GENES AND MEMES: PART II

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0.1 PREFACE

Brief summary of TGD

Towards the end of the year 2023 I became convinced that it would be appropriate to prepare collections about books related to TGD and its applications. The finiteness of human lifetime was my first motivation. My second motivation was the deep conviction that TGD will mean a revolution of the scientific world view and I must do my best to make it easier.

The first collection would relate to the TGD proper and its applications to physics. Second collection would relate to TGD inspired theory of consciousness and the third collection to TGD based quantum biology. The books in these collections would focus on much more precise topics than the earlier books and would be shorter. This would make it much easier for the reader to understand what TGD is, when the time is finally mature for the TGD to be taken seriously. This particular book belongs to a collection of books about TGD proper.

The basic ideas of TGD

TGD can be regarded as a unified theory of fundamental interactions but is not the kind of unified theory as so called GUTs constructed by graduate students in the seventies and eighties using detailed recipes for how to reduce everything to group theory. Nowadays this activity has been completely computerized and it probably takes only a few hours to print out the predictions of this kind of unified theory as an article in the desired format. TGD is something different and I am not ashamed to confess that I have devoted the last 45 years of my life to this enterprise and am still unable to write The Rules.

If I remember correctly, I got the basic idea of Topological Geometrodynamics (TGD) during autumn 1977, perhaps it was October. What I realized was that the representability of physical space-times as 4-dimensional surfaces of some higher-dimensional space-time obtained by replacing the points of Minkowski space with some very small compact internal space could resolve the conceptual difficulties of general relativity related to the definition of the notion of energy. This belief was too optimistic and only with the advent of what I call zero energy ontology the understanding of the notion of Poincare invariance has become satisfactory. This required also the understanding of the relationship to General Relativity.

It soon became clear that the approach leads to a generalization of the notion of space-time with particles being represented by space-time surfaces with finite size so that TGD could be also seen as a generalization of the string model. Much later it became clear that this generalization is consistent with conformal invariance only if space-time is 4-dimensional and the Minkowski space factor of the embedding space is 4-dimensional. During last year it became clear that 4-D Minkowski space and 4-D complex projective space CP_2 are completely unique in the sense that they allow twistor space with Kähler structure.

It took some time to discover that also the geometrization of also gauge interactions and elementary particle quantum numbers could be possible in this framework: it took two years to find the unique internal space (CP_2) providing this geometrization involving also the realization that family replication phenomenon for fermions has a natural topological explanation in TGD framework and that the symmetries of the standard model symmetries are much more profound than pragmatic TOE builders have believed them to be. If TGD is correct, the mainstream particle physics chose the wrong track leading to the recent deep crisis when people decided that quarks and leptons belong to the same multiplet of the gauge group implying instability of the proton.

Instead of trying to describe in detail the path, which led to TGD as it is now with all its side tracks, it is better to summarize the recent view which of course need not be final.

TGD can be said to be a fusion of special and general relativities. The Relativity Principle (Poincare Invariance) of Special Relativity is combined with the General Coordinate Invariance and Equivalence Principle of General Relativity. TGD involves 3 views of physics: physics geometry, physics as number theory and physics as topological physics in some sense.

Physics as geometry

"Geometro-" in TGD refers to the idea about the geometrization of physics. The geometrization program of Einstein is extended to gauge fields allowing realization in terms of the geometry of surfaces so that Einsteinian space-time as abstract Riemann geometry is replaced with sub-manifold geometry. The basic motivation is the loss of classical conservation laws in General Relativity Theory (GRT)(see **Fig. 12**). Also the interpretation as a generalization of string models by replacing string with 3-D surface is natural.

- Standard model symmetries uniquely fix the choice of 8-D space in which space-time surfaces live to $H = M^4 \times CP_2$ [L152]. Also the notion of twistor is geometrized in terms of surface geometry and the existence of twistor lift fixes the choice of H completely so that TGD is unique [L52, L72](see **Fig. 13**). The geometrization applies even to the quantum theory itself and the space of space-time surfaces - "world of classical worlds" (WCW) - becomes the basic object endowed with Kähler geometry (see **Fig. 14**). The mere mathematical existence of WCW geometry requires that it has maximal isometries, which together twistor lift and number theoretic vision fixes it uniquely [L154].

- General Coordinate Invariance (GCI) for space-time surfaces has dramatic implications. A given 3-surface fixes the space-time surface almost completely as analog of Bohr orbit (preferred extremal). This implies holography and leads to zero energy ontology (ZEO) in which quantum states are superpositions of space-time surfaces [K93, L92].

- From the beginning it was clear that the theory predicts the presence of long ranged classical electro-weak and color gauge fields and that these fields necessarily accompany classical electromagnetic fields in all scales. It took about 26 years to gain the maturity to admit the obvious: these fields are classical correlates for long range color and weak interactions assignable to the phases of ordinary matter predicted by the number theoretic vision and behaving like dark matter but identifiable as matter explaining the missing baryon problem whereas the galactic dark matter would correspond to the dark energy assignable monopole flux tubes as deformations of cosmic strings. The only possible conclusion is that TGD physics is a fractal consisting of an entire hierarchy of fractal copies of standard model physics. Also the understanding of electro-weak massivation and screening of weak charges has been a long standing problem and p-adic physics solved this problem in terms of p-adic thermodynamics [K19, K46] [L145].

- One of the most recent discoveries of classical TGD is exact general solution of the field equations. Holography can be realized as a generalized holomorphy realized in terms of what I call Hamilton-Jacobi structure [L149]. Space-time surfaces correspond to holomorphic imbeddings of the space-time surface to H with a generalized complex structure defined by the vanishing of 2 analytic functions of 4 generalized complex coordinates of H. These surfaces are automatically minimal surfaces. This is true for any geneneral coordinate invariant action constructed in terms of the induced geometric structures so that the dynamics is universal. Different actions differ only in the sense that singularities at which the minimal surface property fails depend on the action. This affects the scattering amplitudes, which can be constructed in terms of the data related to the singularities [L158].

- Generalized conformal symmetries define an extension of conformal symmetries and one can assign to them Noether charges. Besides this the so called super-symplectic symmetries associated with $\delta M^4_+ \times CP_2$ define isometries of the "world of classical worlds" (WCW), which by holography is essentially the space of Bohr orbits of 3-surfaces as particles so that quantum TGD is expected to reduce to a generalization of wave mechanics.

Physics as number theory

During these years TGD led to a rather profound generalization of the space-time concept. Quite general properties of the theory led to the notion of many-sheeted space-time with sheets representing physical subsystems of various sizes. At the beginning of 90s I became dimly aware of the

importance of p-adic number fields and soon ended up with the idea that p-adic thermodynamics for a conformally invariant system allows to understand elementary particle massivation with amazingly few input assumptions. The attempts to understand p-adicity from basic principles led gradually to the vision about physics as a generalized number theory as an approach complementary to the physics as an infinite-dimensional spinor geometry of WCW approach. One of its elements was a generalization of the number concept obtained by fusing real numbers and various p-adic numbers along common rationals. The number theoretical trinity involves besides p-adic number fields also quaternions and octonions and the notion of infinite prime.

Adelic physics [L50, L51] fusing real and various p-adic physics is part of the number theoretic vision, which provides a kind of dual description for the description based on space-time geometry and the geometry of "world of classical words". Adelic physics predicts two fractal length scale hierarchies: p-adic length scale hierarchy and the hierarchy of dark length scales labelled by $h_{eff} = nh_0$, where n is the dimension of extension of rational. The interpretation of the latter hierarchy is as phases of ordinary matter behaving like dark matter. Quantum coherence is possible in arbitarily long scales. These two hierarchies are closely related. p-Adic primes correspond to ramified primes for a polynomial, whose roots define the extension of rationals: for a given extension this polynomial is not unique.

$M^8 - H$ duality

The concrete realization of the number theoretic vision is based on $M^8 - H$ duality (see **Fig. 15**). What the precise form is this duality is, has been far from clear but the recent form is the simplest one and corresponds to the original view [L156]. M^8 corresponds to octonions O but with the number theoretic metric defined by $Re(o^2)$ rather than the standard norm and giving Minkowskian signature.

The physics in M^8 can be said to be algebraic whereas in H field equations are partial differential equations. The dark matter hierarchy corresponds to a hierarchy of algebraic extensions of rationals inducing that for adeles and has interpretation as an evolutionary hierarchy (see **Fig. 16**). p-Adic physics is an essential part of number theoretic vision and the space-time surfaces are such that at least their M^8 counterparts exists also in p-adic sense. This requires that the analytic function defining the space-time surfaces are polynomials with rational coefficients.

M^8-H duality relates two complementary visions about physics (see **Fig. 17**), and can be seen as a generalization of the momentum-position duality of wave mechanics, which fails to generalize to quantum field theories (QFTs). M^8-H duality applies to particles which are 3-surfaces instead of point-like particles.

p-Adic physics

The idea about p-adic physics as physics of cognition and intentionality emerged also rather naturally and implies perhaps the most dramatic generalization of the space-time concept in which most points of p-adic space-time sheets are infinite in real sense and the projection to the real imbedding space consists of discrete set of points. One of the most fascinating outcomes was the observation that the entropy based on p-adic norm can be negative. This observation led to the vision that life can be regarded as something in the intersection of real and p-adic worlds. Negentropic entanglement has interpretation as a correlate for various positively colored aspects of conscious experience and means also the possibility of strongly correlated states stable under state function reduction and different from the conventional bound states and perhaps playing key role in the energy metabolism of living matter.

If one requires consistency of Negentropy Mazimization Principle with standard measurement theory, negentropic entanglement defined in terms of number theoretic negentropy is necessarily associated with a density matrix proportional to unit matrix and is maximal and is characterized by the dimension n of the unit matrix. Negentropy is positive and maximal for a p-adic unique prime dividing n.

Hierarchy of Planck constants labelling phases ordinary matter dark matter behaving like dark matter

One of the latest threads in the evolution of ideas is not more than nine years old. Learning about the paper of Laurent Nottale about the possibility to identify planetary orbits as Bohr orbits with a gigantic value of gravitational Planck constant made once again possible to see the obvious. Dynamical quantized Planck constant is strongly suggested by quantum classical correspondence and the fact that space-time sheets identifiable as quantum coherence regions can have arbitrarily large sizes. Second motivation for the hierarchy of Planck constants comes from bio-electromagnetism suggesting that in living systems Planck constant could have large values making macroscopic quantum coherence possible. The interpretation of dark matter as a hierarchy of phases of ordinary matter characterized by the value of Planck constant is very natural.

During summer 2010 several new insights about the mathematical structure and interpretation of TGD emerged. One of these insights was the realization that the postulated hierarchy of Planck constants might follow from the basic structure of quantum TGD. The point is that due to the extreme non-linearity of the classical action principle the correspondence between canonical momentum densities and time derivatives of the imbedding space coordinates is one-to-many and the natural description of the situation is in terms of local singular covering spaces of the imbedding space. One could speak about effective value of Planck constant $h_{eff} = n \times h$ coming as a multiple of minimal value of Planck constant. Quite recently it became clear that the non-determinism of Kähler action is indeed the fundamental justification for the hierarchy: the integer n can be also interpreted as the integer characterizing the dimension of unit matrix characterizing negentropic entanglement made possible by the many-sheeted character of the space-time surface.

Due to conformal invariance acting as gauge symmetry the n degenerate space-time sheets must be replaced with conformal equivalence classes of space-time sheets and conformal transformations correspond to quantum critical deformations leaving the ends of space-time surfaces invariant. Conformal invariance would be broken: only the sub-algebra for which conformal weights are divisible by n act as gauge symmetries. Thus deep connections between conformal invariance related to quantum criticality, hierarchy of Planck constants, negentropic entanglement, effective p-adic topology, and non-determinism of Kähler action perhaps reflecting p-adic non-determinism emerges.

The implications of the hierarchy of Planck constants are extremely far reaching so that the significance of the reduction of this hierarchy to the basic mathematical structure distinguishing between TGD and competing theories cannot be under-estimated.

TGD as an analog of topological QFT

Consider next the attribute "Topological". In condensed matter physical topological physics has become a standard topic. Typically one has fields having values in compact spaces, which are topologically non-trivial. In the TGD framework space-time topology itself is non-trivial as also the topology of $H = M^4 \times CP_2$. Since induced metric is involved with TGD, it is too much to say that TGD is topological QFT but one can for instance say, that space-time surfaces as preferred extremals define representatives for 4-D homological equivalence classes.

The space-time as 4-surface $X^4 \subset H$ has a non-trivial topology in all scales and this together with the notion of many-sheeted space-time brings in something completely new. Topologically trivial Einsteinian space-time emerges only at the QFT limit in which all information about topology is lost (see **Fig. 18**).

Any GCI action satisfying holography=holomorphy principle has the same universal basic extremals: CP_2 type extremals serving basic building bricks of elementary particles, cosmic strings and their thickenings to flux tubes defining a fractal hierarchy of structure extending from CP_2 scale to cosmic scales, and massless extremals (MEs) define space-time correletes for massless particles. World as a set or particles is replaced with a network having particles as nodes and flux tubes as bonds between them serving as correlates of quantum entanglement.

"Topological" could refer also to p-adic number fields obeying p-adic local topology differing radically from the real topology (see **Fig. 19**).

Zero energy ontology

TGD inspired theory of consciousness entered the scheme after 1995 as I started to write a book about consciousness. Gradually it became difficult to say where physics ends and consciousness theory begins since consciousness theory could be seen as a generalization of quantum measurement theory by identifying quantum jump as a moment of consciousness and by replacing the observer with the notion of self identified as a system which is conscious as long as it can avoid entanglement with environment. The somewhat cryptic statement "Everything is conscious and consciousness can be only lost" summarizes the basic philosophy neatly.

General coordinate invariance leads to the identification of space-time surfaces are analogous to Bohr orbits inside causal diamond (CD). CD obtained as intersection of future and past directed light-cones (with CP_2 factor included). By the already described hologamphy, 3-dimensional data replaces the boundary conditions at single 3-surface involving also normal derivatives with conditions involving no derivates.

In zero energy ontology (ZEO), the superpositions of space-time surfaces inside causal diamond (CD) having their ends at the opposite light-like boundaries of CD, define quantum states. CDs form a scale hierarchy (see **Fig. 20** and **Fig. 21**). Quantum states are modes of WCW spinor fields, essentially wave functions in the space WCW consisting of Bohr orbit-like 4-surfaces.

Quantum jumps occur between these and the basic problem of standard quantum measurement theory disappears. Ordinary state function reductions (SFRs) correspond to "big" SFRs (BSFRs) in which the arrow of time changes (see **Fig. 13.5**). This has profound thermodynamic implications and the question about the scale in which the transition from classical to quantum takes place becomes obsolete. BSFRs can occur in all scales but from the point of view of an observer with an opposite arrow of time they look like smooth time evolutions.

In "small" SFRs (SSFRs) as counterparts of "weak measurements" the arrow of time does not change and the passive boundary of CD and states at it remain unchanged (Zeno effect).

Equivalence Principle in TGD framework

There have been also longstanding problems related to the relationship between inertial mass and gravitational mass, whose identification has been far from obvious.

- Gravitational energy is well-defined in cosmological models but is not conserved. Hence the conservation of the inertial energy does not seem to be consistent with the Equivalence Principle. In this framework the quantum numbers are assigned with zero energy states located at the boundaries of CDs defined as intersections of future and past directed light-cones. The notion of energy-momentum becomes length scale dependent since one has a scale hierarchy for causal diamonds. This allows to understand the non-conservation of energy as apparent.

  Equivalence Principle in the form expressed by Einstein's equations follows from Poincare invariance once it is realized that GRT space-time is obtained from the many-sheeted space-time of TGD by lumping together the space-time sheets to a regionof Minkowski space and endowing it with an effective metric given as a sum of Minkowski metric and deviations of the metrices of space-time sheets from Minkowski metric. Similar description relates classical gauge potentials identified as components of induced spinor connection to Yang-Mills gauge potentials in GRT space-time. Various topological inhomogenities below resolution scale identified as particles are described using energy momentum tensor and gauge currents.

  At quantum level, the Equivalence Principle has a surprisingly strong content. In linear Minkowski coordinates, space-time projection of the M^4 spinor connection representing gravitational gauge potentials the coupling to induced spinor fields vanishes. Also the modified Dirac action for the solutions of the modified Dirac equation seems to vanish identically and in TGD perturbative approach separating interaction terms is not possible.

  The modified Dirac equation however fails at the singularities of the minimal surface representing space-time surface and Dirac action reduces to an integral over singularities for the trace of the second fundamental form slashed between the induced spinor field and its conjugate. Also the M^4 part of the trace is non-vanishing and gives rise to the gravitational coupling. The trace gives both standard model vertices and graviton emission vertices. One

could say that at the quantum level gravitational and gauge interactions are eliminated everywhere except at the singularities identifiable as defects of the ordinary smooth structure. The exotic smooth structures [L138], possible only in dimension 4, are ordinary smooth structures apart from these defects serving as vertex representing a creation of a fermion-antifermion pair in the induced gauge potentials. The vertex is universal and essentially the trace of the second fundamental form as an analog of the Higgs field and the gravitational constant is proportional to the square of CP_2 radius.

- There is a delicate difference between inertial and gravitational masses. One can assume that the modes of the imbedding space spinor fields are solutions of massles Dirac equation in either $M^4 \times CP_2$ and therefore eigenstates of inertial momentum or in $CD = cd \times CP_2$: in this case they are only mass eigenstates. The mass spectra are identical for these options. Inertial momenta correspond naturally to the Poincare charges in the space of CDs. For the CD option the spinor modes correspond to mass squared eigenstates for which the mode for H^3 with a given value of light-proper time is a unitary irreducible $SO(1,3)$ representation rather than a representation of translation group. These two eigenmode basis correspond to gravitational basis for spinor modes.

Quantum TGD as a generalization of Einstein's geometrization program

I started the serious attempts to construct quantum TGD after my thesis around 1982. The original optimistic hope was that path integral formalism or canonical quantization might be enough to construct the quantum theory but it turned that this approach fails due to the extreme non-linearity of the theory.

It took some years to discover that the only working approach is based on the generalization of Einstein's program. Quantum physics involves the geometrization of the infinite-dimensional "world of classical worlds" (WCW) identified as the space of 3-dimensional surfaces. Later 3-surfaces where replaced with 4-surfaces satifying holography and therefore as analogs of Bohr orbits.

- If one assumes Bohr orbitology, then strong correlations between the 3-surfaces at the ends of CD follow and mean holography. It is natural to identify the quantum states of the Universe (and sub-Univeverses) as modes of a formally classical spinor field in WCW. WCW gamma matrices are expressible in terms of oscillator operators of free second quantized spinor fields of H. The induced spinor fields identified projections of H spinor fields to the space-time surfaces satisfy modified Dirac equation for the modified Dirac equation. Only quantum jump remains the genuinely quantal aspect of quantum physics.

- Quantum TGD can be seen as a theory for free spinor fields in WCW having maximal isometries and the generalization of the Super Virasoro conditions gives rise to the analog massless Dirac equation at the level of WCW.

The world of classical worlds and its symmetries

The notion of "World of Classical Worlds" (WCW) emerged around 1985 but found its basic form around 1990. Holography forced by the realization of General Coordinate Invariance forced/allowed to give up the attempts to make sense of the path integral.

A more concrete way to express this view is that WCW does not consist of 3-surfaces as particle-like entities but almost deterministic Bohr orbits assignable to them as preferred extremals of Kähler action so that quantum TGD becomes wave mechanics in WCW combined with Bohr orbitology. This view has profound implications, which can be formulated in terms of zero energy ontology (ZEO), solving among other things the basic paradox of quantum measurement theory. ZEO forms also the backbone of TGD inspired theory of consciousness and quantum biology.

WCW geometry exists only if it has maximal isometries: this statement is a generalization of the discovery of Freed for loop space geometries [A26]. I have proposed [K43, K20, K91, K72, L154] that WCW could be regarded as a union of generalized symmetric spaces labelled by zero modes which do not contribute to the metric. The induced Kähler field is invariant under symplectic transformations of CP_2 and would therefore define zero mode degrees of freedom if one assumes

that WCW metric has symplectic transformations as isometries. In particular, Kähler magnetic fluxes would define zero modes and are quantized closed 2-surfaces. The induced metric appearing in Kähler action is however not zero mode degree of freedom. If the action contains volume term, the assumption about union of symmetric spaces is not well-motivated.

Symplectic transformations are not the only candidates for the isometries of WCW. The basic picture about what these maximal isometries could be, is partially inspired by string models.

- A weaker proposal is that the symplectomorphisms of H define only symplectomorphisms of WCW. Extended conformal symmetries define also a candidate for isometry group. Remarkably, light-like boundary has an infinite-dimensional group of isometries which are in 1-1 correspondence with conformal symmetries of $S^2 \subset S^2 \times R_+ = \delta M^4_+$.

- Extended Kac Moody symmetries induced by isometries of δM^4_+ are also natural candidates for isometries. The motivation for the proposal comes from physical intuition deriving from string models. Note they do not include Poincare symmetries, which act naturally as isometries in the moduli space of causal diamonds (CDs) forming the "spine" of WCW.

- The light-like orbits of partonic 2-surfaces might allow separate symmetry algebras. One must however notice that there is exchange of charges between interior degrees of freedom and partonic 2-surfaces. The essential point is that one can assign to these surface conserved charges when the dual light-like coordinate defines time coordinate. This picture also assumes a slicing of space-time surface by by the partonic orbits for which partonic orbits associated with wormrhole throats and boundaries of the space-time surface would be special. This slicing would correspond to Hamilton-Jacobi structure.

- Fractal hierarchy of symmetry algebras with conformal weights, which are non-negative integer multiples of fundamental conformal weights, is essential and distinguishes TGD from string models. Gauge conditions are true only the isomorphic subalgebra and its commutator with the entire algebra and the maximal gauge symmetry to a dynamical symmetry with generators having conformal weights below maximal value. This view also conforms with p-adic mass calculations.

- The realization of the symmetries for 3-surfaces at the boundaries of CD and for light-like orbits of partonic 2-surfaces is known. The problem is how to extend the symmetries to the interior of the space-time surface. It is natural to expect that the symmetries at partonic orbits and light-cone boundary extend to the same symmetries.

After the developments towards the end of 2023, it seems that the extension of conformal and Kac-Moody symmetries of string models to the TGD framework is understood. What about symplectic symmetries, which were originally proposed as isometries of WCW? In this article this question is discussed in detail and it will be found that these symmetries act naturally on 3-D holographic data and one can identify conserved charges. By holography this is in principle enough and might imply that the actions of holomorphic and symplectic symmetry algebras are dual. Holography=holomorphy hypothesis is discussed also in the case of the modified Dirac equation.

About the construction of scattering amplitudes

From the point of view of particle physics the ultimate goal is of course a practical construction recipe for the S-matrix of the theory. I have myself regarded this dream as quite too ambitious taking into account how far-reaching re-structuring and generalization of the basic mathematical structure of quantum physics is required. After having made several guesses for what the counterpart of S-matrix could be, it became clear that the dream about explicit formulas is unrealistic before one has understood what happens in quantum jump.

- In ZEO [K93, L92] one must distinguish between "small" state function reductions (SSFRs) and "big" SFRs (BSFRs). BSFR is the TGD counterpart of the ordinary SFRs and the arrow of the geometric time changes in it. SSFR follows the counterpart of a unitary time evolution and the arrow of the geometric time is preserved in SSFR. The sequence of SSFRs

is the TGD counterpart for the sequence of repeated quantum measurements of the same observables in which nothing happens to the state. In TGD something happens in SSFRs and this gives rise to the flow of consciousness. When the set of the observables measured in SSFR does not commute with the previous set of measured observables, BSFR occurs.

The evolution by SSFRs means that also the causal diamond changes. At quantum level one has a wave function in the finite-dimensional moduli space of CDs which can be said to form a spine of WCW [L151]. CDs form a scale hierarchy. SSFRs are preceded by a dispersion in the moduli space of CDs and SSFR means localization in this space.

- There are several S-matrix like entities. One can assign an analog of the S-matrix to each analog of unitary time evolution preceding a given SSFR. One can also assign an analog S-matrix between the eigenstate basis of the previous set of observables and the eigenstate basis of new observers: this S-matrix characterizes BSFR. One can also assign to zero energy states an S-matrix like entity between the states assignable to the two boundaries of CD. These S-matrix like objects can be interpreted as a complex square root of the density matrix representable as a diagonal and positive square root of density matrix and unitary S-matrix so that quantum theory in ZEO can be said to define a square root of thermodynamics at least formally.

In standard QFTs Feynman diagrams provide the description of scattering amplitudes. The beauty of Feynman diagrams is that they realize unitarity automatically via the so-called Cutkosky rules. In contrast to Feynman's original beliefs, Feynman diagrams and virtual particles are taken only as a convenient mathematical tool in quantum field theories. The QFT approach is however plagued by UV and IR divergences and one must keep mind open for the possibility that a genuine progress might mean opening of the black box of the virtual particle.

In the TGD framework this generalization of Feynman diagrams indeed emerges unavoidably.

- The counterparts of elementary particles can be identified as closed monopole flux tubes connecting two parallel Minkowskian space-time sheets and have effective ends which are Euclidean wormhole contacts. The 3-D light-like boundaries of wormhole contacts as orbits of partonic 2-surfaces.

  The intuitive picture is that the 3-D light-like partonic orbits replace the lines of Feynman diagrams and vertices are replaced by 2-D partonic 2-surfaces. A stronger condition is that fermion number is carried by light-like fermion lines at the partonic orbits, which can be identified as boundaries string world sheets.

- The localization of the nodes of induced spinor fields to 2-D string world sheets (and possibly also to partonic 2-surfaces) implies a stringy formulation of the theory analogous to stringy variant of twistor formalism with string world sheets having interpretation as 2-braids. In the TGD framework, the fermionic variant of twistor Grassmann formalism combined with the number theoretic vision [L133, L134] led to a stringy variant of the twistor diagrammatics.

- Fundamental fermions are off-mass-shell in the sense that their momentum components are real algebraic integers in an extension of rationals associated with the space-time surfaces inside CD with a momentum unit determined by the CD size scale. Galois confinement states that the momentum components are integer valued for the physical states.

- The twistorial approach suggests also the generalization of the Yangian symmetry to infinite-dimensional super-conformal algebras, which would determine the vertices and scattering amplitudes in terms of poly-local symmetries.

The twistorial approach is however extremely abstract and lacks a concrete physical interpretation. The holography=holomorphy vision led to a breakthough in the construction of the scattering amplitudes by solving the problem of identifying interaction vertices [L158].

1. The basic prediction is that space-time surfaces as analogs of Bohr orbits are holomorphic in a generalized sense and are therefore minimal surfaces. The minimal surface property fails at lower-dimensional singularities and the trace of the second fundamental form (SFF) analogous to acceleration associated with the Bohr orbit of the particle as 3-surface has a delta function like singularity but vanishes elsewhere.

2. The minimal surface property expressess masslessness for both fields and particles as 3-surfaces. At singularities masslessness property fails and singularities can be said to serve as sources which also in QFT define scattering amplitudes.

3. The singularities are analogs of poles and cuts for the 4-D generalization of the ordinary holomorphic functions. Also for the ordinary holomorphic functions the Laplace equation as analog massless field equation and expressing analyticity fails. Complex analysis generalizes to dimension 4.

4. The conditions at the singularity give a generalization of Newton's "F=ma"! I ended up where I started more than 50 years ago!

5. In dimension 4, and only there, there is an infinite number of exotic diff structures [**?**], which differ from ordinary ones at singularities of measure zero analogous to defects. These defects correspond naturally to the singularities of minimal surfaces. One can say that for the exotic diff structure there is no singularity.

6. Group theoretically the trace of the SFF can be regarded as a generalization of the Higgs field, which is non-vanishing only at the vertices and this is enough. Singularities take the role of generalized particle vertices and determine the scattering amplitudes. The second fundamental form contracted with the embedding space gamma matrices and slashed between the second quantized induced spinor field and its conjugate gives the universal vertex involving only fermions (bosons are bound states of fermions in TGD). It contains both gauge and gravitational contributions to the scattering amplitudes and there is a complete symmetry between gravitational and gauge interactions. Gravitational couplings come out correctly as the radius squared of CP_2 as also in the classical picture.

7. The study of the modified Dirac equation leads to the conclusion that vertices as singularities and defects contain the standard electroweak gauge contribution coming from the induced spinor connection and a contribution from the M^4 spinor connection. M^4 part of the generalized Higgs can give rise to a graviton as an $L = 1$ rotational state of the flux tube representing the graviton. It is not clear whether M^4 Kähler gauge potential can give rise to a spin 1 particle. The vielbein part of M^4 spinor connection is pure gauge and could give rise to gravitational topological field theory.

Figures

Basic ideas of TGD inspired quantum biology

The following list gives the basic elements of TGD inspired quantum biology.

- Many-sheeted space-time allows the interpretation of the structures of macroscopic world around us in terms of space-time topology. Magnetic/field body acts as intentional agent using biological body as a sensory receptor and motor instrument and controlling biological body and inheriting its hierarchical fractal structure. Fractal hierarchy of EEGs and its variants can be seen as communication and control tools of magnetic body. Also collective levels of consciousness have a natural interpretation in terms of magnetic body. Magnetic body makes also possible entanglement in macroscopic length scales. The braiding of magnetic flux tubes makes possible topological quantum computations and provides a universal mechanism of memory. One can also undersand the real function of various information molecules and corresponding receptors by interpreting the receptors as addresses in quantum computer memory and information molecules as ends of flux tubes which attach to these receptors to form a connection in quantum web.

  Note that also the notion of electric body makes sense [L148]. Quite generally, long range classical gravitational, electric and magnetic fields give rise to very large values of effective Planckl constants. The Nottale's hypothesis of gravitational Planck constant generalizes to electric interactions.

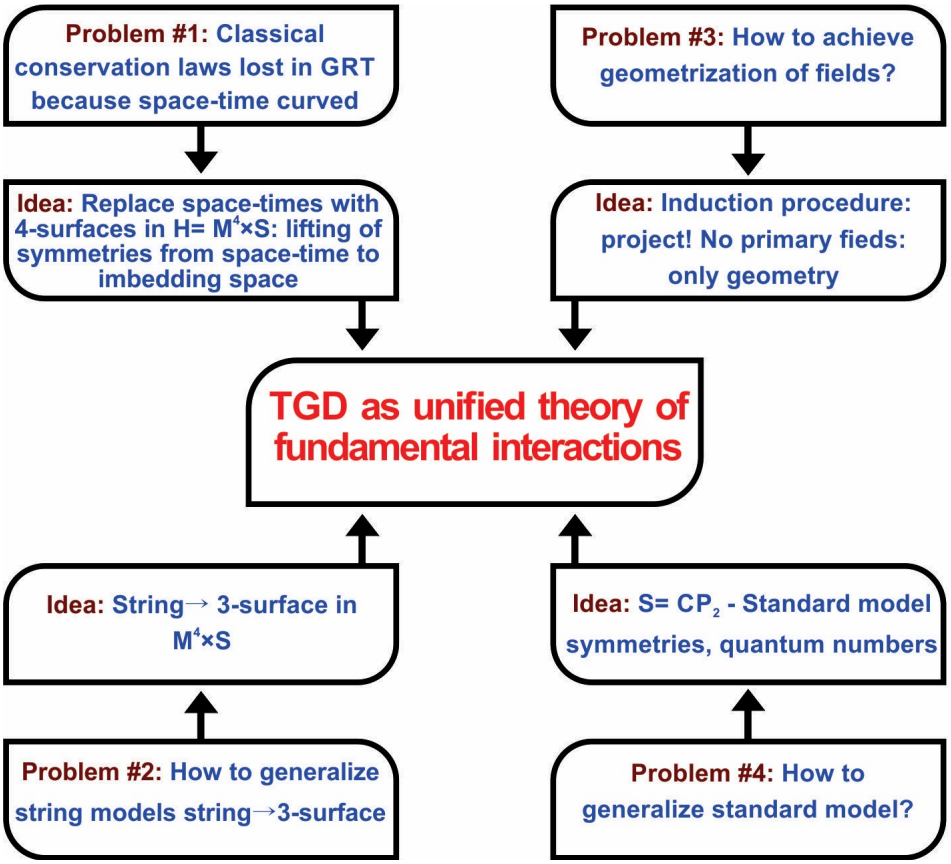


Figure 1: The problems leading to TGD as their solution.

- Magnetic body carrying dark matter and forming an onion-like structure with layers characterized by large values of Planck constant is the key concept of TGD inspired view about Quantum Mind to biology.. Magnetic body is identified as intentional agent using biological body as sensory receptor and motor instrument. EEG and its fractal variants are identified as a communication and control tool of the magnetic body and a fractal hierarchy of analogs of EEG is predicted. Living system is identified as a kind of Indra's net with biomolecules representing the nodes of the net and magnetic flux tubes connections between then.

  The reconnection of magnetic flux tubes and phase transitions changing Planck constant and therefore the lengths of the magnetic flux tubes are identified as basic mechanisms behind DNA replication and analogous processes and also behind the phase transitions associated with the gel phase in cell interior. The braiding of magnetic flux makes possible universal memory representation recording the motions of the basic units connected by flux tubes. Braiding also defines topological quantum computer programs updated continually by the flows of the basic units. The model of DNA as topological quantum computer is discussed as an application. In zero energy ontology the braiding actually generalize to 2-braiding for string world sheets in 4-D space-time and brings in new elements.

- Zero energy ontology (ZEO) makes possible the proposed p-adic description of intentions and cognitions and their transformations to action. Time mirror mechanism based on sending of negative energy signal to geometric past would apply to both long term memory recall, remote metabolism, and realization of intentional acting as an activity beginning in the geometric past in accordance with the findings of Libet. ZEO gives a precise content to the notion of negative energy signal in terms of zero energy state for which the arrow of geometric time is opposite to the standard one.

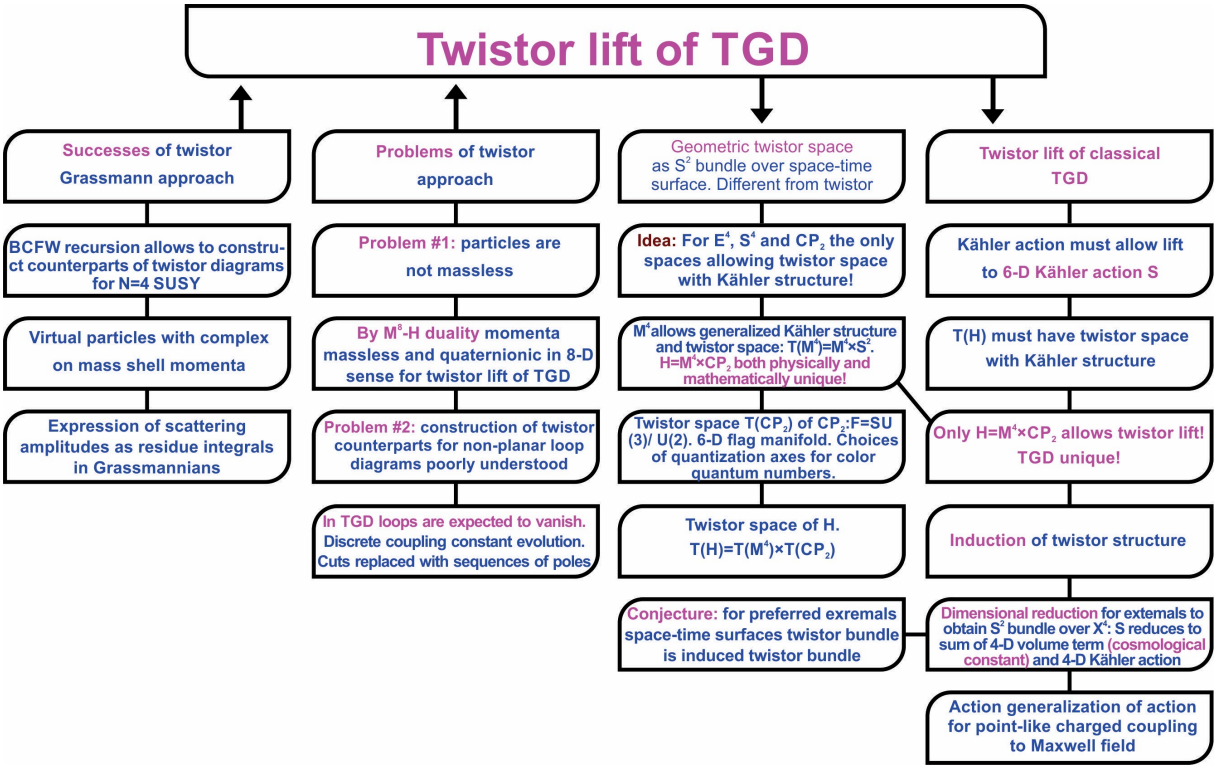


Figure 2: Twistor lift

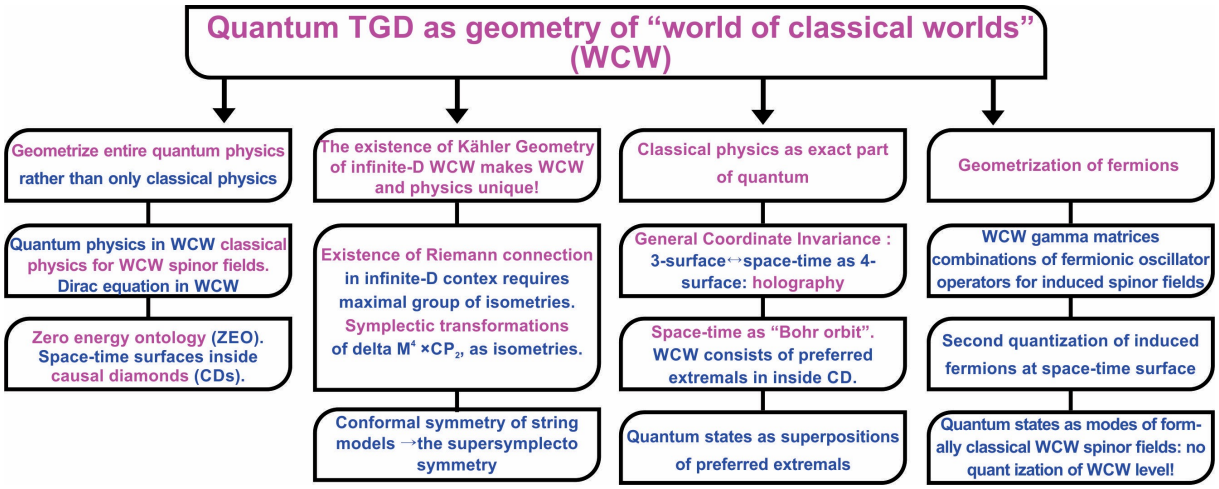


Figure 3: Geometrization of quantum physics in terms of WCW

The associated notion of causal diamond (CD) is essential element and assigns to elementary particles new fundamental time scales which are macroscopic: for electron the time scale is .1 seconds, the fundamental biorhythm. An essentially new element is time-like entanglement which allows to understand among other things the quantum counterparts of Boolean functions in terms of time-like entanglement in fermionic degrees of freedom.

- The assignment of dark matter with a hierarchy of Planck constants gives rise to a hierarchy of macroscopic quantum phases making possible macroscopic and macrotemporal quantum coherence and allowing to understand evolution as a gradual increase of Planck constant. The model for dark nucleons leads to a surprising conclusion: the states of nucleons correspond to DNA, RNA, tRNA, and amino-acids in a natural manner and vertebrate genetic code as correspondence between DNA and amino-acids emerges naturally. This suggests that genetic code is realized at the level of dark hadron physics and living matter in the usual sense provides a secondary representation for it. The hierarchy of Planck constants emerges from basic TGD under rather general assumptions.

- p-Adic physics can be identified as physics of cognition and intentionality. Negentropic entanglement possible for number theoretic entanglement entropy makes sense for rational (and even algebraic) entanglement and leads to the identification of life as something residing in the intersection of real and p-adic worlds. NMP respects negentropic entanglement and the attractive idea is that the experience of understanding and positively colored emotions relate to negentropic entanglement.

- Living matter as conscious hologram is one of the basic ideas of TGD inspired biology and consciousness theory. The basic objection against TGD is that the interference of classical

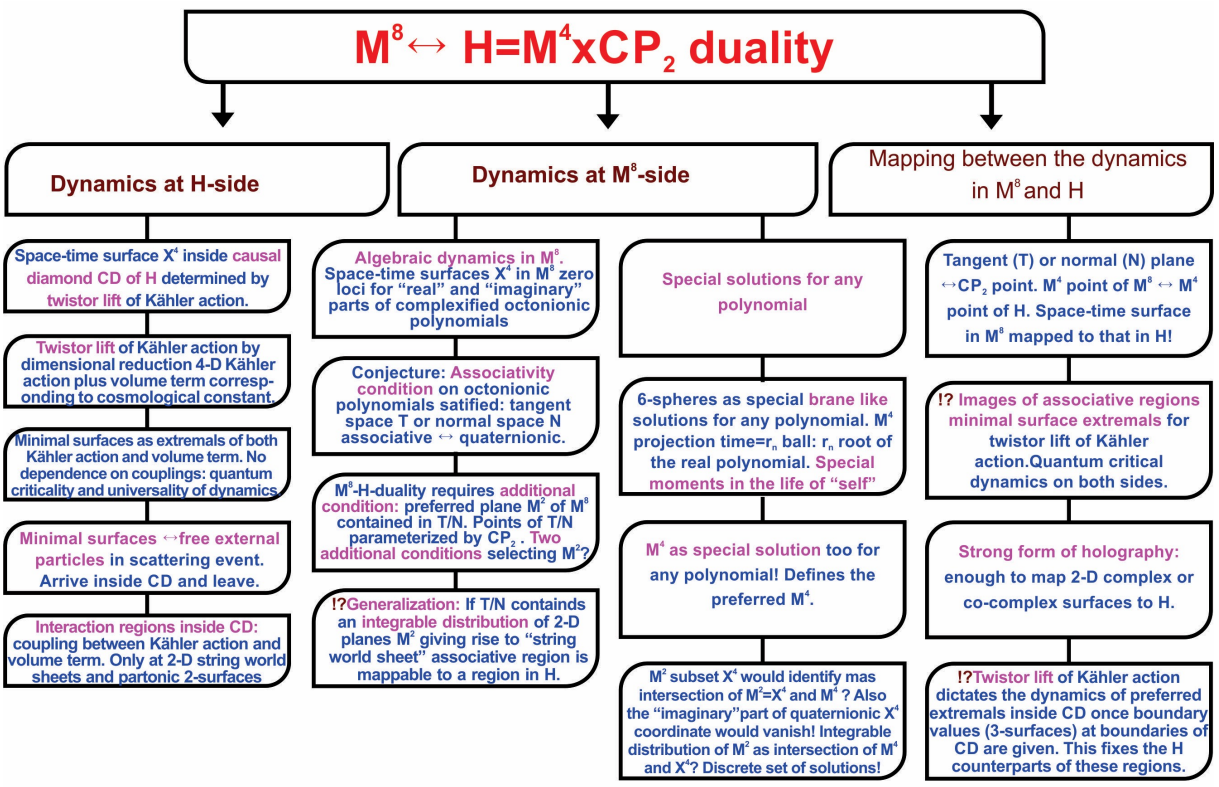


Figure 4: $M^8 - H$ duality

fields is impossible in the standard sense for the reason that that classical fields are not primary dynamical variables in TGD Universe. The resolution is based on the observation that only the interference of the effects caused by these fields can be observed experimentally and that many-sheeted space-time allows to realized the summation of effects in terms of multiple topological condensations of particles to several parallel space-time sheets. One concrete implication is fractality of qualia. Qualia appear in very wide range of scales: our qualia could in fact be those of magnetic body. The proposed mechanism for the generation of qualia realizes the fractality idea.

Various anomalies of living matter have been in vital role in the development of not only TGD view about living matter but also TGD itself.

- TGD approach to living matter was strongly motivated by the findings about the strange behavior of cell membrane and of cellular water, and gel behavior of cytoplasm. Also the findings about effects of ELF em fields on vertebrate brain were decisive and led to the proposal of the hierarchy of Planck constants found later to emerge naturally from the non-determinism of Kähler action. Rather satisfactorily, the other manner to introduce the hierarchy of Planck constants is in terms of gravitational Planck constant: at least in microscopic scales the equivalence of these approaches makes sense and leads to highly non-trivial predictions. The basic testable prediction is that dark photons have cyclotron frequencies inversely proportional to their masses but universal energy spectrum in visible and UV range which corresponds to the transition energies for biomolecules so that they are ideal for biocontrol at the level of both magnetic bodies and at the level of biochemistry.

- Water is in key role in living matter and also in TGD inspired view about living matter. The

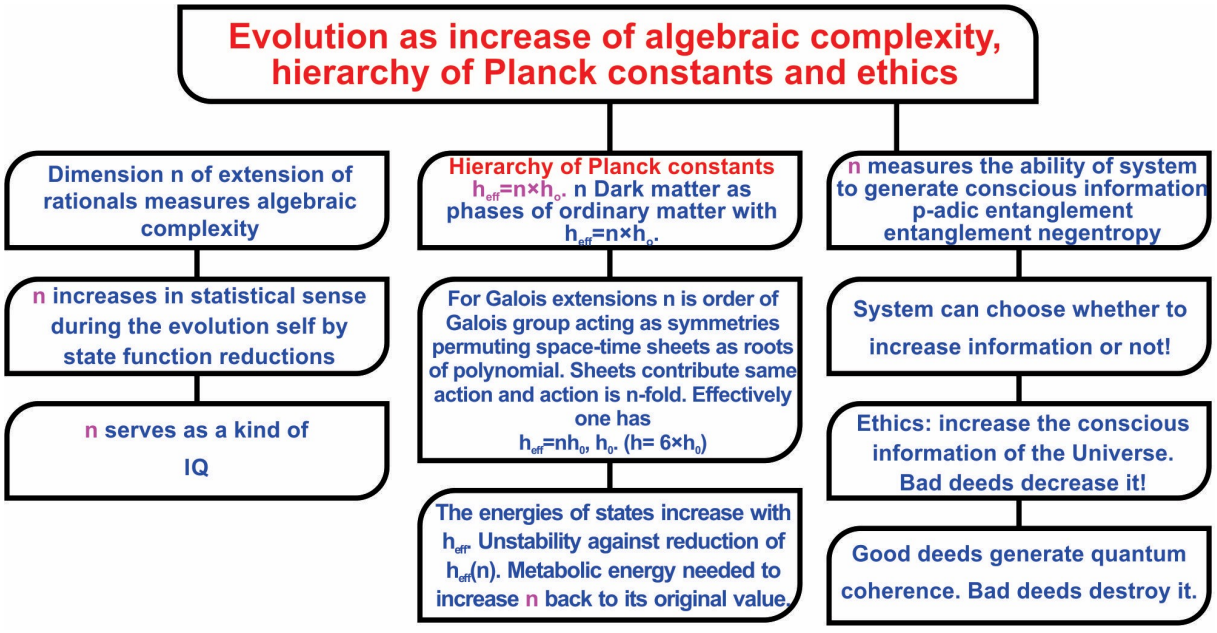


Figure 5: Number theoretic view of evolution

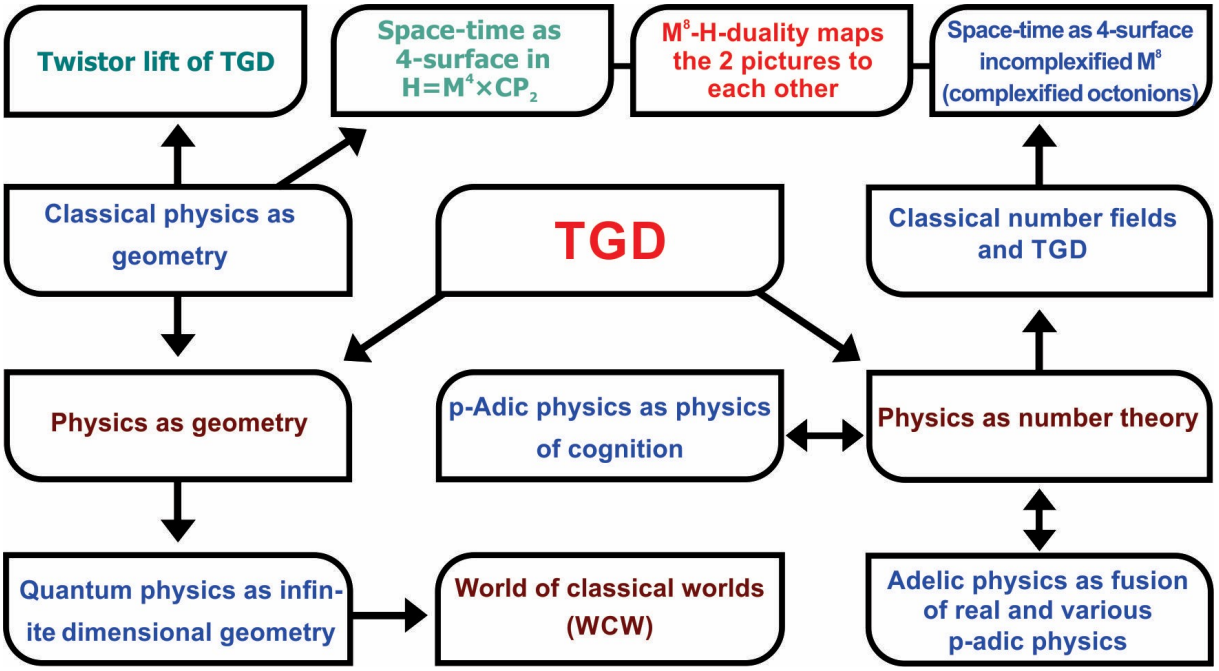


Figure 6: TGD is based on two complementary visions: physics as geometry and physics as number theory.

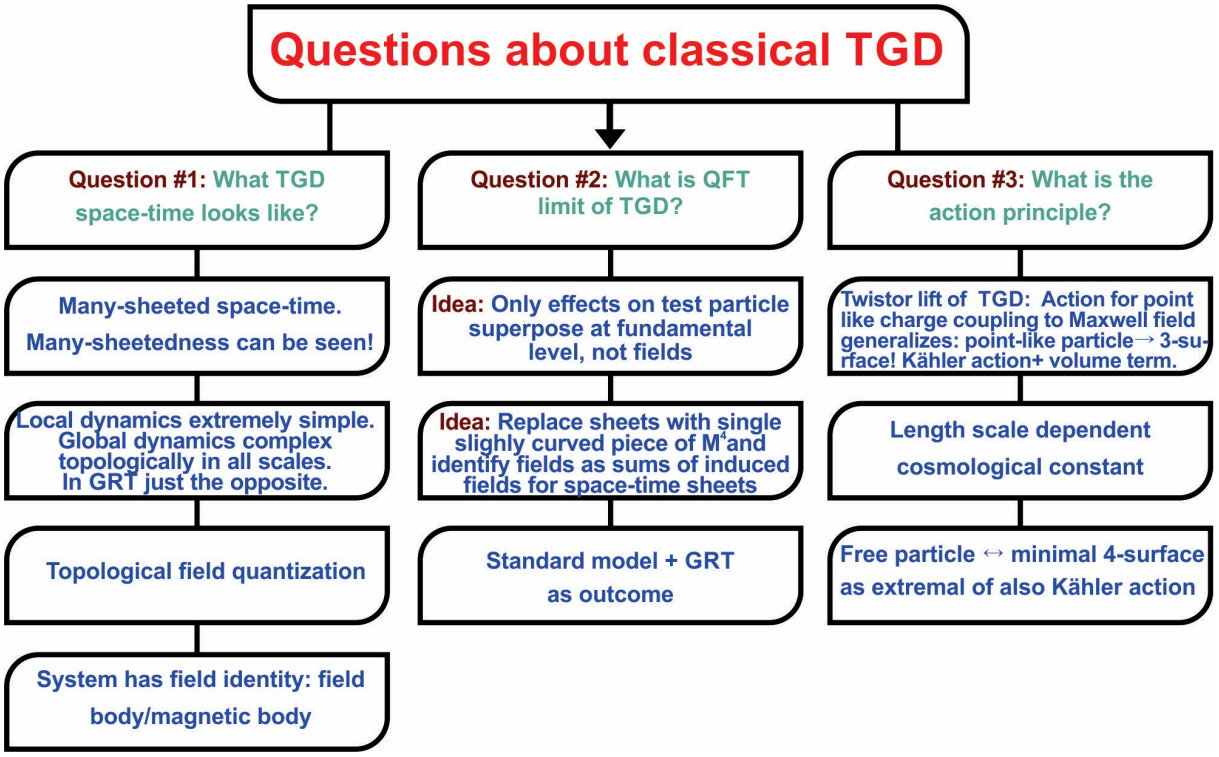


Figure 7: Questions about classical TGD.

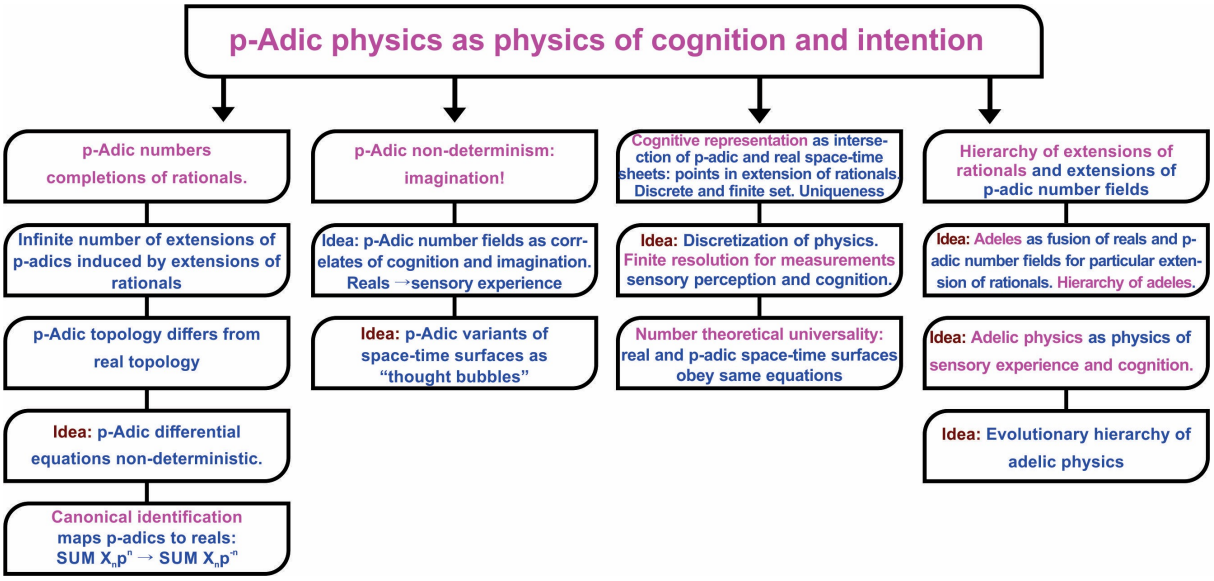


Figure 8: p-Adic physics as physics of cognition and imagination.

anomalies of water lead to a model for dark nuclei as dark proton strings with the surprising prediction that DNA, RNA, aninoacids and even tRNA are in one-one correspondence with the resulting 3-quark states and that vertebrate genetic code emerges naturally. This leads to a vision about water as primordial lifeform still playing a vital role in living organisms. The model of water memory and homeopathy in turn generalizes to a vision about how immune system might have evolved.

- Metabolic energy is necessary for conscious information processing in living matter. This suggests that metabolism should be basically tranfer of negentropic entanglement from nutrients to the organism. ATP could be seen as a molecule of consciousness in this picture and high energy phosphate bond would make possible the transfer of negentropy.

- Pollack effect and its generalizations are in a central role in the TGD inspire quantum biology. In the Pollack effect, the feed of energy allows to increase the value of effective Planck constant so that an ordinary charged particle transforms to its dark variant, being kicked to, say, the gravitational magnetic body of the system itself or some other system such as the Earth or Sun. Charge separation takes place between ordinary biomatter and its magnetic body. Dissipation is extremely small at the magnetic /field body so that Pollack effect makes it possible to realize various biological functions at the magnetic/field body. Photons, in particular solar photons, can provide the energy needed to increase the value of h_{eff} but there are many other possibilities. For instance, the formation of molecular bound states of atoms liberates energy which can be used in the Pollack effect and this process could generate dark matter at the magnetic and more general field bodies.

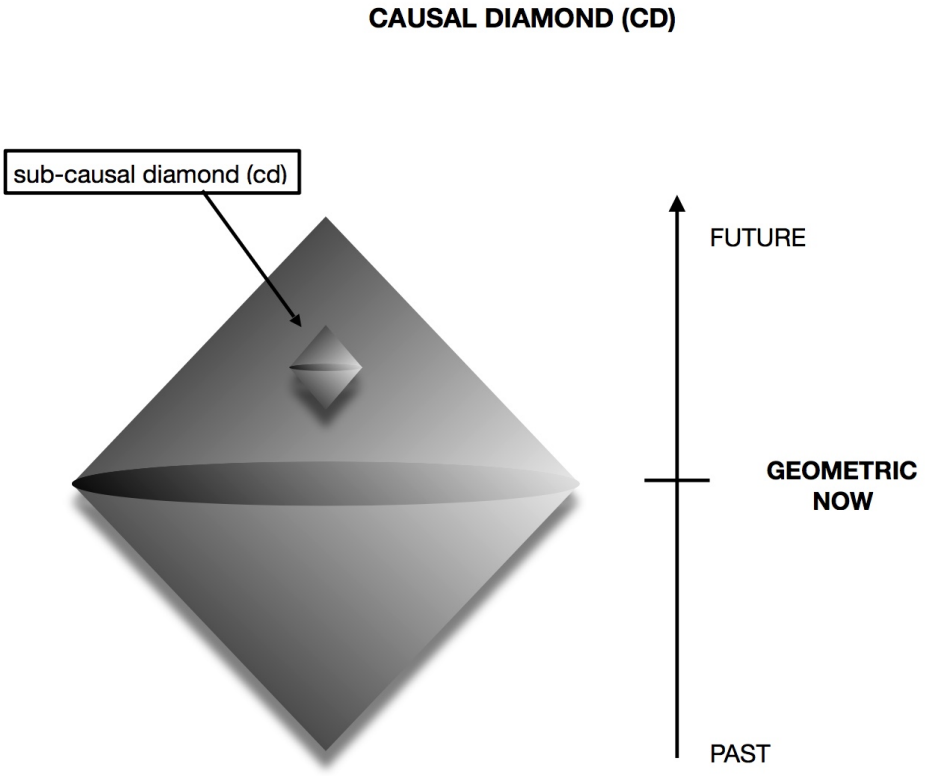


Figure 9: Causal diamond

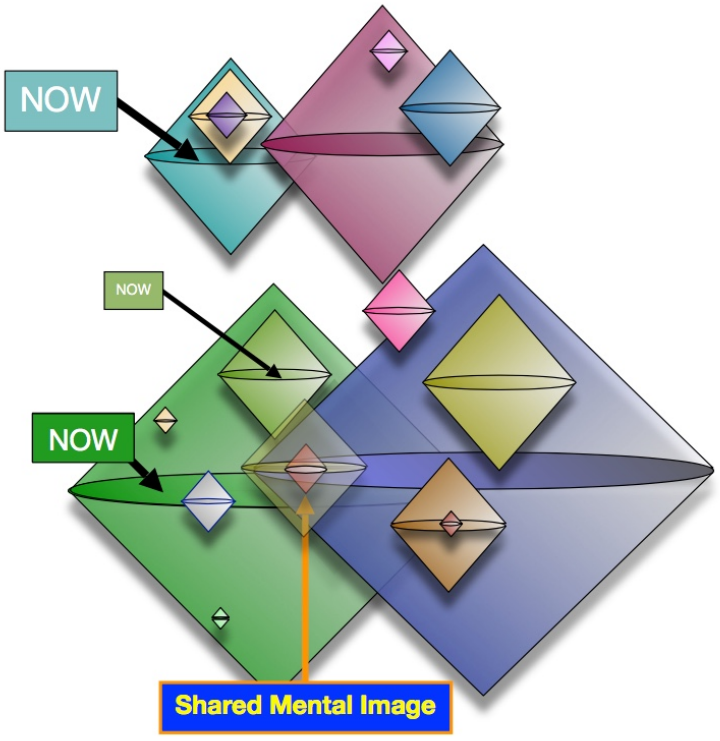


Figure 10: CDs define a fractal "conscious atlas"

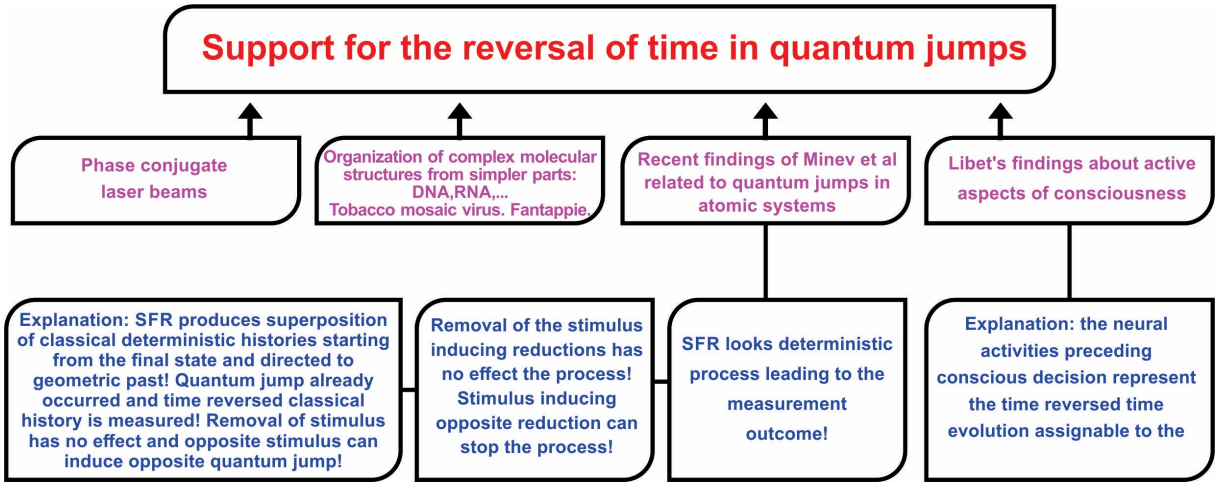


Figure 11: Time reversal occurs in BSFR

Figures

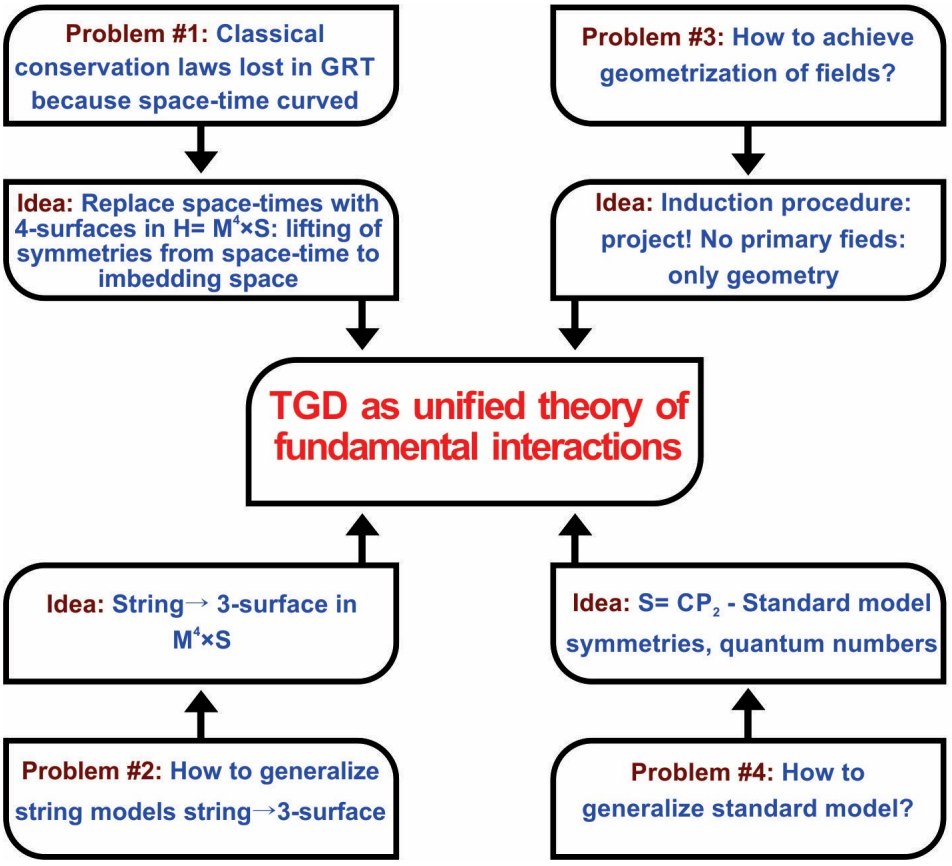


Figure 12: The problems leading to TGD as their solution.

What I have said above is strongly biased view about the recent situation in quantum TGD. This vision is single man's view and doomed to contain unrealistic elements as I know from experience. My dream is that young critical readers could take this vision seriously enough to try to demonstrate that some of its basic premises are wrong or to develop an alternative based on these or better premises. I must be however honest and tell that 45 years of TGD is a really vast bundle of thoughts and quite a challenge for anyone who is not able to cheat himself by taking the attitude of a blind believer or a light-hearted debunker trusting on the power of easy rhetoric tricks.

Karkkila, April 22, 2024, Finland

Matti Pitkänen

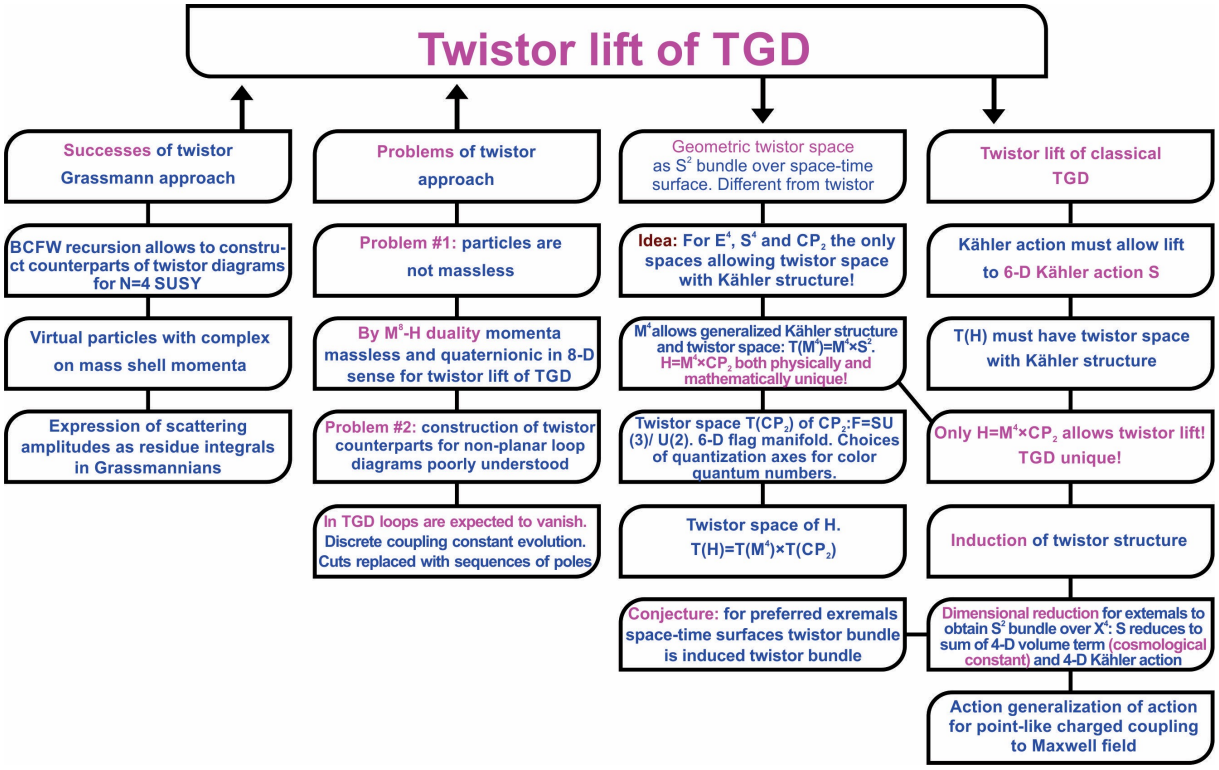


Figure 13: Twistor lift

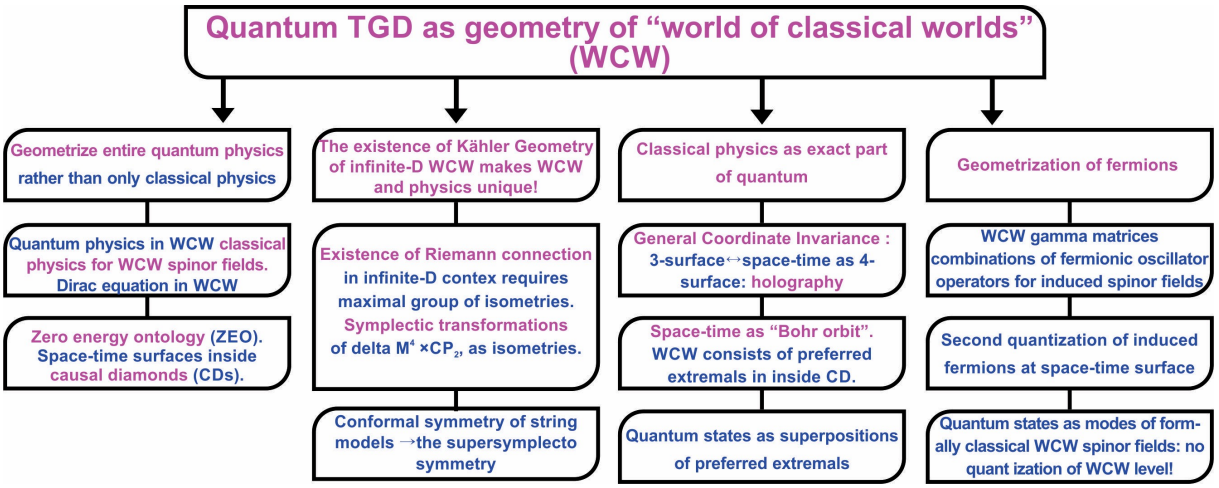


Figure 14: Geometrization of quantum physics in terms of WCW

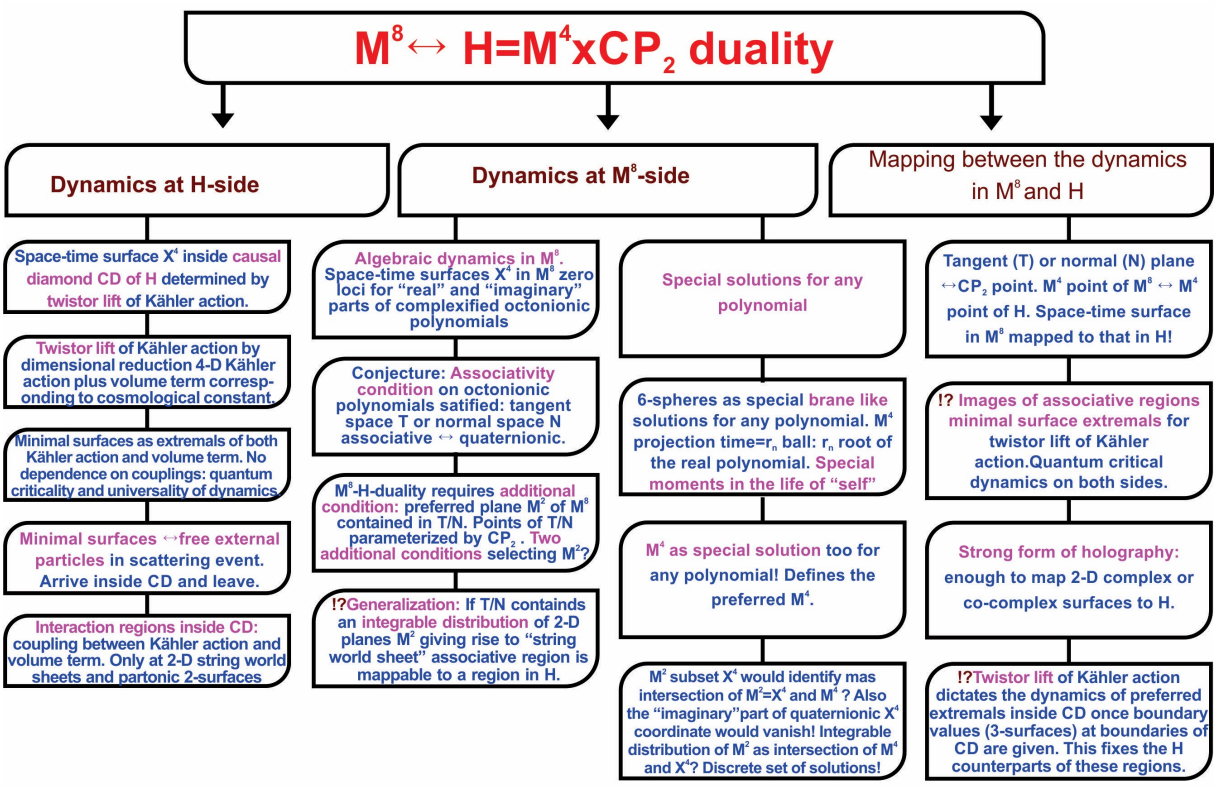


Figure 15: $M^8 - H$ duality

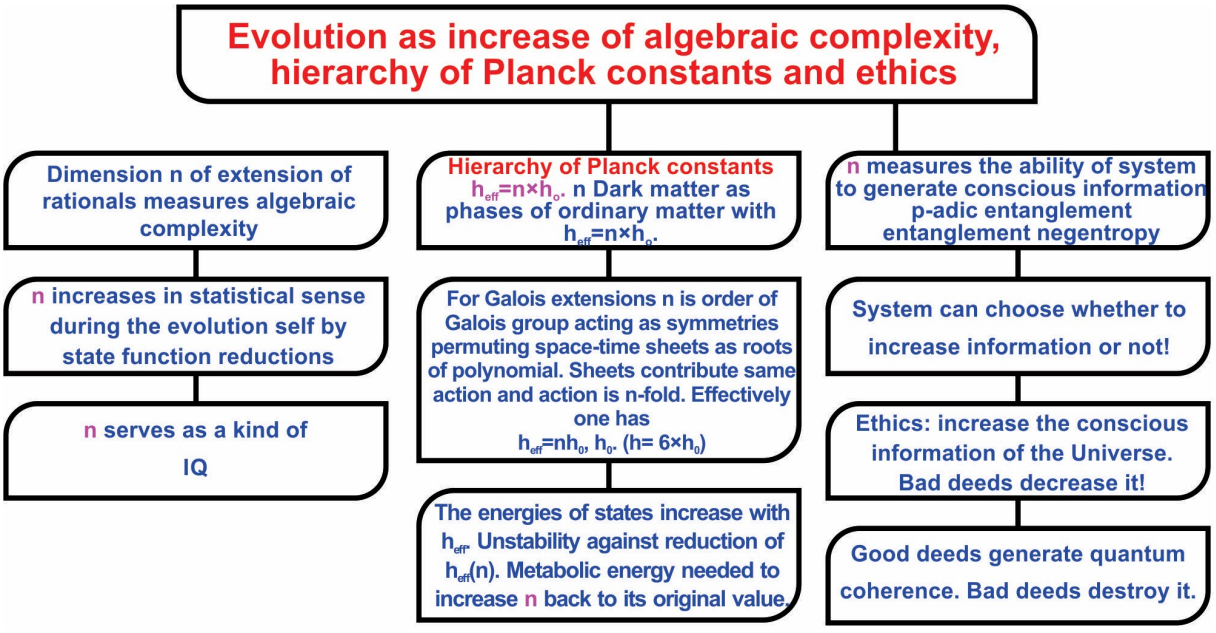
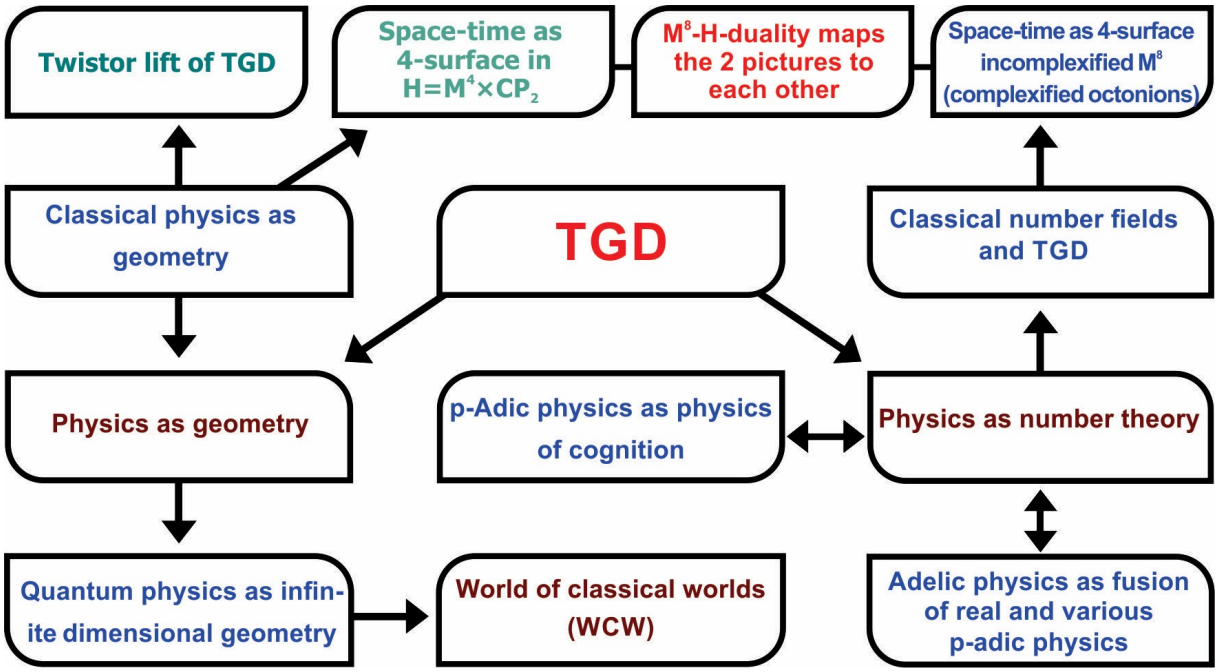


Figure 16: Number theoretic view of evolution



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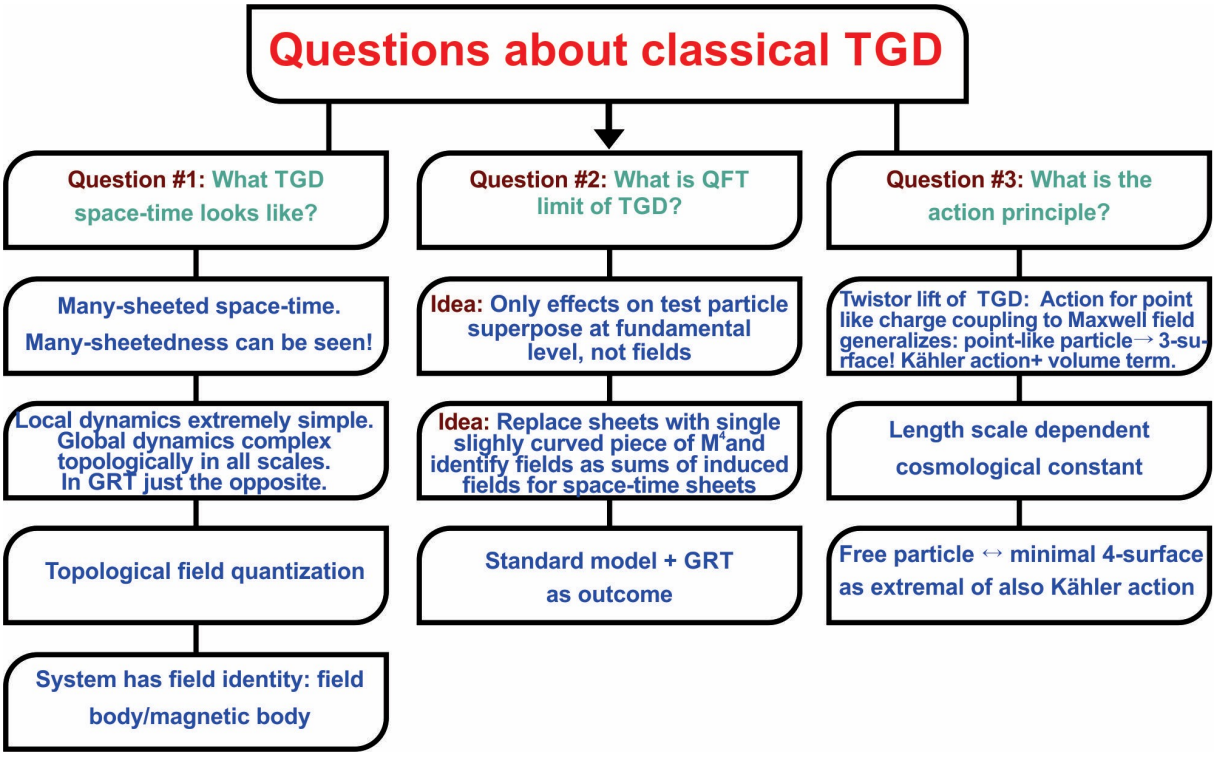

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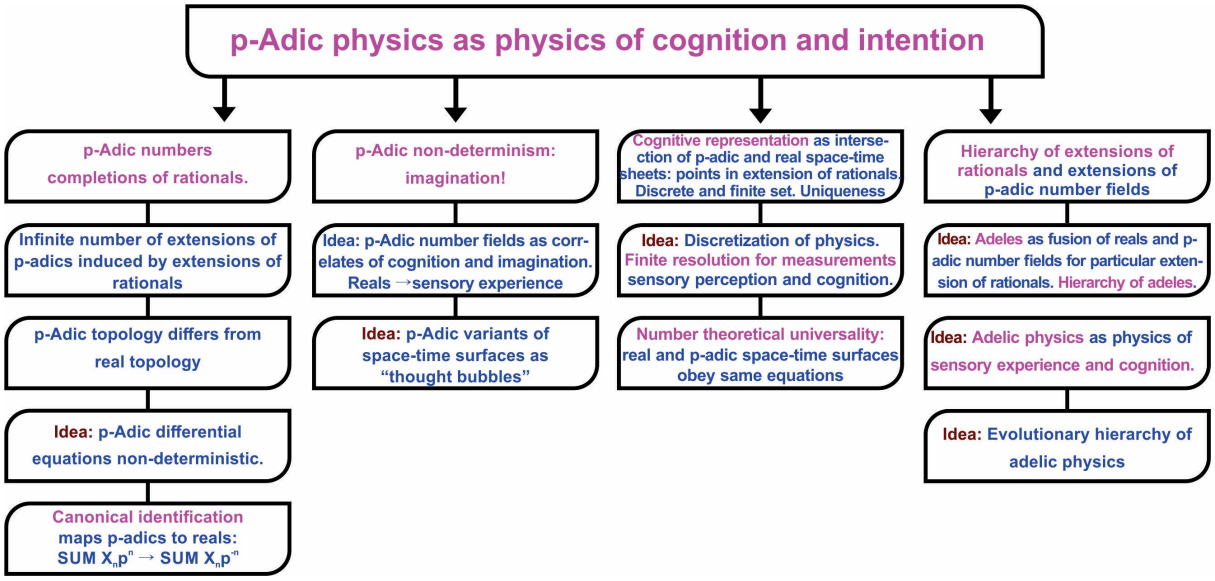

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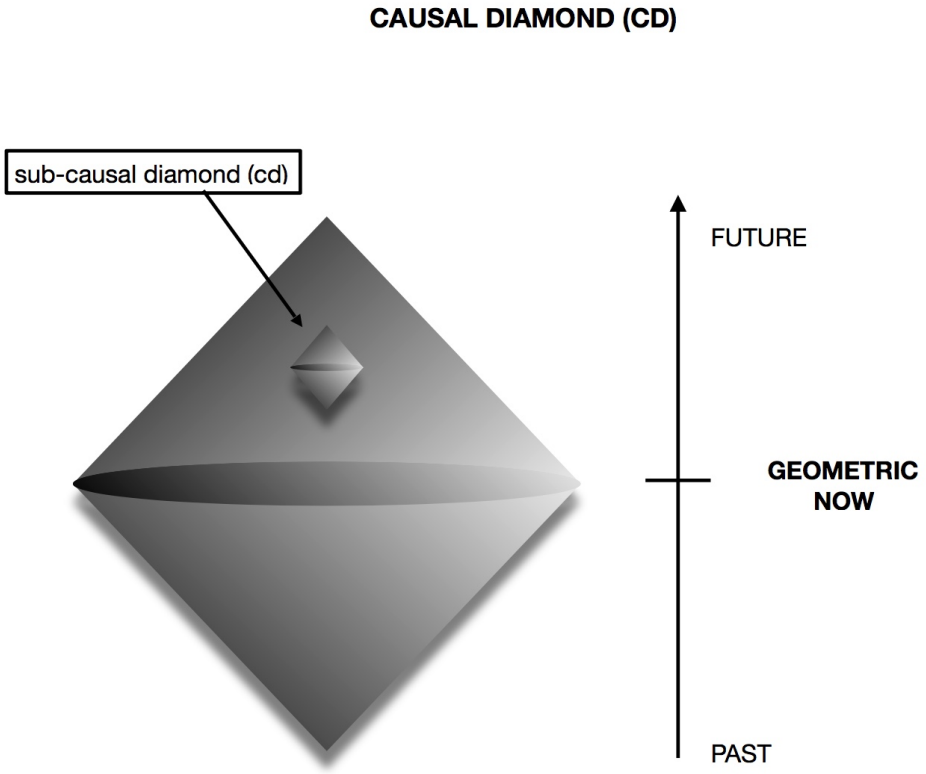
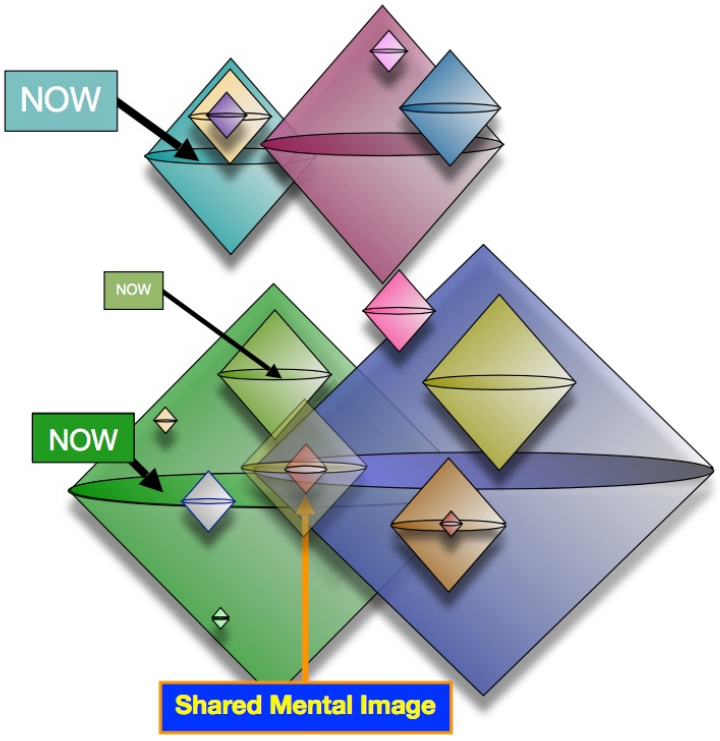


Figure 20: Causal diamond



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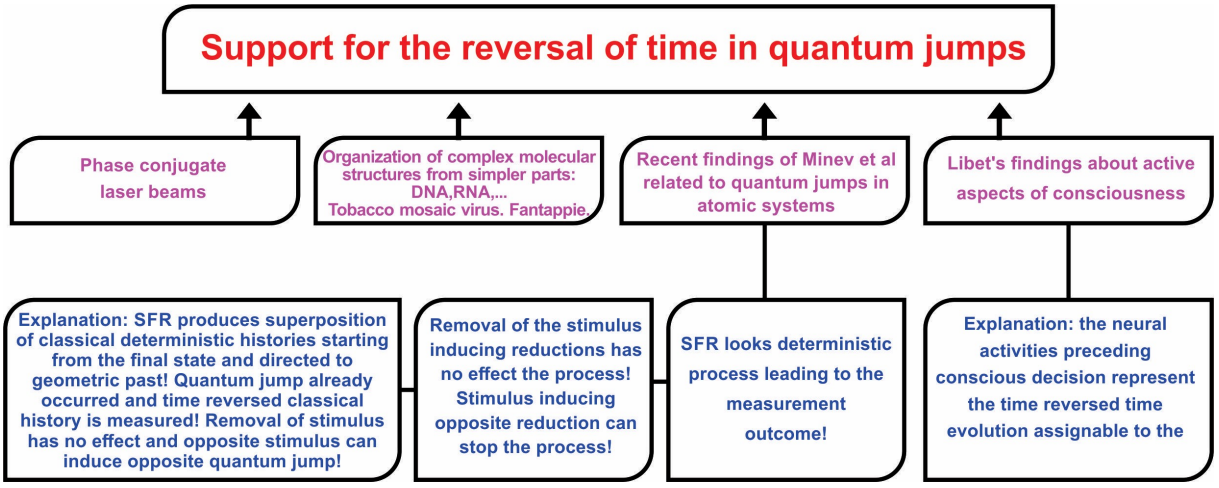

Figure 22: Time reversal occurs in BSFR

ACKNOWLEDGEMENTS

Neither TGD nor these books would exist without the help and encouragement of many people. The friendship with Heikki and Raija Haila and their family and Kalevi and Ritva Tikkanen and their family have been kept me in contact with the everyday world and without this friendship I would not have survived through these lonely 45 lonely years most of which I have remained unemployed as a scientific dissident. I am happy that my children have understood my difficult position and like my friends have believed that what I am doing is something valuable although I have not received any official recognition for it.

During the last decade Tapio Tammi has helped me quite concretely by providing the necessary computer facilities and being one of the few persons in Finland with whom to discuss my work. Pertti Kärkkäinen is my old physicist friend and has provided continued economic support for a long time. I have also had stimulating discussions with Samuli Penttinen who has also helped to get through the economical situations in which there seemed to be no hope. The continual updating of fifteen online books means quite a heavy bureaucracy at the level of bits and without a systemization one ends up with endless copying and pasting and internal consistency is soon lost. Tommi Ullgren has provided both economic support and encouragement during years. Pekka Rapinoja has offered his help in this respect and I am especially grateful to him for my Python skills.

During the last five years I have had inspiring discussions with many people in Finland interested in TGD. We have had video discussions with Sini Kunnas and had podcast discussions with Marko Manninen related to the TGD based view of physics and consciousness. Marko has also helped in the practical issues related to computers and quite recently he has done a lot of testing of chatGPT helping me to get an overall view of what it is. The discussions in a Zoom group involving Marko Manninen, Tuomas Sorakivi and Rode Majakka have given me the valuable opportunity to clarify my thoughts.

The collaboration with Lian Sidorov was extremely fruitful and she also helped me to survive economically through the hardest years. The participation in CASYS conferences in Liege has been an important window to the academic world and I am grateful for Daniel Dubois and Peter Marcer for making this participation possible. The discussions and collaboration with Eduardo de Luna and Istvan Dienes stimulated the hope that the communication of new vision might not be a mission impossible after all. Also blog discussions have been very useful. During these years I have received innumerable email contacts from people around the world. I am grateful to Mark McWilliams, Paul Kirsch, Gary Ehlenberg, and Ulla Matfolk and many others for providing links to possibly interesting websites and articles. We have collaborated with Peter Gariaev and Reza Rastmanesh. These contacts have helped me to avoid the depressive feeling of being some kind of Don Quixote of Science and helped me to widen my views: I am grateful for all these people.

In the situation in which the conventional scientific communication channels are strictly closed it is important to have some loop hole through which the information about the work done can at least in principle leak to the public through the iron wall of academic censorship. Without any exaggeration I can say that without the world wide web I would not have survived as a scientist nor as an individual. Homepage and blog are however not enough since only the formally published result is a result in recent day science. Publishing is however impossible without direct support from power holders- even in archives like arXiv.org.

Situation changed as Andrew Adamatsky proposed the writing of a book about TGD when I had already gotten used to the thought that my work would not be published during my lifetime. The Prespacetime Journal and two other journals related to quantum biology and consciousness - all of them founded by Huping Hu - have provided this kind of loophole. In particular, Dainis Zeps,

Phil Gibbs, and Arkadiusz Jadczyk deserve my gratitude for their kind help in the preparation of an article series about TGD catalyzing a considerable progress in the understanding of quantum TGD. Also the viXra archive founded by Phil Gibbs and its predecessor Archive Freedom have been of great help: Victor Christianto deserves special thanks for doing the hard work needed to run Archive Freedom. Also the Neuroquantology Journal founded by Sultan Tarlaci deserves a special mention for its publication policy.

And last but not least: there are people who experience as a fascinating intellectual challenge to spoil the practical working conditions of a person working with something which might be called unified theory: I am grateful for the people who have helped me to survive through the virus attacks, an activity which has taken roughly one month per year during the last half decade and given a strong hue of grey to my hair.

For a person approaching his 73th birthday it is somewhat easier to overcome the hard feelings due to the loss of academic human rights than for an inpatient youngster. Unfortunately the economic situation has become increasingly difficult during the twenty years after the economic depression in Finland which in practice meant that Finland ceased to be a constitutional state in the strong sense of the word. It became possible to depose people like me from society without fear about public reactions and the classification as dropout became a convenient tool of ridicule to circumvent the ethical issues. During the period when the right wing held political power this trend was steadily strengthening and the situation is the same as I am writing this. In this kind of situation the concrete help from individuals has been and will be of utmost importance. Against this background it becomes obvious that this kind of work is not possible without the support from outside and I apologize for not being able to mention all the people who have helped me during these years.

Karkkila, August 30, 2023, Finland

Matti Pitkänen

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Chapter 1

Introduction

1.1 Basic Ideas of Topological Geometrodynamics (TGD)

Standard model describes rather successfully both electroweak and strong interactions but sees them as totally separate and contains a large number of parameters which it is not able to predict. For about four decades ago unified theories known as Grand Unified Theories (GUTs) trying to understand electroweak interactions and strong interactions as aspects of the same fundamental gauge interaction assignable to a larger symmetry group emerged. Later superstring models trying to unify even gravitation and strong and weak interactions emerged. The shortcomings of both GUTs and superstring models are now well-known. If TGD - whose basic idea emerged towards the end of 1977 - would emerge now it would be seen as an attempt to solve the difficulties of these approaches to unification.

The basic physical picture behind the geometric vision of TGD corresponds to a fusion of two rather disparate approaches: namely TGD as a Poincare invariant theory of gravitation and TGD as a generalization of the old-fashioned string model. After 1995 number theoretic vision started to develop and was initiated by the success of mass calculations based on p-adic thermodynamics. Number theoretic vision involves all number fields and is complementary to the geometric vision: one can say that this duality is analogous to momentum-position duality of wave mechanics. TGD can be also regarded as topological quantum theory in a very general sense as already the attribute "Topological" in "TGD" makes clear. Space-time surfaces as minimal surfaces can be regarded as representatives of homology equivalence classes and p-adic topologies generalize the notion of local topology and apply to the description of correlates of cognition.

1.1.1 Geometric Vision Very Briefly

T(opological) G(eometro)D(ynamics) is one of the many attempts to find a unified description of basic interactions. The development of the basic ideas of TGD to a relatively stable form took time of about half decade [K2].

The basic vision and its relationship to existing theories is now rather well understood.

1. Space-times are representable as 4-surfaces in the 8-dimensional embedding space $H = M^4 \times CP_2$, where M^4 is 4-dimensional (4-D) Minkowski space and CP_2 is 4-D complex projective space (see Appendix).

2. Induction procedure (a standard procedure in fiber bundle theory, see Appendix) allows to geometrize various fields. Space-time metric characterizing gravitational fields corresponds to the induced metric obtained by projecting the metric tensor of H to the space-time surface. Electroweak gauge potentials are identified as projections of the components of CP_2 spinor connection to the space-time surface, and color gauge potentials as projections of CP_2 Killing vector fields representing color symmetries. Also spinor structure can be induced: induced spinor gamma matrices are projections of gamma matrices of H and induced spinor fields just H spinor fields restricted to space-time surface. Spinor connection is also projected. The interpretation is that distances are measured in embedding space metric and parallel translation using spinor connection of embedding space.

Twistor lift of TGD means that one can lift space-time surfaces in H to 6-D surfaces a analogs of twistor space of space-time surface in the Cartesian product of the twistor spaces of M^4 and CP_2, which are the only 4-manifolds allowing twistor space with Kähler structure [A33]. The twistor structure would be induced in some sense, and should coincide with that associated with the induced metric. Clearly, the 2-spheres defining the fibers of twistor spaces of M^4 and CP_2 must allow identification: this 2-sphere defines the S^2 fiber of the twistor space of the space-time surface. This poses a constraint on the embedding of the twistor space of space-time surfaces as sub-manifold in the Cartesian product of twistor spaces. The existence of Kähler structure allows to lift 4-D Kähler action to its 6-D counterparts and the 6-D counterpart of twistor space is obtained by its dimensional reduction so that one obtains a sphere bundle. This makes possible twistorialization for all space-time surfaces: in general relativity the general metric does not allow this.

3. A geometrization of quantum numbers is achieved. The isometry group of the geometry of CP_2 codes for the color gauge symmetries of strong interactions. Vierbein group codes for electroweak symmetries, and explains their breaking in terms of CP_2 geometry so that standard model gauge group results. There are also important deviations from the standard model: color quantum numbers are not spin-like but analogous to orbital angular momentum: this difference is expected to be seen only in CP_2 scale. In contrast to GUTs, quark and lepton numbers are separately conserved and family replication has a topological explanation in terms of topology of the partonic 2-surface carrying fermionic quantum numbers.

   M^4 and CP_2 are unique choices for many other reasons. For instance, they are the unique 4-D space-times allowing twistor space with Kähler structure. M^4 light-cone boundary allows a huge extension of 2-D conformal symmetries. M^4 and CP_2 allow quaternionic structures. Therefore standard model symmetries have number theoretic meaning.

4. Induced gauge potentials are expressible in terms of embedding space coordinates and their gradients and general coordinate invariance implies that there are only 4 field-like variables locally. Situation is thus extremely simple mathematically. The objection is that one loses linear superposition of fields. The resolution of the problem comes from the generalization of the concepts of particle and space-time.

   Space-time surfaces can be also particle like having thus finite size. In particular, space-time regions with Euclidian signature of the induced metric (temporal and spatial dimensions in the same role) emerge and have interpretation as lines of generalized Feynman diagrams. Particles in space-time can be identified as a topological inhomogeneities in background space-time surface which looks like the space-time of general relativity in long length scales.

   One ends up with a generalization of space-time surface to many-sheeted space-time with space-time sheets having extremely small distances of about 10^4 Planck lengths (CP_2 size). As one adds a particle to this kind of structure, it touches various space-time sheets and thus interacts with the associated classical fields. Their effects superpose linearly in good approximation and linear superposition of fields is replaced with that for their effects.

   This resolves the basic objection. It also leads to the understanding of how the space-time of general relativity and quantum field theories emerges from TGD space-time as effective space-time when the sheets of many-sheeted space-time are lumped together to form a region of Minkowski space with metric replaced with a metric identified as the sum of empty Minkowski metric and deviations of the metrics of sheets from empty Minkowski metric. Gauge potentials are identified as sums of the induced gauge potentials. TGD is therefore a microscopic theory from which the standard model and general relativity follow as a topological simplification, however forcing a dramatic increase of the number of fundamental field variables.

5. A further objection is that classical weak fields identified as induced gauge fields are long ranged and should cause large parity breaking effects due to weak interactions. These effects are indeed observed but only in living matter. The basic problem is that one has long ranged classical electroweak gauge fields. The resolution of the problem is that the quantum averages of induced weak and color gauge fields vanish due to the fact that color rotations affect both space-time surfaces and induced weak and color fields. Only the averages of

electromagnetic fields are nonvanishing. The correlations functions for weak fields are nonvanishing below Compton lengths of weak bosons. In living matter large values of effective Planck constant labelling phases of ordinary matter identified as dark matter make possible long ranged weak fields and color fields.

6. General coordinate invariance requires holography so that space-time surfaces are analogous to Bohr orbits for particles identified as 3-surfaces. Bohr orbit property would be naturally realized by a 4-D generalization of holomorphy of string world sheets and implies that the space-time surfaces are minimal surfaces apart from singularities. This holds true for any action as long as it is general coordinate invariant and constructible in terms of the induced geometry. String world sheets and light-like orbits of partonic 2-surfaces correspond to singularities at which the minimal surface property of the space-time surfaces realizing the preferred extremal property fails. Preferred extremals are not completely deterministic, which implies what I call zero energy ontology (ZEO) meaning that the Bohr orbits are the fundamental objects. This leads to a solution of the basic paradox of quantum measurement theory. Also the mathematically ill-defined path integral disappears and leaves only the well-defined functional integral over the Bohr orbits.

7. A string model-like picture emerges from TGD and one ends up with a rather concrete view about the topological counterpart of Feynman diagrammatics. The natural stringy action would be given by the string world sheet area, which is present only in the space-time regions with Minkowskian signature. Gravitational constant could be present as a fundamental constant in string action and the ratio $\hbar/G/R^2$ would be determined by quantum criticality conditions. The hierarchy of Planck constants $h_{eff}/h = n$ assigned to dark matter in TGD framework would allow to circumvent the objection that only objects of length of order Planck length are possible since string tension given by $T = 1/\hbar_{eff}G$ apart from numerical factor could be arbitrary small. This would make possible gravitational bound states as partonic 2-surfaces as structures connected by strings and solve the basic problem of superstring theories. This option allows the natural interpretation of M^4 type vacuum extremals with CP_2 projection, which is Lagrange manifold as good approximations for space-time sheets at macroscopic length scales. String area does not contribute to the Kähler function at all.

   Whether induced spinor fields associated with Kähler-Dirac action and de-localized inside the entire space-time surface should be allowed remains an open question: super-conformal symmetry strongly suggests their presence. A possible interpretation for the corresponding spinor modes could be in terms of dark matter, sparticles, and hierarchy of Planck constants.

It is perhaps useful to make clear what TGD is not and also what new TGD can give to physics.

1. TGD is *not* just General Relativity made concrete by using embeddings: the 4-surface property is absolutely essential for unifying standard model physics with gravitation and to circumvent the incurable conceptual problems of General Relativity. The many-sheeted space-time of TGD gives rise only at the macroscopic limit to GRT space-time as a slightly curved Minkowski space. TGD is *not* a Kaluza-Klein theory although color gauge potentials are analogous to gauge potentials in these theories.

   TGD space-time is 4-D and its dimension is due to completely unique conformal properties of light-cone boundary and 3-D light-like surfaces implying enormous extension of the ordinary conformal symmetries. Light-like 3-surfaces represent orbits of partonic 2-surfaces and carry fundamental fermions at 1-D boundaries of string world sheets. TGD is *not* obtained by performing Poincare gauging of space-time to introduce gravitation and is plagued by profound conceptual problems.

2. TGD is *not* a particular string model although string world sheets emerge in TGD very naturally as loci for spinor modes: their 2-dimensionality makes among other things possible quantum deformation of quantization known to be physically realized in condensed matter, and conjectured in TGD framework to be crucial for understanding the notion of finite measurement resolution. Hierarchy of objects of dimension up to 4 emerge from TGD: this obviously means analogy with branes of super-string models.

TGD is *not* one more item in the collection of string models of quantum gravitation relying on Planck length mystics. Dark matter becomes an essential element of quantum gravitation and quantum coherence in astrophysical scales is predicted just from the assumption that strings connecting partonic 2-surfaces are responsible for gravitational bound states.

TGD is *not* a particular string model although AdS/CFT duality of super-string models generalizes due to the huge extension of conformal symmetries and by the identification of WCW gamma matrices as Noether super-charges of super-symplectic algebra having a natural conformal structure.

3. TGD is *not* a gauge theory. In TGD framework the counterparts of also ordinary gauge symmetries are assigned to super-symplectic algebra (and its Yangian [A17] [B9, B7, B8]), which is a generalization of Kac-Moody algebras rather than gauge algebra and suffers a fractal hierarchy of symmetry breakings defining hierarchy of criticalities. TGD is *not* one more quantum field theory like structure based on path integral formalism: path integral is replaced with functional integral over 3-surfaces, and the notion of classical space-time becomes an exact part of the theory. Quantum theory becomes formally a purely classical theory of WCW spinor fields: only state function reduction is something genuinely quantal.

4. TGD view about spinor fields is *not* the standard one. Spinor fields appear at three levels. Spinor modes of the embedding space are analogs of spinor modes characterizing incoming and outgoing states in quantum field theories. Induced second quantized spinor fields at space-time level are analogs of stringy spinor fields. Their modes are localized by the well-definedness of electro-magnetic charge and by number theoretic arguments at string world sheets. Kähler-Dirac action is fixed by supersymmetry implying that ordinary gamma matrices are replaced by what I call Kähler-Dirac gamma matrices - this something new. WCW spinor fields, which are classical in the sense that they are not second quantized, serve as analogs of fields of string field theory and imply a geometrization of quantum theory.

5. TGD is in some sense an extremely conservative geometrization of entire quantum physics: *no* additional structures such as gauge fields as independent dynamical degrees of freedom are introduced: Kähler geometry and associated spinor structure are enough. "Topological" in TGD should not be understood as an attempt to reduce physics to torsion (see for instance [B6]) or something similar. Rather, TGD space-time is topologically non-trivial in all scales and even the visible structures of the everyday world represent non-trivial topology of space-time in the TGD Universe.

6. Twistor space - or rather, a generalization of twistor approach replacing masslessness in 4-D sense with masslessness in 8-D sense and thus allowing description of also massive particles - emerged originally as a technical tool, and its Kähler structure is possible only for $H = M^4 \times CP_2$. It however turned out that much more than a technical tool is in question. What is genuinely new is the infinite-dimensional character of the Kähler geometry making it highly unique, and its generalization to p-adic number fields to describe correlates of cognition. Also the hierarchy of Planck constants $h_{eff} = n \times h$ reduces to the quantum criticality of the TGD Universe and p-adic length scales and Zero Energy Ontology represent something genuinely new.

The great challenge is to construct a mathematical theory around these physically very attractive ideas and I have devoted the last 45 years to the realization of this dream and this has resulted in 26 online books about TGD and nine online books about TGD inspired theory of consciousness and of quantum biology.

A collection of 30 online books is now (August 2023) under preparation. The goal is to minimize overlap between the topics of the books and make the focus of a given book sharper.

1.1.2 Two Visions About TGD as Geometrization of Physics and Their Fusion

As already mentioned, TGD as a geometrization of physics can be interpreted both as a modification of general relativity and generalization of string models.

TGD as a Poincare Invariant Theory of Gravitation

The first approach was born as an attempt to construct a Poincare invariant theory of gravitation. Space-time, rather than being an abstract manifold endowed with a pseudo-Riemannian structure, is regarded as a surface in the 8-dimensional space $H = M^4_{\times} CP_2$, where M^4 denotes Minkowski space and $CP_2 = SU(3)/U(2)$ is the complex projective space of two complex dimensions [A28, A32, A24, A31].

The identification of the space-time as a sub-manifold [A29, A39] of $M^4 \times CP_2$ leads to an exact Poincare invariance and solves the conceptual difficulties related to the definition of the energy-momentum in General Relativity.

It soon however turned out that sub-manifold geometry, being considerably richer in structure than the abstract manifold geometry, leads to a geometrization of all basic interactions. First, the geometrization of the elementary particle quantum numbers is achieved. The geometry of CP_2 explains electro-weak and color quantum numbers. The different H-chiralities of H-spinors correspond to the conserved baryon and lepton numbers. Secondly, the geometrization of the field concept results. The projections of the CP_2 spinor connection, Killing vector fields of CP_2 and of H-metric to four-surface define classical electro-weak, color gauge fields and metric in X^4.

The choice of H is unique from the condition that TGD has standard model symmetries. Also number theoretical vision selects $H = M^4 \times CP_2$ uniquely. M^4 and CP_2 are also unique spaces allowing twistor space with Kähler structure.

TGD as a Generalization of the Hadronic String Model

The second approach was based on the generalization of the mesonic string model describing mesons as strings with quarks attached to the ends of the string. In the 3-dimensional generalization 3-surfaces correspond to free particles and the boundaries of the 3- surface correspond to partons in the sense that the quantum numbers of the elementary particles reside on the boundaries. Various boundary topologies (number of handles) correspond to various fermion families so that one obtains an explanation for the known elementary particle quantum numbers. This approach leads also to a natural topological description of the particle reactions as topology changes: for instance, two-particle decay corresponds to a decay of a 3-surface to two disjoint 3-surfaces.

This decay vertex does not however correspond to a direct generalization of trouser vertex of string models. Indeed, the important difference between TGD and string models is that the analogs of string world sheet diagrams do not describe particle decays but the propagation of particles via different routes. Particle reactions are described by generalized Feynman diagrams for which 3-D light-like surface describing particle propagating join along their ends at vertices. As 4-manifolds the space-time surfaces are therefore singular like Feynman diagrams as 1-manifolds.

Quite recently, it has turned out that fermionic strings inside space-time surfaces define an exact part of quantum TGD and that this is essential for understanding gravitation in long length scales. Also the analog of AdS/CFT duality emerges in that the Kähler metric can be defined either in terms of Kähler function identifiable as Kähler action assignable to Euclidian space-time regions or Kähler action + string action assignable to Minkowskian regions.

The recent view about construction of scattering amplitudes is very "stringy". By strong form of holography string world sheets and partonic 2-surfaces provide the data needed to construct scattering amplitudes. Space-time surfaces are however needed to realize quantum-classical correspondence necessary to understand the classical correlates of quantum measurement. There is a huge generalization of the duality symmetry of hadronic string models.

The proposal is that scattering amplitudes can be regarded as sequences of computational operations for the Yangian of super-symplectic algebra. Product and co-product define the basic vertices and realized geometrically as partonic 2-surfaces and algebraically as multiplication for the elements of Yangian identified as super-symplectic Noether charges assignable to strings. Any computational sequences connecting given collections of algebraic objects at the opposite boundaries of causal diamond (CD) produce identical scattering amplitudes.

Fusion of the Two Approaches via a Generalization of the Space-Time Concept

The problem is that the two approaches to TGD seem to be mutually exclusive since the orbit of a particle like 3-surface defines 4-dimensional surface, which differs drastically from the topologically

trivial macroscopic space-time of General Relativity. The unification of these approaches forces a considerable generalization of the conventional space-time concept. First, the topologically trivial 3-space of General Relativity is replaced with a "topological condensate" containing matter as particle like 3-surfaces "glued" to the topologically trivial background 3-space by connected sum operation. Secondly, the assumption about connectedness of the 3-space is given up. Besides the "topological condensate" there could be "vapor phase" that is a "gas" of particle like 3-surfaces and string like objects (counterpart of the "baby universes" of GRT) and the non-conservation of energy in GRT corresponds to the transfer of energy between different sheets of the space-time and possible existence vapour phase.

. What one obtains is what I have christened as many-sheeted space-time (see **Fig.** `http://tgdtheory.fi/appfigures/manysheeted.jpg` or **Fig. ??** in the appendix of this book). One particular aspect is topological field quantization meaning that various classical fields assignable to a physical system correspond to space-time sheets representing the classical fields to that particular system. One can speak of the field body of a particular physical system. Field body consists of topological light rays, and electric and magnetic flux quanta. In Maxwell's theory the physical system does not possess this kind of field identity. The notion of the magnetic body is one of the key players in TGD inspired theory of consciousness and quantum biology. The existence of monopole flux tubes requiring no current as a source of the magnetic field makes it possible to understand the existence of magnetic fields in cosmological and astrophysical scales.

This picture became more detailed with the advent of zero energy ontology (ZEO). The basic notion of ZEO is causal diamond (CD) identified as the Cartesian product of CP_2 and of the intersection of future and past directed light-cones and having scale coming as an integer multiple of CP_2 size is fundamental. CDs form a fractal hierarchy and zero energy states decompose to products of positive and negative energy parts assignable to the opposite boundaries of CD defining the ends of the space-time surface. The counterpart of zero energy state in positive energy ontology is the pair of initial and final states of a physical event, say particle reaction.

At space-time level ZEO means that 3-surfaces are pairs of space-like 3-surfaces at the opposite light-like boundaries of CD. Since the extremals of Kähler action connect these, one can say that by holography the basic dynamical objects are the space-time surface connecting these 3-surfaces and identifiable as analogs of Bohr orbits. This changes totally the vision about notions like self-organization: self-organization by quantum jumps does not take for a 3-D system but for the entire 4-D field pattern associated with it.

General Coordinate Invariance (GCI) allows to identify the basic dynamical objects as space-like 3-surfaces at the ends of space-time surface at boundaries of CD: this means that space-time surface is analogous to Bohr orbit. An alternative identification of the lines of generalized Feynman diagrams is as light-like 3-surfaces at which the signature of the induced metric changes from Minkowskian to Euclidian . Also the Euclidian 4-D regions can have a similar interpretation. The requirement that the two interpretations are equivalent, leads to a strong form of General Coordinate Invariance. The outcome is effective 2-dimensionality stating that the partonic 2-surfaces identified as intersections of the space-like ends of space-time surface and light-like wormhole throats are the fundamental objects. That only effective 2-dimensionality is in question is due to the effects caused by the failure of strict determinism of Kähler action. In finite length scale resolution these effects can be neglected below UV cutoff and above IR cutoff. One can also speak about a strong form of holography.

The understanding of the super symplectic invariance leads to the proposal that super symplectic algebra and other Kac-Moody type algebras labelled by non-negative multiples of basic conformal weights allow a hierarchy of symmetry breakings in which the analog of gauge symmetry breaks down to a genuine dynamical symmetry. This gives rise to fractal hierarchies of algebras and symmetry breakings. This breaking can occur also for ordinary conformal algebras if one restricts the conformal weights to be non-negative integers.

1.1.3 Basic Objections

Objections are the most powerful tool in theory building. The strongest objection against TGD is the observation that all classical gauge fields are expressible in terms of four embedding space coordinates only- essentially CP_2 coordinates. The linear superposition of classical gauge fields taking place independently for all gauge fields is lost. This would be a catastrophe without many-

sheeted space-time. Instead of gauge fields, only the effects such as gauge forces are superposed. Particles topologically condense to several space-time sheets simultaneously and experience the sum of gauge forces. This transforms the weakness to extreme economy: in a typical unified theory the number of primary field variables is countered in hundreds if not thousands, now it is just four.

Second objection is that TGD space-time is quite too simple as compared to GRT space-time due to the embeddability to 8-D embedding space. One can also argue that Poincare invariant theory of gravitation cannot be consistent with General Relativity. The above interpretation makes it possible to understand the relationship to GRT space-time and how the Equivalence Principle (EP) follows from Poincare invariance of TGD. The interpretation of GRT space-time is as effective space-time obtained by replacing many-sheeted space-time with Minkowski space with effective metric determined as a sum of Minkowski metric and sum over the deviations of the induced metrics of the space-time sheets from Minkowski metric. Poincare invariance strongly suggests classical EP for the GRT limit in long length scales at least. One can also consider other kinds of limits such as the analog of GRT limit for Euclidian space-time regions assignable to elementary particles. In this case deformations of CP_2 metric define a natural starting point and CP_2 indeed defines a gravitational instanton with a very large cosmological constant in Einstein-Maxwell theory. Also gauge potentials of the standard model correspond classically to superpositions of induced gauge potentials over space-time sheets.

Topological Field Quantization

Topological field quantization distinguishes between TGD based and more standard - say Maxwellian - notion of field. In Maxwell's fields created by separate systems superpose and one cannot tell which part of field comes from which system except theoretically. In TGD these fields correspond to different space-time sheets and only their effects on test particle superpose. Hence physical systems have well-defined field identifies - field bodies - in particular magnetic bodies.

The notion of magnetic body carrying dark matter with non-standard large value of Planck constant has become central concept in TGD inspired theory of consciousness and living matter, and by starting from various anomalies of biology one ends up to a rather detailed view about the role of magnetic body as intentional agent receiving sensory input from the biological body and controlling it using EEG and its various scaled up variants as a communication tool. Among other thins this leads to models for cell membrane, nerve pulse, and EEG.

1.1.4 Quantum TGD as Spinor Geometry of World of Classical Worlds

A turning point in the attempts to formulate a mathematical theory was reached after seven years from the birth of TGD. The great insight was "Do not quantize". The basic ingredients to the new approach have served as the basic philosophy for the attempt to construct Quantum TGD since then and have been the following ones.

World of Classical Worlds

The notion of WCW reduces the interacting quantum theory to a theory of free WCW spinor fields.

1. Quantum theory for extended particles is free(!), classical(!) field theory for a generalized Schrödinger amplitude identified as WCW spinor in the configuration space CH ("world of classical worlds", WCW) consisting of all possible 3-surfaces in H. "All possible" means that surfaces with arbitrary many disjoint components and with arbitrary internal topology and also singular surfaces topologically intermediate between two different manifold topologies are included.

2. 4-D general coordinate invariance forces holography and replaces the ill-defined path integral over all space-time surfaces with a discrete sum over 4-D analogs of Bohr orbits for particles identified as 3-surfaces. Holography means that basic objects are these analogs of Bohr orbits. Since there is no quantization at the level of WCW, one has an analog of wave mechanics with point-like particles replaced with 4-D Bohr orbits.

3. One must geometrize WCW as the space of Bohr orbits. In an infinite-dimensional situation the existence of geometry requires maximal symmetries already in the case of loop spaces. Physics is unique from its mathematical existence.

   WCW is endowed with metric and spinor structure so that one can define various metric related differential operators, say Dirac operators, appearing in the field equations of the theory [1]

Identification of Kähler function

The evolution of these basic ideas has been rather slow but has gradually led to a rather beautiful vision. One of the key problems has been the definition of Kähler function. Kähler function is Kähler action for a preferred extremal assignable to a given 3-surface but what this preferred extremal is? The obvious first guess was as absolute minimum of Kähler action but could not be proven to be right or wrong. One big step in the progress was boosted by the idea that TGD should reduce to almost topological QFT in which braids would replace 3-surfaces in finite measurement resolution, which could be inherent property of the theory itself and imply discretization at partonic 2-surfaces with discrete points carrying fermion number.

It took long time to realize that there is no discretization in 4-D sense - this would lead to difficulties with basic symmetries. Rather, the discretization occurs for the parameters characterizing co-dimension 2 objects representing the information about space-time surface so that they belong to some algebraic extension of rationals. These 2-surfaces - string world sheets and partonic 2-surfaces - are genuine physical objects rather than a computational approximation. Physics itself approximates itself, one might say! This is of course nothing but strong form of holography.

1. TGD as almost topological QFT vision suggests that Kähler action for preferred extremals reduces to Chern-Simons term assigned with space-like 3-surfaces at the ends of space-time (recall the notion of causal diamond (CD)) and with the light-like 3-surfaces at which the signature of the induced metric changes from Minkowskian to Euclidian. Minkowskian and Euclidian regions would give at wormhole throats the same contribution apart from coefficients and in Minkowskian regions the $\sqrt{g_4}$ factorc coming from metric would be imaginary so that one would obtain sum of real term identifiable as Kähler function and imaginary term identifiable as the ordinary Minkowskian action giving rise to interference effects and stationary phase approximation central in both classical and quantum field theory.

   Imaginary contribution - the presence of which I realized only after 33 years of TGD - could also have topological interpretation as a Morse function. On physical side the emergence of Euclidian space-time regions is something completely new and leads to a dramatic modification of the ideas about black hole interior.

2. The way to achieve the reduction to Chern-Simons terms is simple. The vanishing of Coulomb contribution to Kähler action is required and is true for all known extremals if one makes a general ansatz about the form of classical conserved currents. The so called weak form of electric-magnetic duality defines a boundary condition reducing the resulting 3-D terms to Chern-Simons terms. In this way almost topological QFT results. But only "almost" since the Lagrange multiplier term forcing electric-magnetic duality implies that Chern-Simons action for preferred extremals depends on metric.

WCW spinor fields

Classical WCW spinor fields are analogous to Schrödinger amplitudes and the construction of WCW Kähler geometry reduces to the second quantization of free spinor fields of H.

[1] There are four kinds of Dirac operators in TGD. The geometrization of quantum theory requires Kähler metric definable either in terms of Kähler function identified as a the bosonic action for Euclidian space-time regions or as anti-commutators for WCW gamma matrices identified as conformal Noether super-charges associated with the second quantized modified Dirac action consisting of string world sheet term and possibly also modified Dirac action in Minkowskian space-time regions. These two possible definitions reflect a duality analogous to AdS/CFT duality.

1. The WCW metric is given by anticommutators of WCW gamma matrices which also have interpretation as supercharges assignable to the generators of WCW isometries and allowing expression as non-conserved Noether charges. Holography implies zero energy ontology (ZEO) meaning that zero energy states are superpositions of Bohr orbits connecting boundaries of causal diamond (CD). CDs form a fractal hierarchy and their space forming the spine of WCW is finite-dimensional and can be geometrized. The alternative interpretation is as a superposition of pairs of ordinary 3-D fermionic states assignable to the ends of the space-time surfaces.

2. There are several Dirac operators. WCW Dirac operator D_{WCW} appears in Super-symplectic gauge conditions analogous to Super Virasoro conditions. The algebraic variant of the H Dirac operator D_H appears in fermionic correlation functions: this is due to the fact that free fermions appearing as building bricks of WCW gamma matrices are modes of D_H. The modes of ${}_DH$ define the ground states of super-symplectic representations. There is also the modified Dirac operator D_{X^4} acting on the induced spinors at space-time surfaces and it is dictated by symmetry one the action fixing the space-time surfaces as Bohr orbits is fixed. D_H is needed since it determines the expressions of WCW gamma matrices as Noether charges assignable to 3-surfaces at the ends of WCW.

The role of modified Dirac action

1. By quantum classical correspondence, the construction of WCW spinor structure in sectors assignable to CDs reduces to the second quantization of the induced spinor fields of H. The basic action is so called modified Dirac action in which gamma matrices are replaced with the modified) gamma matrices defined as contractions of the canonical momentum currents of the bosonic action defining the space-time surfaces with the embedding space gamma matrices. In this way one achieves super-conformal symmetry and conservation of fermionic currents among other things and a consistent Dirac equation.

   Modified Dirac action is needed to define WCW gamma matrices as super charges assignable to WCW isometry generators identified as generators of symplectic transformations and by holography are needed only at the 3-surface at the boundaries of WCW. It is important to notice that the modified Dirac equation does not determine propagators since induced spinor fields are obtained from free second quantized spinor fields of H. This means enormous simplification and makes the theory calculable.

2. An important interpretational problem relates to the notion of the induced spinor connection. The presence of classical W boson fields is in conflict with the classical conservation of em charge since the coupling to classical W fields changes em charge.

   One way out of the problem is the fact that the quantum averages of weak and gluon fields vanish unlike the quantum average of the em field. This leads to a rather precise understanding of electroweak symmetry breaking as being due the fact that color symmetries rotate space-time surfaces and also affect the induced weak fields.

   One can also consider a stronger condition. If one requires that the spinor modes have well-defined em charge, one must assume that the modes in the generic situation are localized at 2-D surfaces - string world sheets or perhaps also partonic 2-surfaces - at which classical W boson fields vanish. Covariantly constant right handed neutrinos generating super-symmetries forms an exception. The vanishing of the Z^0 field is possible for Kähler-Dirac action and should hold true at least above weak length scales. This implies that the string model in 4-D space-time becomes part of TGD. Without these conditions classical weak fields can vanish above weak scale only for the GRT limit of TGD for which gauge potentials are sums over those for space-time sheets.

   The localization would simplify the mathematics enormously and one can solve exactly the Kähler-Dirac equation for the modes of the induced spinor field just like in super string models.

   At the light-like 3-surfaces the signature of the induced metric changes from Euclidian to Minkowskian so that $\sqrt{g_4}$ vanishes. One can pose the condition that the algebraic analog of

the massless Dirac equation is satisfied by the modes of the modified-Dirac action assignable to the Chern-Simons-Kähler action.

1.1.5 Construction of scattering amplitudes

Reduction of particle reactions to space-time topology

Particle reactions are identified as topology changes [A35, A42, A46]. For instance, the decay of a 3-surface to two 3-surfaces corresponds to the decay $A \to B + C$. Classically this corresponds to a path of WCW leading from 1-particle sector to 2-particle sector. At quantum level this corresponds to the dispersion of the generalized Schrödinger amplitude localized to 1-particle sector to two-particle sector. All coupling constants should result as predictions of the theory since no nonlinearities are introduced.

During years this naïve and very rough vision has of course developed a lot and is not anymore quite equivalent with the original insight. In particular, the space-time correlates of Feynman graphs have emerged from theory as Euclidian space-time regions and the strong form of General Coordinate Invariance has led to a rather detailed and in many respects un-expected visions. This picture forces to give up the idea about smooth space-time surfaces and replace space-time surface with a generalization of Feynman diagram in which vertices represent the failure of manifold property. I have also introduced the word "world of classical worlds" (WCW) instead of rather formal "configuration space". I hope that "WCW" does not induce despair in the reader having tendency to think about the technicalities involved!

Construction of the counterparts of S-matrices

What does one mean with the counterpart of S-matrix in the TGD framework has been a long standing problem. The development of ZEO based quantum measurement theory has led to a rough overall view of the situation.

1. There are two kinds of state function reductions (SFRs). "Small" SFRs (SSFRs) following the TGD counterpart of a unitary time evolution defines a sequence of SFRs, which is analogous to a sequence of repeated quantum measurements associated with the Zeno effect. In wave mechanics nothing happens in these measurements. In quantum optics these measurements correspond to weak measurements. In TGD SSFR affects the zero energy state but leaves the 3-D state at the passive boundary of CD unaffected.

2. In TGD framework each SSFR is preceded by a counterpart of a unitary time evolution, which means dispersion in the space of CDs and unitary time evolution in fermionic degrees of freedom such that the passive boundary of CDs and 3-D states at it are unaffected but a superposition of CDs with varying active boundaries in the space of CDs is formed. In SSFR a localization in the space of CDs occurs such that the active is fixed. In a statistical sense the size of the CD increases and the increasing distance between the tips of the CD gives rise to the arrow of geometric time.

3. Also "big" SFRS (BSFRs) can occur and they correspond to ordinary SFRs. In BSFR the roles of the active and passive boundary are changed and this means that the arrow of time is changed. Big SFR occurs when the SSFR corresponds to a quantum measurement, which does not commute with the operators, which define the states at the passive boundary of CD as their eigenstates. This means a radical deviation from standard quantum measurement theory and has predictions in all scales.

4. One can assign the counterpart of S-matrix to the unitary time evolution between two subsequent SSFRs and also to the counterpart of S-matrix associated with BSFR. At least in the latter case the dimension of the state space can increase since at least BSFRs lead to the increase of the dimension of algebraic extension of rationals assignable to the space-time surface by $M^8 - H$ duality. Unitarity is therefore replaced with isometry.

5. I have also considered the possibility that unitary S-matrix could be replaced in the fermionic degrees of freedom with Kähler metric of the state space satisfying analogs of unitarity conditions but it seems that this is un-necessary and also too outlandish an idea.

The notion of M-matrix

1. The most ambitious dream is that zero energy states correspond to a complete solution basis for the Dirac operators associated with WCWs associated with the spaces of CDs with fixed passive boundary: this would define an S-matrix assignable to SFR. Also the analog of S-matrix for the localizations of the states to the active boundary assignable to the BSFR changing the state at the passive boundary of CD is needed.

2. If one allows entanglement between positive and energy parts of the zero energy state but assumes that the states at the passive boundary are fixed, one must introduce the counterpart of the density matrix, or rather its square root. This classical free field theory would dictate what I have called M-matrices defined between positive and negative energy parts of zero energy states which form orthonormal rows of what I call U-matrix as a matrix defined between zero energy states. A biven M-matrix in turn would decompose to a product of a hermitian square root of density matrix and unitary S-matrix.

3. M-matrix would define time-like entanglement coefficients between positive and negative energy parts of zero energy states (all net quantum numbers vanish for them) and can be regarded as a hermitian square root of density matrix multiplied by a unitary S-matrix. Quantum theory would be in a well-defined sense a square root of thermodynamics. The orthogonality and hermiticity of the M-matrices commuting with S-matrix means that they span infinite-dimensional Lie algebras acting as symmetries of the S-matrix. Therefore quantum TGD would reduce to group theory in a well-defined sense.

4. In fact the Lie algebra of Hermitian M-matrices extends to Kac-Moody type algebra obtained by multiplying hermitian square roots of density matrices with powers of the S-matrix. Also the analog of Yangian algebra involving only non-negative powers of S-matrix is possible and would correspond to a hierarchy of CDs with the temporal distances between tips coming as integer multiples of the CP_2 time.

   The M-matrices associated with CDs are obtained by a discrete scaling from the minimal CD and characterized by integer n are naturally proportional to a representation matrix of scaling: $S(n) = S^n$, where S is unitary S-matrix associated with the minimal CD [K54]. This conforms with the idea about unitary time evolution as exponent of Hamiltonian discretized to integer power of S and represented as scaling with respect to the logarithm of the proper time distance between the tips of CD.

5. I have also considered the notion of U-matrix. U-matrix elements between M-matrices for various CDs are proportional to the inner products $Tr[S^{-n_1} \circ H^i H^j \circ S^{n_2} \lambda]$, where λ represents unitarily the discrete Lorentz boost relating the moduli of the active boundary of CD and H^i form an orthonormal basis of Hermitian square roots of density matrices. $\circ$ tells that S acts at the active boundary of CD only. I have proposed a general representation for the U-matrix, reducing its construction to that of the S-matrix.

1.1.6 TGD as a generalized number theory

Quantum T(opological)D(ynamics) as a classical spinor geometry for infinite-dimensional configuration space ("world of classical worlds", WCW), p-adic numbers and quantum TGD, and TGD inspired theory of consciousness, have been for last ten years the basic three strongly interacting threads in the tapestry of quantum TGD. The fourth thread deserves the name "TGD as a generalized number theory". It involves three separate threads: the fusion of real and various p-adic physics to a single coherent whole by requiring number theoretic universality discussed already, the formulation of quantum TGD in terms of complexified counterparts of classical number fields, and the notion of infinite prime. Note that one can identify subrings such as hyper-quaternions and hyper-octonions as sub-spaces of complexified classical number fields with Minkowskian signature of the metric defined by the complexified inner product.

The Threads in the Development of Quantum TGD

The development of TGD has involved several strongly interacting threads: physics as infinite-dimensional geometry; TGD as a generalized number theory, the hierarchy of Planck constants interpreted in terms of dark matter hierarchy, and TGD inspired theory of consciousness. In the following these threads are briefly described.

1. Quantum T(opological) G(eometro)D(ynamics) as a classical spinor geometry for infinite-dimensional WCW, p-adic numbers and quantum TGD, and TGD inspired theory of consciousness and of quantum biology have been for last decade of the second millenium the basic three strongly interacting threads in the tapestry of quantum TGD.

2. The discussions with Tony Smith initiated a fourth thread which deserves the name "TGD as a generalized number theory". The basic observation was that classical number fields might allow a deeper formulation of quantum TGD. The work with Riemann hypothesis made time ripe for realization that the notion of infinite primes could provide, not only a reformulation, but a deep generalization of quantum TGD. This led to a thorough and rather fruitful revision of the basic views about what the final form and physical content of quantum TGD might be. Together with the vision about the fusion of p-adic and real physics to a larger coherent structure these sub-threads fused to the "physics as generalized number theory" thread.

3. A further thread emerged from the realization that by quantum classical correspondence TGD predicts an infinite hierarchy of macroscopic quantum systems with increasing sizes, that it is not at all clear whether standard quantum mechanics can accommodate this hierarchy, and that a dynamical quantized Planck constant might be necessary and strongly suggested by the failure of strict determinism for the fundamental variational principle. The identification of hierarchy of Planck constants labelling phases of dark matter would be natural. This also led to a solution of a long standing puzzle: what is the proper interpretation of the predicted fractal hierarchy of long ranged classical electro-weak and color gauge fields. Quantum classical correspondences allows only single answer: there is infinite hierarchy of p-adically scaled up variants of standard model physics and for each of them also dark hierarchy. Thus TGD Universe would be fractal in very abstract and deep sense.

The chronology based identification of the threads is quite natural but not logical and it is much more logical to see p-adic physics, the ideas related to classical number fields, and infinite primes as sub-threads of a thread which might be called "physics as a generalized number theory". In the following I adopt this view. This reduces the number of threads to three corresponding to geometric, number theoretic and topological views of physics.

TGD forces the generalization of physics to a quantum theory of consciousness, and TGD as a generalized number theory vision leads naturally to the emergence of p-adic physics as physics of cognitive representations.

Number theoretic vision very briefly

Number theoretic vision about quantum TGD involves notions like adelic physics, $M^8 - H$ duality and number theoretic universality. A short review of the basic ideas that have developed during years is in order.

1. The physical interpretation of M^8 is as an analog of momentum space and $M^8 - H$ duality is analogous to momentum-position duality of ordinary wave mechanics.

2. Adelic physics means that all classical number fields, all p-adic number fields and their extensions induced by extensions of rationals and defining adeles, and also finite number fields are basic mathematical building bricks of physics.

   The complexification of M^8, identified as complexified octonions, would provide a realization of this picture and $M^8 - H$ duality would map the algebraic physics in M^8 to the ordinary physics in $M^4 \times CP_2$ described in terms of partial differential equations.

3. Negentropy Maximization Principle (NMP) states that the conscious information assignable with cognition representable measured in terms of p-adic negentropy increases in statistical sense.

   NMP is mathematically completely analogous to the second law of thermodynamics and number theoretic evolution as an unavoidable statistical increase of the dimension of the algebraic extension of rationals characterizing a given space-time region implies it. There is no paradox involved: the p-adic negentropy measures the conscious information assignable to the entanglement of two systems regarded as a conscious entity whereas ordinary entropy measures the lack of information about the quantums state of either entangled system.

4. Number theoretical universality requires that space-time surfaces or at least their $M^8 - H$ duals in M_c^8 are defined for both reals and various p-adic number fields. This is true if they are defined by polynomials with integer coefficients as surfaces in M^8 obeying number theoretic holography realized as associativity of the normal space of 4-D surface using as holographic data 3-surfaces at mass shells identified in terms of roots of a polynomial. A physically motivated additional condition is that the coefficients of the polynomials are smaller than their degrees.

5. Galois confinement is a key piece of the number theoretic vision. It states that the momenta of physical states are algebraic integers in the extensions of rationals assignable to the space-time region considered. These numbers are in general complex and are not consistent with particle in box quantization. The proposal is that physical states satisfy Galois confinement being thus Galois singlets and having therefore total momenta, whose components are ordinary integers, when momentum unit defined by the scale of causal diamond (CD) is used.

6. The notion of p-adic prime was introduced in p-adic mass calculations that started the developments around 1995. p-Adic length scale hypothesis states that p-adic primes near powers of 2 have a special physical role (as possibly also the powers of other small primes such as $p = 3$).

   The proposal is that p-adic primes correspond to ramified primes assignable to the extension and identified as divisors of the polynomial defined by the products of the root differences for the roots of the polynomial defining space-time space and having interpretation as values of, in general complex, virtual mass squared.

p-Adic TGD and fusion of real and p-adic physics to single coherent whole

The p-adic thread emerged for roughly ten years ago as a dim hunch that p-adic numbers might be important for TGD. Experimentation with p-adic numbers led to the notion of canonical identification mapping reals to p-adics and vice versa. The breakthrough came with the successful p-adic mass calculations using p-adic thermodynamics for Super-Virasoro representations with the super-Kac-Moody algebra associated with a Lie-group containing standard model gauge group. Although the details of the calculations have varied from year to year, it was clear that p-adic physics reduces not only the ratio of proton and Planck mass, the great mystery number of physics, but all elementary particle mass scales, to number theory if one assumes that primes near prime powers of two are in a physically favored position. Why this is the case, became one of the key puzzles and led to a number of arguments with a common gist: evolution is present already at the elementary particle level and the primes allowed by the p-adic length scale hypothesis are the fittest ones.

It became very soon clear that p-adic topology is not something emerging in Planck length scale as often believed, but that there is an infinite hierarchy of p-adic physics characterized by p-adic length scales varying to even cosmological length scales. The idea about the connection of p-adics with cognition motivated already the first attempts to understand the role of the p-adics and inspired "Universe as Computer" vision but time was not ripe to develop this idea to anything concrete (p-adic numbers are however in a central role in TGD inspired theory of consciousness). It became however obvious that the p-adic length scale hierarchy somehow corresponds to a hierarchy of intelligences and that p-adic prime serves as a kind of intelligence quotient. Ironically, the almost obvious idea about p-adic regions as cognitive regions of space-time providing cognitive representations for real regions had to wait for almost a decade for the access into my consciousness.

In string model context one tries to reduces the physics to Planck scale. The price is the inability to say anything about physics in long length scales. In TGD p-adic physics takes care of this shortcoming by predicting the physics also in long length scales.

There were many interpretational and technical questions crying for a definite answer.

1. What is the relationship of p-adic non-determinism to the classical non-determinism of the basic field equations of TGD? Are the p-adic space-time region genuinely p-adic or does p-adic topology only serve as an effective topology? If p-adic physics is direct image of real physics, how the mapping relating them is constructed so that it respects various symmetries? Is the basic physics p-adic or real (also real TGD seems to be free of divergences) or both? If it is both, how should one glue the physics in different number field together to get *the* Physics? Should one perform p-adicization also at the level of the WCW? Certainly the p-adicization at the level of super-conformal representation is necessary for the p-adic mass calculations.

2. Perhaps the most basic and most irritating technical problem was how to precisely define p-adic definite integral which is a crucial element of any variational principle based formulation of the field equations. Here the frustration was not due to the lack of solution but due to the too large number of solutions to the problem, a clear symptom for the sad fact that clever inventions rather than real discoveries might be in question. Quite recently I however learned that the problem of making sense about p-adic integration has been for decades central problem in the frontier of mathematics and a lot of profound work has been done along same intuitive lines as I have proceeded in TGD framework. The basic idea is certainly the notion of algebraic continuation from the world of rationals belonging to the intersection of real world and various p-adic worlds.

Despite various uncertainties, the number of the applications of the poorly defined p-adic physics has grown steadily and the applications turned out to be relatively stable so that it was clear that the solution to these problems must exist. It became only gradually clear that the solution of the problems might require going down to a deeper level than that represented by reals and p-adics.

The key challenge is to fuse various p-adic physics and real physics to single larger structure. This has inspired a proposal for a generalization of the notion of number field by fusing real numbers and various p-adic number fields and their extensions along rationals and possible common algebraic numbers. This leads to a generalization of the notions of embedding space and space-time concept and one can speak about real and p-adic space-time sheets. One can talk about adelic space-time, embedding space, and WCW.

The corresponds of real 4-surfaces with the p-adic ones is induced by number theoretical discretization using points of 4-surfaces $Y^4 \subset M_c^8$ identifiable as 8-momenta, whose components are assumed to be algebraic integers in an extension of rationals defined by the extension of rationals associated with a polynomial P with integer coefficients smaller than the degree of P. These points define a cognitive representation, which is universal in the sense that it exists also in the algebraic extensions of p-adic numbers. The points of the cognitive representations associated with the mass shells with mass squared values identified as roots of P are enough since $M^8 - H$ duality can be used at both M^8 and H sides and also in the p-adic context. The mass shells are special in that they allow for Minkowski coordinates very large cognitive representations unlike the interiors of the 4-surfaces determined by holography by using the data defined by the 3-surfaces at the mass shells. The higher the dimension of the algebraic extension associated with P, the better the accuracy of the cognitive representation.

Adelization providing number theoretical universality reduces to algebraic continuation for the amplitudes from this intersection of reality and various p-adicities - analogous to a back of a book - to various number fields. There are no problems with symmetries but canonical identification is needed: various group invariant of the amplitude are mapped by canonical identification to various p-adic number fields. This is nothing but a generalization of the mapping of the p-adic mass squared to its real counterpart in p-adic mass calculations.

This leads to surprisingly detailed predictions and far reaching conjectures. For instance, the number theoretic generalization of entropy concept allows negentropic entanglement central for the applications to living matter (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book). One can also understand how preferred p-adic primes could

emerge as so called ramified primes of algebraic extension of rationals in question and characterizing string world sheets and partonic 2-surfaces. Preferred p-adic primes would be ramified primes for extensions for which the number of p-adic continuations of two-surfaces to space-time surfaces (imaginations) allowing also real continuation (realization of imagination) would be especially large. These ramifications would be winners in the fight for number theoretical survival. Also a generalization of p-adic length scale hypothesis emerges from NMP [K50].

The characteristic non-determinism of the p-adic differential equations suggests strongly that p-adic regions correspond to "mind stuff", the regions of space-time where cognitive representations reside. This interpretation implies that p-adic physics is physics of cognition. Since Nature is probably a brilliant simulator of Nature, the natural idea is to study the p-adic physics of the cognitive representations to derive information about the real physics. This view encouraged by TGD inspired theory of consciousness clarifies difficult interpretational issues and provides a clear interpretation for the predictions of p-adic physics.

Infinite primes

The discovery of the hierarchy of infinite primes and their correspondence with a hierarchy defined by a repeatedly second quantized arithmetic quantum field theory gave a further boost for the speculations about TGD as a generalized number theory.

After the realization that infinite primes can be mapped to polynomials possibly representable as surfaces geometrically, it was clear how TGD might be formulated as a generalized number theory with infinite primes forming the bridge between classical and quantum such that real numbers, p-adic numbers, and various generalizations of p-adics emerge dynamically from algebraic physics as various completions of the algebraic extensions of complexified quaternions and octonions. Complete algebraic, topological and dimensional democracy would characterize the theory.

The infinite primes at the first level of hierarchy, which represent analogs of bound states, can be mapped to irreducible polynomials, which in turn characterize the algebraic extensions of rationals defining a hierarchy of algebraic physics continuable to real and p-adic number fields. The products of infinite primes in turn define more general algebraic extensions of rationals. The interesting question concerns the physical interpretation of the higher levels in the hierarchy of infinite primes and integers mappable to polynomials of $n > 1$ variables.

1.1.7 An explicit formula for $M^8 - H$ duality

$M^8 - H$ duality is a generalization of momentum-position duality relating the number theoretic and geometric views of physics in TGD and, despite that it still involves poorly understood aspects, it has become a fundamental building block of TGD. One has 4-D surfaces $Y^4 \subset M^8_c$, where M^8_c is complexified M^8 having interpretation as an analog of complex momentum space and 4-D spacetime surfaces $X^4 \subset H = M^4 \times CP_2$. M^8_c, equivalently E^8_c, can be regarded as complexified octonions. M^8_c has a subspace M^4_c containing M^4.

Comment: One should be very cautious with the meaning of "complex". Complexified octonions involve a complex imaginary unit i commuting with the octonionic imaginary units I_k. i is assumed to also appear as an imaginary unit also in complex algebraic numbers defined by the roots of polynomials P defining holographic data in M^8_c.

In the following $M^8 - H$ duality and its twistor lift are discussed and an explicit formula for the dualities are deduced. Also possible variants of the duality are discussed.

Holography in H

$X^4 \subset H$ satisfies holography and is analogous to the Bohr orbit of a particle identified as a 3-surface. The proposal is that holography reduces to a 4-D generalization of holomorphy so that X^4 is a simultaneous zero of two functions of complex CP_2 coordinates and of what I have called Hamilton-Jacobi coordinates of M^4 with a generalized Kähler structure.

The simplest choice of the Hamilton-Jacobi coordinates is defined by the decomposition $M^4 = M^2 \times E^2$, where M^2 is endowed with hypercomplex structure defined by light-like coordinates (u, v), which are analogous to z and $\overline{z}$. Any analytic map $u \to f(u)$ defines a new set

of light-like coordinates and corresponds to a solution of the massless d'Alembert equation in M^2. E^2 has some complex coordinates with imaginary unit defined by i.

The conjecture is that also more general Hamilton-Jacobi structures for which the tangent space decomposition is local are possible. Therefore one would have $M^4 = M^2(x) \times E^2(x)$. These would correspond to non-equivalent complex and Kähler structures of M^4 analogous to those possessed by 2-D Riemann surfaces and parametrized by moduli space.

Number theoretic holography in M_c^8

$Y^4 \subset M_c^8$ satisfies number theoretic holography defining dynamics, which should reduce to associativity in some sense. The Euclidian complexified normal space $N^4(y)$ at a given point y of Y^4 is required to be associative, i.e. quaternionic. Besides this, $N^4(i)$ contains a preferred complex Euclidian 2-D subspace $Y^2(y)$. Also the spaces $Y^2(x)$ define an integrable distribution. I have assumed that $Y^2(x)$ can depend on the point y of Y^4.

These assumptions imply that the normal space $N(y)$ of Y^4 can be parameterized by a point of $CP_2 = SU(3)/U(2)$. This distribution is always integrable unlike quaternionic tangent space distributions. $M^8 - H$ duality assigns to the normal space $N(y)$ a point of CP_2. M_c^4 point y is mapped to a point $x \in M^4 \subset M^4 \times CP_2$ defined by the real part of its inversion (conformal transformation): this formula involves effective Planck constant for dimensional reasons.

The 3-D holographic data, which partially fixes 4-surfaces Y^4 is partially determined by a polynomial P with real integer coefficients smaller than the degree of P. The roots define mass squared values which are in general complex algebraic numbers and define complex analogs of mass shells in $M_c^4 \subset M_c^8$, which are analogs of hyperbolic spaces H^3. The 3-surfaces at these mass shells define 3-D holographic data continued to a surface Y^4 by requiring that the normal space of Y^4 is associative, i.e. quaternionic. These 3-surfaces are not completely fixed but an interesting conjecture is that they correspond to fundamental domains of tessellations of H^3.

What does the complexity of the mass shells mean? The simplest interpretation is that the space-like M^4 coordinates (3-momentum components) are real whereas the time-like coordinate (energy) is complex and determined by the mass shell condition. One would have $Re^2(E) - Im(E)^2 - p^2 = Re(m^2)$ and $2Re(E)Im(E) = Im(m^2)$. The condition for the real parts gives H^3 when $\sqrt{Re^2(E) - Im(E)^2}$ is taken as a time coordinate. The second condition allows to solve $Im(E)$ in terms of $Re(E)$ so that the first condition reduces to an equation of mass shell when $\sqrt{(Re(E)^2 - Im(E)^2)}$, expressed in terms of $Re(E)$, is taken as new energy coordinate $E_{eff} = \sqrt{(Re(E)^2 - Im(E)^2)}$. Is this deformation of H^3 in imaginary time direction equivalent with a region of the hyperbolic 3-space H^3?

One can look at the formula in more detail. Mass shell condition gives $Re^2(E) - Im(E)^2 - p^2 = Re(m^2)$ and $2Re(E)Im(E) = Im(m^2)$. The condition for the real parts gives H^3, when $\sqrt{Re^2(E) - Im(E)^2}$ is taken as an effective energy. The second condition allows to solve $Im(E)$ in terms of $Re(E)$ so that the first condition reduces to a dispersion relation for $Re(E)^2$.

$$Re(E)^2 = \frac{1}{2}(Re(m^2) - Im(m^2) + p^2)(1 \pm \sqrt{1 + \frac{2Im(m^2)^2}{(Re(m^2) - Im(m^2) + p^2)^2}}) \quad . \tag{1.1.1}$$

Only the positive root gives a non-tachyonic result for $Re(m^2) - Im(m^2) > 0$. For real roots with $Im(m^2) = 0$ and at the high momentum limit the formula coincides with the standard formula. For $Re(m^2) = Im(m^2)$ one obtains $Re(E)^2 \to Im(m^2)/\sqrt{2}$ at the low momentum limit $p^2 \to 0$. Energy does not depend on momentum at all: the situation resembles that for plasma waves.

Can one find an explicit formula for $M^8 - H$ duality?

The dream is an explicit formula for the $M^8 - H$ duality mapping $Y^4 \subset M_c^8$ to $X^4 \subset H$. This formula should be consistent with the assumption that the generalized holomorphy holds true for X^4.

The following proposal is a more detailed variant of the earlier proposal for which Y^4 is determined by a map g of $M_c^4 \to SU(3)_c \subset G_{2,c}$, where $G_{2,c}$ is the complexified automorphism group of octonions and $SU(3)_c$ is interpreted as a complexified color group.

This map defines a trivial $SU(3)_c$ gauge field. The real part of g however defines a non-trivial real color gauge field by the non-linearity of the non-abelian gauge field with respect to the gauge potential. The quadratic terms involving the imaginary part of the gauge potential give an additional condition to the real part in the complex situation and cancel it. If only the real part of g contributes, this contribution would be absent and the gauge field is non-vanishing.

How could the automorphism $g(x) \subset SU(3) \subset G_2$ give rise to $M^8 - H$ duality?

1. The interpretation is that $g(y)$ at given point y of Y^4 relates the normal space at y to a fixed quaternionic/associative normal space at point y_0, which corresponds is fixed by some subgroup $U(2)_0 \subset SU(3)$. The automorphism property of g guarantees that the normal space is quaternionic/associative at y. This simplifies the construction dramatically.

2. The quaternionic normal sub-space (which has Euclidian signature) contains a complex sub-space which corresponds to a point of sphere $S^2 = SO(3)/O(2)$, where $SO(3)$ is the quaternionic automorphism group. The interpretation could be in terms of a selection of spin quantization axes. The local choice of the preferred complex plane would not be unique and is analogous to the possibility of having non-trivial Hamilton Jacobi structures in M^4 characterized by the choice of $M^2(x)$ and equivalently its normal subspace $E^2(x)$.

   These two structures are independent apart from dependencies forced by the number theoretic dynamics. Hamilton-Jacobi structure means a selection of the quantization axis of spin and energy by fixing a distribution of light-like tangent vectors of M^4 and the choice of the quaternionic normal sub-space fixes a choice of preferred quaternionic imaginary unit defining a quantization axis of the weak isospin.

3. The real part $Re(g(y))$ defines a point of $SU(3)$ and the bundle projection $SU(3) \to CP_2$ in turn defines a point of $CP_2 = SU(3)/U(2)$. Hence one can assign to g a point of CP_2 as $M^8 - H$ duality requires and deduce an explicit formula for the point. This means a realization of the dream.

4. The construction requires a fixing of a quaternionic normal space N_0 at y_0 containing a preferred complex subspace at a single point of Y^4 plus a selection of the function g. If M^4 coordinates are possible for Y^4, the first guess is that g as a function of complexified M^4 coordinates obeys generalized holomorphy with respect to complexified M^4 coordinates in the same sense and in the case of X^4. This might guarantee that the $M^8 - H$ image of Y^4 satisfies the generalized holomorphy.

5. Also space-time surfaces X^4 with M^4 projection having a dimension smaller than 4 are allowed. I have proposed that they might correspond to singular cases for the above formula: a kind of blow-up would be involved. One can also consider a more general definition of Y^4 allowing it to have a M^4 projection with dimension smaller than 4 (say cosmic strings). Could one have implicit equations for the surface Y^4 in terms of the complex coordinates of $SU(3)_c$ and M^4? Could this give for instance cosmic strings with a 2-D M^4 projection and CP_2 type extremals with 4-D CP_2 projection and 1-D light-like M^4 projection?

What could the number theoretic holography mean physically?

What could be physical meaning of the number theoretic holography? The condition that has been assumed is that the CP_2 coordinates at the mass shells of $M^4_c \subset M^8_c$ mapped to mass shells H^3 of $M^4 \subset M^4 \times CP_2$ are constant at the H^3. This is true if the $g(y)$ defines the same CP_2 point for a given component X^3_i of the 3-surface at a given mass shell. g is therefore fixed apart from a local $U(2)$ transformation leaving the CP_2 point invariant. A stronger condition would be that the CP_2 point is the same for each component of X^3_i and even at each mass shell but this condition seems to be unnecessarily strong.

Comment: One can o criticize this condition as too strong and one can consider giving up this condition. The motivation for this condition is that the number of algebraic points at the 3-surfaces associated with H^3 explodes since the coordinates associated with normal directions vanish. Kind of cognitive explosion would be in question.

$SU(3)$ corresponds to a subgroup of G_2 and one can wonder what the fixing of this subgroup could mean physically. G_2 is 14-D and the coset space $G_2/SU(3)$ is 6-D and a good guess is that

it is just the 6-D twistor space $SU(3)/U(1) \times U(1)$ of CP_2: at least the isometries are the same. The fixing of the $SU(3)$ subgroup means fixing of a CP_2 twistor. Physically this means the fixing of the quantization axis of color isospin and hypercharge.

Twistor lift of the holography

What is interesting is that by replacing $SU(3)$ with G_2, one obtains an explicit formula form the generalization of $M^8 - H$ duality to that for the twistorial lift of TGD!

One can also consider a twistorial generalization of the above proposal for the number theoretic holography by allowing local G_2 automorphisms interpreted as local choices of the color quantization axis. G_2 elements would be fixed apart from a local $SU(3)$ transformation at the components of 3-surfaces at mass shells. The choice of the color quantization axes for a connected 3-surface at a given mass shell would be the same everywhere. This choice is indeed very natural physically since 3-surface corresponds to a particle.

Is this proposal consistent with the boundary condition of the number theoretical holography mean in the case of 4-surfaces in M_c^8 and $M^4 \times CP_2$?

1. The selection of $SU(3) \subset G_2$ for ordinary $M^8 - H$ duality means that the $G_{2,c}$ gauge field vanishes everywhere and the choice of color quantization axis is the same at all points of the 4-surface. The fixing of the CP_2 point to be constant at H^3 implies that the color gauge field at $H^3 \subset M_c^8$ and its image $H^3 \subset H$ vanish. One would have color confinement at the mass shells H_i^3, where the observations are made. Is this condition too strong?

2. The constancy of the G_2 element at mass shells makes sense physically and means a fixed color quantization axis. The selection of a fixed $SU(3) \subset G_2$ for entire space-time surface is in conflict with the non-constancy of G_2 element unless G_2 element differs at different points of 4-surface only by a multiplication of a local $SU(3)_0$ element, that is local $SU(3)$ transformation. This kind of variation of the G_2 element would mean a fixed color group but varying choice of color quantization axis.

3. Could one consider the possibility that the local $G_{2,c}$ element is free and defines the twistor lift of $M^8 - H$ duality as something more fundamental than the ordinary $M^8 - H$ duality based on $SU(3)_c$. This duality would make sense only at the mass shells so that only the spaces $H^3 \times CP_2$ assignable to mass shells would make sense physically? In the interior CP_2 would be replaced with the twistor space $SU(3)/U(1) \times U(1)$. Color gauge fields would be non-vanishing at the mass shells but outside the mass shells one would have G_2 gauge fields.

   There is also a physical objection against the G_2 option. The 14-D Lie algebra representation of G_2 acts on the imaginary octonions which decompose with respect to the color group to $1 \oplus 3 \oplus \overline{3}$. The automorphism property requires that 1 can be transformed to 3 or $\overline{3}$ to themselves: this requires that the decomposition contains $3 \oplus \overline{3}$. Furthermore, it must be possible to transform 3 and $\overline{3}$ to themselves, which requires the presence of 8. This leaves only the decomposition $8 \oplus 3 \oplus \overline{3}$. G_2 gluons would both color octet and triplets. In the TDG framework the only conceivable interpretation would be in terms of ordinary gluons and leptoquark-like gluons. This does not fit with the basic vision of TGD.

The choice of twistor as a selection of quantization axes should make sense also in the M^4 degrees of freedom. M^4 twistor corresponds to a choice of light-like direction at a given point of M^4. The spatial component of the light-like vector fixes the spin quantization axis. Its choice together with the light-likeness fixes the time direction and therefore the rest system and energy quantization axis. Light-like vector fixes also the choice of M^2 and of E^2 as its orthogonal complement. Therefore the fixing of M^4 twistor as a point of $SU(4)/SU(3) \times U(1)$ corresponds to a choice of the spin quantization axis and the time-like axis defining the rest system in which the energy is measured. This choice would naturally correspond to the Hamilton-Jacobi structure fixing the decompositions $M^2(x) \times E^2(x)$. At a given mass shell the choice of the quantization axis would be constant for a given X_i^3.

1.1.8 Hierarchy of Planck Constants and Dark Matter Hierarchy

By quantum classical correspondence space-time sheets can be identified as quantum coherence regions. Hence the fact that they have all possible size scales more or less unavoidably implies that Planck constant must be quantized and have arbitrarily large values. If one accepts this then also the idea about dark matter as a macroscopic quantum phase characterized by an arbitrarily large value of Planck constant emerges naturally as does also the interpretation for the long ranged classical electro-weak and color fields predicted by TGD. Rather seldom the evolution of ideas follows simple linear logic, and this was the case also now. In any case, this vision represents the fifth, relatively new thread in the evolution of TGD and the ideas involved are still evolving.

Dark Matter as Large $\hbar$ Phases

D. Da Rocha and Laurent Nottale [E1] have proposed that Schrödinger equation with Planck constant $\hbar$ replaced with what might be called gravitational Planck constant $\hbar_{gr} = \frac{GmM}{v_0}$ ($\hbar = c = 1$). v_0 is a velocity parameter having the value $v_0 = 144.7 \pm .7$ km/s giving $v_0/c = 4.6 \times 10^{-4}$. This is rather near to the peak orbital velocity of stars in galactic halos. Also subharmonics and harmonics of v_0 seem to appear. The support for the hypothesis coming from empirical data is impressive.

Nottale and Da Rocha believe that their Schrödinger equation results from a fractal hydrodynamics. Many-sheeted space-time however suggests that astrophysical systems are at some levels of the hierarchy of space-time sheets macroscopic quantum systems. The space-time sheets in question would carry dark matter.

Nottale's hypothesis would predict a gigantic value of h_{gr}. Equivalence Principle and the independence of gravitational Compton length on mass m implies however that one can restrict the values of mass m to masses of microscopic objects so that h_{gr} would be much smaller. Large h_{gr} could provide a solution of the black hole collapse (IR catastrophe) problem encountered at the classical level. The resolution of the problem inspired by TGD inspired theory of living matter is that it is the dark matter at larger space-time sheets which is quantum coherent in the required time scale [K75].

It is natural to assign the values of Planck constants postulated by Nottale to the space-time sheets mediating gravitational interaction and identifiable as magnetic flux tubes (quanta) possibly carrying monopole flux and identifiable as remnants of cosmic string phase of primordial cosmology. The magnetic energy of these flux quanta would correspond to dark energy and magnetic tension would give rise to negative "pressure" forcing accelerate cosmological expansion. This leads to a rather detailed vision about the evolution of stars and galaxies identified as bubbles of ordinary and dark matter inside magnetic flux tubes identifiable as dark energy.

Certain experimental findings suggest the identification $h_{eff} = n\times = h_{gr}$. The large value of h_{gr} can be seen as a way to reduce the string tension of fermionic strings so that gravitational (in fact all!) bound states can be described in terms of strings connecting the partonic 2-surfaces defining particles (analogous to AdS/CFT description). The values $h_{eff}/h = n$ can be interpreted in terms of a hierarchy of breakings of super-conformal symmetry in which the super-conformal generators act as gauge symmetries only for a sub-algebras with conformal weights coming as multiples of n. Macroscopic quantum coherence in astrophysical scales is implied. If also Kähler-Dirac action is present, part of the interior degrees of freedom associated with the Kähler-Dirac part of conformal algebra become physical. A possible is that tfermionic oscillator operators generate super-symmetries and sparticles correspond almost by definition to dark matter with $h_{eff}/h = n > 1$. One implication would be that at least part if not all gravitons would be dark and be observed only through their decays to ordinary high frequency graviton ($E = hf_{high} = h_{eff}f_{low}$) of bunch of n low energy gravitons.

Hierarchy of Planck Constants from the Anomalies of Neuroscience and Biology

The quantal ELF effects of ELF em fields on vertebrate brain have been known since seventies. ELF em fields at frequencies identifiable as cyclotron frequencies in magnetic field whose intensity is about 2/5 times that of Earth for biologically important ions have physiological effects and affect also behavior. What is intriguing that the effects are found only in vertebrates (to my best knowledge). The energies for the photons of ELF em fields are extremely low - about 10^{-10} times

lower than thermal energy at physiological temperatures- so that quantal effects are impossible in the framework of standard quantum theory. The values of Planck constant would be in these situations large but not gigantic.

This inspired the hypothesis that these photons correspond to so large a value of Planck constant that the energy of photons is above the thermal energy. The proposed interpretation was as dark photons and the general hypothesis was that dark matter corresponds to ordinary matter with non-standard value of Planck constant. If only particles with the same value of Planck constant can appear in the same vertex of Feynman diagram, the phases with different value of Planck constant are dark relative to each other. The phase transitions changing Planck constant can however make possible interactions between phases with different Planck constant but these interactions do not manifest themselves in particle physics. Also the interactions mediated by classical fields should be possible. Dark matter would not be so dark as we have used to believe.

The hypothesis $h_{eff} = h_{gr}$ - at least for microscopic particles - implies that cyclotron energies of charged particles do not depend on the mass of the particle and their spectrum is thus universal although corresponding frequencies depend on mass. In bio-applications this spectrum would correspond to the energy spectrum of bio-photons assumed to result from dark photons by h_{eff} reducing phase transition and the energies of bio-photons would be in visible and UV range associated with the excitations of bio-molecules.

Also the anomalies of biology (see for instance [K65, K66, K63]) support the view that dark matter might be a key player in living matter.

Dark Matter as a Source of Long Ranged Weak and Color Fields

Long ranged classical electro-weak and color gauge fields are unavoidable in TGD framework. The smallness of the parity breaking effects in hadronic, nuclear, and atomic length scales does not however seem to allow long ranged electro-weak gauge fields. The problem disappears if long range classical electro-weak gauge fields are identified as space-time correlates for massless gauge fields created by dark matter. Also scaled up variants of ordinary electro-weak particle spectra are possible. The identification explains chiral selection in living matter and unbroken $U(2)_{ew}$ invariance and free color in bio length scales become characteristics of living matter and of bio-chemistry and bio-nuclear physics.

The recent view about the solutions of Kähler- Dirac action assumes that the modes have a well-defined em charge and this implies that localization of the modes to 2-D surfaces (right-handed neutrino is an exception). Classical W boson fields vanish at these surfaces and also classical Z^0 field can vanish. The latter would guarantee the absence of large parity breaking effects above intermediate boson scale scaling like h_{eff}.

1.1.9 Twistors in TGD and connection with Veneziano duality

The twistorialization of TGD has two aspects. The attempt to generalize twistor Grassmannian approach emerged first. It was however followed by the realization that also the twistor lift of TGD at classical space-time level is needed. It turned out that the progress in the understanding of the classical twistor lift has been much faster - probably this is due to my rather limited technical QFT skills.

Twistor lift at space-time level

8-dimensional generalization of ordinary twistors is highly attractive approach to TGD [K83]. The reason is that M^4 and CP_2 are completely exceptional in the sense that they are the only 4-D manifolds allowing twistor space with Kähler structure [A33]. The twistor space of $M^4 \times CP_2$ is Cartesian product of those of M^4 and CP_2. The obvious idea is that space-time surfaces allowing twistor structure if they are orientable are representable as surfaces in H such that the properly induced twistor structure coincides with the twistor structure defined by the induced metric.

In fact, it is enough to generalize the induction of spinor structure to that of twistor structure so that the induced twistor structure need not be identical with the ordinary twistor structure possibly assignable to the space-time surface. The induction procedure reduces to a dimensional reduction of 6-D Kähler action giving rise to 6-D surfaces having bundle structure with twistor

sphere as fiber and space-time as base. The twistor sphere of this bundle is imbedded as sphere in the product of twistor spheres of twistor spaces of M^4 and CP_2.

This condition would define the dynamics, and the original conjecture was that this dynamics is equivalent with the identification of space-time surfaces as preferred extremals of Kähler action. The dynamics of space-time surfaces would be lifted to the dynamics of twistor spaces, which are sphere bundles over space-time surfaces. What is remarkable that the powerful machinery of complex analysis becomes available.

It however turned out that twistor lift of TGD is much more than a mere technical tool. First of all, the dimensionally reduction of 6-D Kähler action contained besides 4-D Kähler action also a volume term having interpretation in terms of cosmological constant. This need not bring anything new, since all known extremals of Kähler action with non-vanishing induced Kähler form are minimal surfaces. There is however a large number of embeddings of twistor sphere of space-time surface to the product of twistor spheres. Cosmological constant has spectrum and depends on length scale, and the proposal is that coupling constant evolution reduces to that for cosmological constant playing the role of cutoff length. That cosmological constant could transform from a mere nuisance to a key element of fundamental physics was something totally new and unexpected.

1. The twistor lift of TGD at space-time level forces to replace 4-D Kähler action with 6-D dimensionally reduced Kähler action for 6-D surface in the 12-D Cartesian product of 6-D twistor spaces of M^4 and CP_2. The 6-D surface has bundle structure with twistor sphere as fiber and space-time surface as base.

   Twistor structure is obtained by inducing the twistor structure of 12-D twistor space using dimensional reduction. The dimensionally reduced 6-D Kähler action is sum of 4-D Kähler action and volume term having interpretation in terms of a dynamical cosmological constant depending on the size scale of space-time surface (or of causal diamond CD in zero energy ontology (ZEO)) and determined by the representation of twistor sphere of space-time surface in the Cartesian product of the twistor spheres of M^4 and CP_2.

2. The preferred extremal property as a representation of quantum criticality would naturally correspond to minimal surface property meaning that the space-time surface is separately an extremal of both Kähler action and volume term almost everywhere so that there is no coupling between them. This is the case for all known extremals of Kähler action with non-vanishing induced Kähler form.

   Minimal surface property could however fail at 2-D string world sheets, their boundaries and perhaps also at partonic 2-surfaces. The failure is realized in minimal sense if the 3-surface has 1-D edges/folds (strings) and 4-surface 2-D edges/folds (string world sheets) at which some partial derivatives of the embedding space coordinates are discontinuous but canonical momentum densities for the entire action are continuous.

   There would be no flow of canonical momentum between interior and string world sheet and minimal surface equations would be satisfied for the string world sheet, whose 4-D counterpart in twistor bundle is determined by the analog of 4-D Kähler action. These conditions allow the transfer of canonical momenta between Kähler- and volume degrees of freedom at string world sheets. These no-flow conditions could hold true at least asymptotically (near the boundaries of CD).

   $M^8 - H$ duality suggests that string world sheets (partonic 2-surfaces) correspond to images of complex 2-sub-manifolds of M^8 (having tangent (normal) space which is complex 2-plane of octonionic M^8).

3. Cosmological constant would depend on p-adic length scales and one ends up to a concrete model for the evolution of cosmological constant as a function of p-adic length scale and other number theoretic parameters (such as Planck constant as the order of Galois group): this conforms with the earlier picture.

   Inflation is replaced with its TGD counterpart in which the thickening of cosmic strings to flux tubes leads to a transformation of Kähler magnetic energy to ordinary and dark matter. Since the increase of volume increases volume energy, this leads rapidly to energy minimum at some flux tube thickness. The reduction of cosmological constant by a phase transition

however leads to a new expansion phase. These jerks would replace smooth cosmic expansion of GRT. The discrete coupling constant evolution predicted by the number theoretical vision could be understood as being induced by that of cosmological constant taking the role of cutoff parameter in QFT picture [L71].

Twistor lift at the level of scattering amplitudes and connection with Veneziano duality

The classical part of twistor lift of TGD is rather well-understood. Concerning the twistorialization at the level of scattering amplitudes the situation is much more difficult conceptually - I already mentioned my limited QFT skills.

1. From the classical picture described above it is clear that one should construct the 8-D twistorial counterpart of theory involving space-time surfaces, string world sheets and their boundaries, plus partonic 2-surfaces and that this should lead to concrete expressions for the scattering amplitudes.

   The light-like boundaries of string world sheets as carriers of fermion numbers would correspond to twistors as they appear in twistor Grassmann approach and define the analog for the massless sector of string theories. The attempts to understand twistorialization have been restricted to this sector.

2. The beautiful basic prediction would be that particles massless in 8-D sense can be massive in 4-D sense. Also the infrared cutoff problematic in twistor approach emerges naturally and reduces basically to the dynamical cosmological constant provided by classical twistor lift.

   One can assign 4-momentum both to the spinor harmonics of the embedding space representing ground states of super-conformal representations and to light-like boundaries of string world sheets at the orbits of partonic 2-surfaces. The two four-momenta should be identical by quantum classical correspondence: this could be seen as a concretization of Equivalence Principle. Also a connection with string model emerges.

3. As far as symmetries are considered, the picture looks rather clear. Ordinary twistor Grassmannian approach boils down to the construction of scattering amplitudes in terms of Yangian invariants for conformal group of M^4. Therefore a generalization of super-symplectic symmetries to their Yangian counterpart seems necessary. These symmetries would be gigantic but how to deduce their implications?

4. The notion of positive Grassmannian is central in the twistor approach to the scattering amplitudes in $calN = 4$ SUSYs. TGD provides a possible generalization and number theoretic interpretation of this notion. TGD generalizes the observation that scattering amplitudes in twistor Grassmann approach correspond to representations for permutations. Since 2-vertex is the only fermionic vertex in TGD, OZI rules for fermions generalizes, and scattering amplitudes are representations for braidings.

   Braid interpretation encourages the conjecture that non-planar diagrams can be reduced to ordinary ones by a procedure analogous to the construction of braid (knot) invariants by gradual un-braiding (un-knotting).

This is however not the only vision about a solution of non-planarity. Quantum criticality provides different view leading to a totally unexpected connection with string models, actually with the Veneziano duality, which was the starting point of dual resonance model in turn leading via dual resonance models to super string models.

1. Quantum criticality in TGD framework means that coupling constant evolution is discrete in the sense that coupling constants are piecewise constant functions of length scale replaced by dynamical cosmological constant. Loop corrections would vanish identically and the recursion formulas for the scattering amplitudes (allowing only planar diagrams) deduced in twistor Grassmann would involve no loop corrections. In particular, cuts would be replaced by sequences of poles mimicking them like sequences of point charge mimic line charges. In momentum discretization this picture follows automatically.

2. This would make sense in finite measurement resolution realized in number theoretical vision by number-theoretic discretization of the space-time surface (cognitive representation) as points with coordinates in the extension of rationals defining the adele [L51]. Similar discretization would take place for momenta. Loops would vanish at the level of discretization but what would happen at the possibly existing continuum limit: does the sequence of poles integrate to cuts? Or is representation as sum of resonances something much deeper?

3. Maybe it is! The basic idea of behind the original Veneziano amplitudes (see `http://tinyurl.com/yyhwvbqb`) was Veneziano duality. This 4-particle amplitude was generalized by Yoshiro Nambu, Holber-Beck Nielsen, and Leonard Susskind to N-particle amplitude (see `http://tinyurl.com/yyvkx7as`) based on string picture, and the resulting model was called dual resonance model. The model was forgotten as QCD emerged. Later came superstring models and led to M-theory. Now it has become clear that something went wrong, and it seems that one must return to the roots. Could the return to the roots mean a careful reconsideration of the dual resonance model?

4. Recall that Veneziano duality (1968) was deduced by assuming that scattering amplitude can be described as sum over s-channel resonances or t-channel Regge exchanges and Veneziano duality stated that hadronic scattering amplitudes have representation as sums over s- or t-channel resonance poles identified as excitations of strings. The sum over exchanges defined by t-channel resonances indeed reduces at larger values of s to Regge form.

   The resonances had zero width, which was not consistent with unitarity. Further, there were no counterparts for the *sum* of s-, t-, and u-channel diagrams with continuous cuts in the kinematical regions encountered in QFT approach. What puts bells ringing is the u-channel diagrams would be non-planar and non-planarity is the problem of twistor Grassmann approach.

5. Veneziano duality is true only for s- and t- channels but not been s- and u-channel. Stringy description makes t-channel and s-channel pictures equivalent. Could it be that in fundamental description u-channels diagrams cannot be distinguished from s-channel diagrams or t-channel diagrams? Could the stringy representation of the scattering diagrams make u-channel twist somehow trivial if handles of string world sheet representing stringy loops in turn representing the analog of non-planarity of Feynman diagrams are absent? The permutation of external momenta for tree diagram in absence of loops in planar representation would be a twist of π in the representation of planar diagram as string world sheet and would not change the topology of the string world sheet and would not involve non-trivial world sheet topology.

   For string world sheets loops would correspond to handles. The presence of handle would give an edge with a loop at the level of 3-surface (self energy correction in QFT). Handles are not allowed if the induced metric for the string world sheet has Minkowskian signature. If the stringy counterparts of loops are absent, also the loops in scattering amplitudes should be absent.

   This argument applies only inside the Minkowskian space-time regions. If string world sheets are present also in Euclidian regions, they might have handles and loop corrections could emerge in this manner. In TGD framework strings (string world sheets) are identified to 1-D edges/folds of 3-surface at which minimal surface property and topological QFT property fails (minimal surfaces as calibrations). Could the interpretation of edge/fold as discontinuity of some partial derivatives exclude loopy edges: perhaps the branching points would be too singular?

A reduction to a sum over s-channel resonances is what the vanishing of loops would suggest. Could the presence of string world sheets make possible the vanishing of continuous cuts even at the continuum limit so that continuum cuts would emerge only in the approximation as the density of resonances is high enough?

The replacement of continuous cut with a sum of *infinitely* narrow resonances is certainly an approximation. Could it be that the stringy representation as a sum of resonances with *finite* width is an essential aspect of quantum physics allowing to get rid of infinities necessarily accompanying loops? Consider now the arguments against this idea.

1. How to get rid of the problems with unitarity caused by the zero width of resonances? Could *finite* resonance widths make unitarity possible? Ordinary twistor Grassmannian approach predicts that the virtual momenta are light-like but complex: obviously, the imaginary part of the energy in rest frame would have interpretation as resonance with.

   In TGD framework this generalizes for 8-D momenta. By quantum-classical correspondence (QCC) the classical Noether charges are equal to the eigenvalues of the fermionic charges in Cartan algebrable (maximal set of mutually commuting observables) and classical TGD indeed predicts complex momenta (Kähler coupling strength is naturally complex). QCC thus supports this proposal.

2. Sum over resonances/exchanges picture is in conflict with QFT picture about scattering of particles. Could *finite* resonance widths due to the complex momenta give rise to the QFT type scattering amplitudes as one develops the amplitudes in Taylor series with respect to the resonance width? Unitarity condition indeed gives the first estimate for the resonance width.

   QFT amplitudes should emerge in an approximation obtained by replacing the discrete set of finite width resonances with a cut as the distance between poles is shorter than the resolution for mass squared.

   In superstring models string tension has single very large value and one cannot obtain QFT type behavior at low energies (for instance, scattering amplitudes in hadronic string model are concentrated in forward direction). TGD however predicts an entire hierarchy of p-adic length scales with varying string tension. The hierarchy of mass scales corresponding roughly to the lengths and thickness of magnetic flux tubes as thickened cosmic strings and characterized by the value of cosmological constant predicted by twistor lift of TGD. Could this give rise to continuous QCT type cuts at the limit when measurement resolution cannot distinguish between resonances?

   The dominating term in the sum over sums of resonances in t-channel gives near forward direction approximately the lowest mass resonance for strings with the smallest string tension. This gives the behavior $1/(t - m_{min}^2)$, where m_{min} corresponds to the longest mass scale involved (the largest space-time sheet involved), approximating the $1/t$-behavior of massless theories. This also brings in IR cutoff, the lack of which is a problem of gauge theories. This should give rise to continuous QFT type cuts at the limit when measurement resolution cannot distinguish between resonances.

1.2 Bird's Eye of View about the Topics of "Genes and Memes: Part II"

The topics of "*Genes and Memes: Part II*" relate to DNA and genome in several ways.

1. The almost exact symmetries of the code table with respect to the first letter lead to the proposal that the genetic code could has evolved from a simpler code involving only two letters and this leads to concrete suggestion about how the genetic code might have evolved as a fusion of two letter code and single letter code. These symmetries were also an essential element of number theoretical models.

2. This model led to a cascade of ideas about quantum control in living matter. Quite generally, magnetic flux tubes would make living matter kind of Indra's net explaining the strange features of gel phase. For instance, the phase transitions changing Planck constant inducing a contraction or lengthening of the flux tubes would explain why bio-molecules are able to find each other extremely selectively in the dense soup of bio-molecules inside cell. The anomalies related to ionic currents find an explanation and a model of nerve pulse and EEG emerges along these lines.

3. It later turned out that the model for dark nucleon consisting of three quarks predicts counterparts of 64 DNAs and RNAs and 20 amino-acids and allows to identify genetic code as a natural mapping of DNA type states to amino-acid type states. The numbers of DNAs

mapped to a given amino-acid are same as for the vertebrate genetic code. This would mean that genetic code would be realized at the level of elementary particle physics and chemical realization would be only one of the many. In fact, the quite recent experimental discoveries suggest that this kind of representation must exist besides the representation based on the temporal patterns of polarization direction discovered by Gariaev.

4. Later several other ideas about genetic code, based on the new physics predicted by TGD, emerged.

1.2.1 The organization of "Genes and Memes: Part II"

The topics of the book are organized in 3 parts.

1. In the first part of the book mostly physics inspired ideas about genetic code are discussed. The basic vision looks natural to anyone living in the computer age: it would be very natural for the genetic code to have several representations. The first chapter describes 3 realizations of genetic code inspired by TGD based new physics. In dark nuclear code codons are represented as 3-proton states but one can also imagine a realization in terms of quark triplets. The protonic realization is supported by the findings of Gerald Pollack.

   The second realization is based on bioharmony defined by the 3-chords formed by 3 dark photons (with large value of $h_{eff} = n \times h_0$) and leads to a model of bio-harmony leading also to the idea of that this music of light serves as correlate for emotions at molecular level. The third chapter discusses the correspondence between ordinary genetic code and dark nuclear code with codons represented as 3-proton states.

   I have also included a chapter written during 2023 about the realization of the genetic code in terms of icosa-tetrahedral tessellation of hyperbolic 3-space playing a key role in TGD. This tessellation has completely unique properties and one can ask whether the genetic code is a completely universal way to realize information processing and could be realized at the level of magnetic bodies also for non-biological systems.

2. In the second part the notion of homonymy of genetic code introduced by Peter Gariaev, horizontal gene transfer, and so called gene tectonics are discussed from the TGD point of view.

3. The third part number theoretic vision of genes is discussed. The notion of adelic physics serves as the cornerstone of the number theoretic vision. There is also a chapter about zero energy ontology, adelic physics, and genes. The TGD view of the role of genes in the evolution of language is also discussed.

1.3 Sources

The eight online books about TGD [K88, K84, K71, K58, K16, K55, K42, K78] and nine online books about TGD inspired theory of consciousness and quantum biology [K81, K15, K62, K14, K38, K45, K47, K77, K80] are warmly recommended for the reader willing to get overall view about what is involved.

My homepage (`http://tinyurl.com/ybv8dt4n`) contains a lot of material about TGD. In particular, a TGD glossary at `http://tinyurl.com/yd6jf3o7`).

I have published articles about TGD and its applications to consciousness and living matter in *Journal of Non-Locality* (`http://tinyurl.com/ycyrxj4o` founded by Lian Sidorov and in *Prespacetime Journal* (`http://tinyurl.com/ycvktjhn`), *Journal of Consciousness Research and Exploration* (`http://tinyurl.com/yba4f672`), and *DNA Decipher Journal* (`http://tinyurl.com/y9z52khg`), all of them founded by Huping Hu. One can find the list about the articles published at `http://tinyurl.com/ybv8dt4n`. I am grateful for these far-sighted people for providing a communication channel, whose importance one cannot overestimate.

1.3.1 PART I: TGD INSPIRED MODELS FOR GENETIC CODE

About dark fermion realizations of the genetic code

TGD inspired quantum biology leads naturally to the idea that several realizations of genetic code exist. Besides the realizations based on temporal patterns of electromagnetic fields I have considered three different new physics realizations of the genetic code based the notions of many-sheeted space-time, magnetic body, and the hierarchy of Planck constants explaining dark matter in TGD framework.

1. The first realization - proposed in the model for DNA as topological quantum computer (tqc) - maps the nucleotides A,G and T,C to dark quarks u,d and their anti-quarks assignable to the ends of magnetic flux tubes representing braid strands and connecting nucleotides to lipids of cell membrane. This requires scaled up variant of QCD made possible the hierarchy of Planck cosntants.

2. Second realization was discovered in the model of dark nuclei as strings of dark baryons. Dark baryons realize codons in terms of quantum entanglement and without decomposition to letters. Dark baryons are strings of 3 quarks connected by two color flux tubes. The neutral states of the dark baryon predicted by the model are in 1-1 correspondence with DNA, RNA, aminoacids. Candidates for the counterparts of tRNA anticodons are also obtained if one accepts that genetic code actually decomposes to 2 steps $64 \to 40 \to 20$ such that there are 40 dark baryon counterparts for tRNA anticodons. The amazing finding is that vertebrate genetic code comes out correctly.

3. The third realization would be a physical realization for the divisor code proposed by Khrennikov and Nilsson. The realization relies on two integers labeling magnetic flux tubes containing dark matter. The dark magnetic flux tubes assignable to DNA codons and amino-acids could be labeled by these integers providing a representation of the genetic code consistent with the divisor code. Also a physical mechanism implying the physical equivalence of the dark baryon code and divisor code can be imagined.

4. Proposals for two further realizations are inspired by the observation that the number of vertices of icosahedron is 12 - the number of notes in 12-note scale - and that of vertices is 20 - the number of amino-acids. This suggests a connection between music and genetic code. The second model allows to "understand" the degeneracies of the genetic code in terms of representations for discrete subgroups if icosahedral group and involves imbedding of 12-note scale as a Hamiltonian cycle to icosahedron.

The basic proposal is that dark baryon counterparts of basic bio-molecules and genetic code were present from beginning and gave rise to pre-biotic life at the magnetic flux tubes so that the evolution of biological life meant the development of translation and transcription mechanisms allowing to transform dark baryon variants of the codons to their chemical variants. These mechanisms would be still at work inside the living cell and allow the living matter to perform genetic engineering. This proposal is consistent with recent findings about large variations of genomes inside organism.

There is a strange experimental finding giving support for this picture. A water solution containing human cells infected by bacteria is sterilized by a filtering procedure and healthy cells are added to the filtrate. Within few weeks the infected cells re-appear. A possible explanation is that dark baryon variant of the bacterial genome realized as nano-sized particles remains in the solution despite the filtering. Another strong support comes from the exclusion zones and fourth phase of water discovered by Pollack.

The codes are discussed from the point of view of DNA as tqc hypothesis and the model for protein folding and bio-catalysis. The basic selection rules of bio-catalysis could be based on the two integers assignable to the dark magnetic flux tubes. Only bio-molecules whose dark magnetic bodies contain a layer characterized by same integers can be connected by dark magnetic flux tubes. The reconnection of the dark magnetic flux tubes selecting the bio-molecules participating the catalytic reaction and the contraction of these flux tubes induced by a phase transition reducing Planck constant and forcing the bio-molecules near to each other would represent basic mechanisms of bio-catalysis.

About the Correspondence of Dark Nuclear Genetic Code and Ordinary Genetic Code

The basic problem in the understanding of the prebiotic evolution is how DNA, RNA, amino-acids and tRNA and perhaps even cell membrane and microtubules . The individual nucleotides and amino-acids emerge without the help of enzymes or ribozymes but the mystery is how their polymers emerged. If the dark variants of these molecules served as templates for their generation one avoids this hen-and-egg problem. The problem how just the biomolecules were picked up from a huge variety of candidates allowed by chemistry could be solved by the resonance condition making possible metabolic energy transfer between biomolecules and dark nuclei.

Simple scaling argument shows that the assumption that ordinary genetic code corresponds to $h_{eff}/h = n = 2^{18}$ and therefore to the p-adic length scale $L(141) \simeq .3$ nm corresponding to the distance between DNA and RNA bases predicts that the scale of dark nuclear excitation energies is .5 eV, the nominal value of metabolic energy quantum. This extends and modifies the vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compre it to PAH world hypothesis.

p-Adic length scale hypothesis and thermodynamical considerations lead to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures. Thermal constraints allow cell membrane of thickness about 5 nm as a realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. Metabolic energy quantum is predicted to be .04 eV, which corresponds to membrane potential. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is below the thermal energy for photons but the notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum.

Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is .02 eV slightly below thermal energy at room temperature: this could relate to the inherent instability of microtubules. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

Geometric Theory of Bio-harmony

For some years ago I developed a model of music harmony. As a surprising side product a model of genetic code predicting correctly the number of codons coding given amino-acid emerged. Since music expresses and creates emotions, one can ask whether genes could have "moods" characterized by these bio-harmonies. The fundamental realization could be in terms of dark photon triplets replacing phonon triplets for ordinary music.

1. The model relies on the geometries of icosahedron and tetrahedron and representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 amino-acids (AAs).

2. One has three basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6, Z_4 or Z_2. For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle.

3. Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA. 4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint.

4. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA. Music expresses and creates emotions and the natural proposal is that these bio-harmonies correlate with moods that would appear already at molecular level. They could be realized in terms of dark photon triplets realized in terms of light and perhaps even music (living matter is full of piezo-electrets). In fact, also the emotions generated by other art forms could be realized using music of dark light.

The model of music harmony is separate from the model of genetic code based on dark proton triplets and one of the challenges has been to demonstrate that they are equivalent. This inspires several questions.

1. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton's cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied.

   (a) There is a purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20?

   (b) There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies.

2. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could AAs couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA? Could coding by the sum of frequencies appear in the coupling of tRNA with mRNA by codewords and coding by separate frequencies to the letterwise coupling of DNA and RNA nucleotides to DNA during replication and transcription?

3. What about tRNA. Could tRNA correspond to pairs of harmonies with 20+20+444 codons? What about single 20+4=24 codon representation as kind of pre-tRNA?

4. What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetric arguments fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible so that it would be possible to listen what DNA sequences sounds in given mood characterized by the harmony.

5. What disharmony could mean? A possible answer comes from 6 Hamiltonian cycles having no symmetries. These disharmonies could express "negative" emotions.

The Realization of Genetic Code in Terms of Dark Nucleon and Dark Photon Triplets

I have worked for more than 10 years with a proposal for two kinds of realizations of the genetic code. The first realization, bioharmony model, represents genetics as light 3-chords consisting of dark photons. The second realization is in terms of dark proton or nucleon triplets forming closed or open strings. I have considered several variants of both realizations but the details have remained poorly understood and I have spent a considerable time on wrong tracks.

It however seems that the dust is finally settling (I am writing this in the beginning of 2022). One can see the dark nucleon model as a generalization of the quark model of nucleon and Δ baryons obtained by replacing u and d quarks with dark nucleons. Galois confinement solves the statistics problem. The nucleons are connected by pionic flux tubes to form a closed string-like entity. The dark variants of DNA, RNA, tRNA, and amino-acids (AAs) follow as a prediction. In the sequel, the notation DDNA, DRNA, DtRNA, DAA will be used for the dark variants of the

basic information molecules. One can also understand the small symmetry breaking associated with the genetic code.

A concrete realization of bioharmony in terms of the dark nucleon model for codons emerges. The small symmetry breaking effects - the members of doublet that should code for the same amino acid (or act as stop codons), code for different amino acid (or amino acid and stop), are understood. Also the differences between vertebrate and bacterial codes are understood.

An Overall View about Models of Genetic Code and Bio-harmony

During last years kind of brain storming period has occurred in the TGD inspired models of bio-harmony and genetic code. A lot of ideas, some of them doomed to be short lived, have emerged, and it seems that now it its time for a thorough cleanup and integration with the general ideas of TGD inspired quantum biology.

TGD leads to 3 basic realizations of the genetic code. One can also consider 3 realization also for bio-harmony. The question is which of them is the realistic one or whether several options can be considered. In this article these ideas are discussed critically and open problems are summarized.

The three genetic codes correspond to a fundamental realization in terms of dark proton sequences (dark nuclei) with 3-proton representing codon. Second realization is the chemical realization and the third realization is in terms of dark photon 3-chords mediating the interaction between various realizations. Frequency resonance is very natural interaction between dark levels and energy resonance between dark level and chemical level. The possibility to modify the value of h_{eff} for flux tube makes possible to have for given codon single resonance energy.

The homonymy of the genetic codes at various levels is discussed. At the dark level the fact that icosahedral harmonies can have common 3-chords implies the first homonymy. The basic difficulty of Pythagorean scale realized in terms of quint cycle realized already by Pythagoras becomes the solution of this problem. The well-known homonymies in RNA-tRNA correspondence and even in RNA-AA correspondence can be understood in the model in which dark photon 3-chords mediate the interactions.

Also questions related to the relationship of bio-harmony with ordinary genetic code are considered. Why 3 copies of icosahedral harmony and only one copy of tetrahedral harmony? A special triangle assignable to the 3 copies of icosahedron and tetrahdron is analogous to a singular point of covering: do these 4 triangles correspond to exceptional codons breaking symmetries? How do the dissonant 3-chords present in some icosahedral harmonies relate to stop codons? How do the codons of bio-harmony and ordinary codons relate and is this relation consistent with what is known about transcription and translation?

About honeycombs of hyperbolic 3-space and their relation to the genetic code

$M^8 - H$ duality and the realization of holography in M^8 strongly suggests the importance of tessellations of H^3 (analogous to lattices of E^3) in the TGD based physics. These tessellations form a scale hierarchy and can thus appear in all scales. The hierarchy of effective Planck constants labelling dark matter as phases of ordinary matter indeed predicts quantum coherence in arbitrarily long scales and gravitational quantum coherence corresponds to the largest scales of quantum coherence among basic interactions.

There are 5 Platonic tessellations known as honeycombs: the 4 regular honeycombs correspond to cubic, icosahedral, and 2 dodecahedral honeycombs and a quasiregular icosa-tetrahedral honeycomb having tetrahedra, octahedra and icosahedra as cells. The icosa-tetrahedral honeycomb might define a universal realization of the genetic code as an induced structure so that the genetic code would be much more than a biochemical accident. These 5 Platonic honeycombs could occur also in astrophysical scales as gravitational tessellations. The recent discovery of gravitational hum might have an explanation as gravitational diffraction in this kind of a honeycomb.

In this chapter the properties of hyperbolic honeycombs are considered in detail and also a detailed view about the realization of DNA double strand in terms of the icosa-tetrahedral honeycomb is considered. The emerging model is surprisingly quantitative. Also a connection with the notion of memetic code and the realization of memetic codons in terms of 21 DNA codons are suggested by the model.

1.3.2 PART II: SOME APPLICATIONS

Homonymy of the Genetic Code from TGD Point of View

Peter Gariaev and colleagues have applied the linguistic notions of synonymy and homonymy to genetic code. Also the notion of syhomy fusing these concepts is introduced. Homonymy is visible in mRNa-tRNA pairing and induced by the 1-to-many pairing of the third mRNA nucleotide with tRNA nucleotide. The homonymy in mRNA-AA (AA for amino-acid) pairing is also present albeit rare.

The codons for the standard code can be divided to two classes. For 32 codons the first two letters fix AA completely. For the remaining 32 codons this is not the case. There is however almost unbroken symmetry in that U and C *resp.* A and G code for the same AA. The breaking of this symmetry is minimal appearing only for 3 4-columns of the code table and present for A-G only. The deviations from the standard code as a rule break A-G or T-C symmetry or re-establish it.

The notion of homonymy is highly interesting from TGD point of view. TGD leads to two basic proposals for non-chemical realization of genetic code predicting the numbers of DNA codons coding for given AA rather successfully. The first proposal relies on TGD based view about dark matter as $h_{eff}/h = n$ phases of ordinary matter and identifies counterparts of DNA, RNA, tNRA, and AAs as entangled dark proton triplets.

Second proposal emerged from the model of music-harmony based on fusion of icosahedral and tetrahedral geometries. Codons are represented as photon triplets (dark or ordinary) defining the allowed 3-chords of given harmony defined by Hamilton cycle at icosahedron extended to Hamilton cycle to the fusion of icosahedron with tetrahedron along common face. Photon triplets give rise to resonant coupling giving rise to physical pairing of biomolecule and its dark counterpart. Remarkably, there are 3 different realizations of tRNA in terms of 3-chords. There is large number of bio-harmonies corresponding to Hamiltonian cycles. Since music expresses and creates emotions, the proposal is that a realization of emotions at molecular level adding additional degrees of freedom not visible at the level of chemistry is in question. This might give rise to a context dependence of the code.

The proposal is that genetic code at dark level extends to a sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA $\rightarrow$ DAA of horizontal pairings analogous to projections is fundamental one. Codon-codon pairings are realized via dark photon triplet resonance and mRNA-AA pairing by resonant coupling to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of 3-chord frequencies: the codons coding same AA would have frequencies f_{XYZ} differing only by a multiple of octave. One might perhaps say that AA sequence defines melody and mRNA sequence the accompaniment.

There is context dependence and homonymies already in DmRNA-DtRNA pairing and due the fact that DtRNA corresponds to a 2-harmony which is sub-harmony of 3-harmony and can be chosen in 3 different manners. The vertical pairings DDNA $\rightarrow$ DNA, DmRNA $\rightarrow$ mRNA, etc. also mediated by frequency couplings induce ordinary genetic code and horizontal pairings in DNA $\rightarrow$ mRNA $\rightarrow$ tRNA $\rightarrow$ AA. DAA $\rightarrow$ AA pairing dictates mRNA $\rightarrow$ AA pairing and mRNA $\rightarrow$ tRNA homonymy does not matter and actually makes the translation safer by increasing the number of tRNAs performing the same task.

The rather rare homonymies in DNA-AA pairing can be understood as accidental degeneracies. AA couples resonantly to the sum $f_{XYZ} = f_1 + f_2 + f_2$ of frequencies associated with codon XYZ and it can occur that the sum frequencies can be identical for two codons.

Horizontal Gene Transfer by Remote Replication?

This chapter was inspired by the discovery that a horizontal gene transfer (HGT) between eukaryotes is possible. The belief has been that HGT is possible only from prokaryotes to prokaryotes or eukaryotes. The basic obstacles are that the host DNA is within the cell nucleus and that DNA is tightly bound to chromosomes. The transfer should also occur to germ cells in order to have a lasting effect.

The case considered is HGT of antifreezing gene (AFG) from herring to smelt, which could have occurred during simultaneous spawning of herring and smelt in the same area. The AFT of herring associated with a transposon could have somehow attached to the sperm cell of the smelt

and carried by it to the egg of the smelt. Vector carrying AFT to the sperm cell of smelt is needed and there are only guesses about what it might be.

That HGT however occurs, justifies a heretical question. Could it be only the genetic information, which is transferred and used to construct DNA in the host as a kind of remote replication analogous to quantum transportation? The findings of Gariaev and Montagnier indeed suggest remote replication and TGD provides a new physics model for it.

Gene tectonics and TGD

"Gene tectonics" represents a remarkable step of progress in genetics. The study of the evolution of chromosomes involving few basic mechanisms such as mixing of genes within chromosome, fusion of chromosomes along their ends, the insertion of chromosome inside chromosome, and fusion followed by permutations of genes within the composite chromosome allows to study the evolution at the level of entire genome and to understand what the differentiation of lineages and species could correspond at the level of genome. It has been found that the mixing of genes occurs often and does not have drastic effects and one can speak of chromosome conservation whereas the mutations involving several chromosomes are rare.

These findings represent a challenge for the TGD point of view of genetics and together with the recent progress in the number theoretical vision about physics, inspire fresh questions and ideas about genes and chromosomes. In particular, the question of how genes could code for biological functions reduces to the level of space-time dynamics at the number-theoretical level.

In the number-theoretical vision about TGD, biological functions would correspond to polynomials and genes would correspond to composition of polynomials assignable to genes. In zero energy ontology (ZEO), a given polynomial would define a space-time region as an analog of deterministic classical computation and quantum computation would involve their superposition.

1.3.3 PART III: NUMBER THEORETICAL VISION AND GENES

Philosophy of Adelic Physics

The p-adic aspects of Topological Geometrodynamics (TGD) will be discussed. Introduction gives a short summary about classical and quantum TGD. This is needed since the p-adic ideas are inspired by TGD based view about physics.

p-Adic mass calculations relying on p-adic generalization of thermodynamics and super-symplectic and super-conformal symmetries are summarized. Number theoretical existence constrains lead to highly non-trivial and successful physical predictions. The notion of canonical identification mapping p-adic mass squared to real mass squared emerges, and is expected to be a key player of adelic physics allowing to map various invariants from p-adics to reals and vice versa.

A view about p-adicization and adelization of real number based physics is proposed. The proposal is a fusion of real physics and various p-adic physics to single coherent whole achieved by a generalization of number concept by fusing reals and extensions of p-adic numbers induced by given extension of rationals to a larger structure and having the extension of rationals as their intersection.

The existence of p-adic variants of definite integral, Fourier analysis, Hilbert space, and Riemann geometry is far from obvious and various constraints lead to the idea of number theoretic universality (NTU) and finite measurement resolution realized in terms of number theory. An attractive manner to overcome the problems in case of symmetric spaces relies on the replacement of angle variables and their hyperbolic analogs with their exponentials identified as roots of unity and roots of e existing in finite-dimensional algebraic extension of p-adic numbers. Only group invariants - typically squares of distances and norms - are mapped by canonical identification from p-adic to real realm and various phases are mapped to themselves as number theoretically universal entities.

Also the understanding of the correspondence between real and p-adic physics at various levels - space-time level, embedding space level, and level of "world of classical worlds" (WCW) - is a challenge. The gigantic isometry group of WCW and the maximal isometry group of embedding space give hopes about a resolution of the problems. Strong form of holography (SH) allows a non-local correspondence between real and p-adic space-time surfaces induced by algebraic continuation from common string world sheets and partonic 2-surfaces. Also local correspondence seems

intuitively plausible and is based on number theoretic discretization as intersection of real and p-adic surfaces providing automatically finite "cognitive" resolution. he existence p-adic variants of Kähler geometry of WCW is a challenge, and NTU might allow to realize it.

I will also sum up the role of p-adic physics in TGD inspired theory of consciousness. Negentropic entanglement (NE) characterized by number theoretical entanglement negentropy (NEN) plays a key role. Negentropy Maximization Principle (NMP) forces the generation of NE. The interpretation is in terms of evolution as increase of negentropy resources.

ZEO, Adelic Physics, and Genes

Zero energy ontology (ZEO) solving the basic problem of quantum measurement theory has become a cornerstone of quantum TGD, and together with the vision about physics as infinite-D geometry of the "world of classical worlds" (WCW) and number theoretical vision about physics as adelic physics fusing the real number based physics of sensory experience and the p-adics physics of cognition and intentionality dictates to high degree the key structures of TGD.

The basic prediction of ZEO is that "big" (ordinary) state function reduction (BSFR) changes the arrow of time meaning "death" and "reincarnation" with opposite arrow of time. In "small" state function identifiable as TGD counterparts of "weak" measurements reduction this does not occur. This leads to a new view about self-organization in which time reversal making possible dissipation with non-standard arrow of time makes possible for a system to extract (for instance thermal) energy from the environment: this allows to circumvent the heat death predicted by standard thermodynamics.

In this chapter the implications of the ZEO for the understanding of genetic code and DNA are considered.

1. The relation between zero energy ontology (ZEO) based quantum measurement theory and adelic vision is clarified. One can generalize classical cognitive representations as number theoretical discretizations of space-time surfaces in the extension of rationals considered to their quantum counterparts as wave functions in the Galois group of the extension and introduce also fermions as spinors in the group algebra of Galois group. The strongest option is purely number theoretical representations of fermionic Fock spaces in terms of spinors in this group algebra. Presumably however M^8 spinors are required as a building brick and have interpretation in terms of octonion structure.

2. Adelic physics, $M^8 - H$ duality, and zero energy ontology lead (ZEO) to a proposal that the dynamics involved with "small" state function reductions (SSFRs) as counterparts of weak measurements could be basically number theoretical dynamics with SSFRs identified as reduction cascades leading to completely un-entangled state in the space of wave functions in Galois group of extension of rationals identifiable as wave functions in the space of cognitive representations. As a side product a prime factorization of the order of Galois group is obtained.

3. The question what basic processes of biology could have time time reversals is discussed. Here the basic restriction comes from CPT theorem and chiral selection in living matter and it turns out that very restricted set of basic bio-processes can have time reversal catalyzed by enzymes.

   The time reversals of the basic processes like transcription and replication turn out to be possible only for the conjugate (passive) strand - this is basically due to the CPT theorem and chiral selection: enzymes can catalyze processes but not their time reversals. The picture involving time reversal is applied to understand recombination which is a poorly understood step of meiosis.

   TGD predicts that consciousness is possible even at the level of DNA. Could also DNA have a longitudinal electric field with direction correlating with the arrow of time of DNA at the (magnetic body) MB of DNA. Could there be a switch changing the direction of this electric field? This inspires a model for the DNA as ferro-electret based on the properties of the negatively charged sticky ends of chromosome and dark DNA codons as proton triplets along a magnetic flux tube parallel to DNA strand.

TGD View about Language

Human languages differ dramatically from their analogos for animals. Animal languages consist mainly of simple signals, warnings and threats for instance. The emotional expression dominates. There seems to be no grammar. Birds can have repertoire of different song patterns and monkeys have gesture language. There is a huge variety of human languages. One can also regard music as a kind language expressing emotions and creating them. Also pictures define linguistic representations. Children and animals learn speech by mimicry and the grammar and syntax without conscious efforts. Human language is also special in that it involves conceptualization, metaphors, and analogies representing abstract concepts in terms of objects and actions of the external world.

One might understand the semantic aspect of language in terms of association and conditioning. Language acquisition involves showing the object and saying the word describing it. This suggests conditioning and association so that a mere word generates an imagined percept of the object. Conditioning and formation of associations is a very general form of learning assumed to relate to the increase of synaptic strengths leading to a generation of association pathways. In computer science pattern recognition and completion models it mathematically.

Amazingly, only a few point mutations for relatively few genes seems so have led to human languages and transformed biological evolution to cultural evolution? What happened for these genes? In the biochemistry framework it is difficult to imagine an answer to this question. Here TGD could come in rescue.

Number theoretic physics is part of quantum TGD and essential for understanding evolution as an increase of algebraic complexity. Evolutionary hierarchies would correspond to hierarchies of algebraic extensions of rationals. The dimension n of extension defines effective Planck constant $h_{eff}/h_0 = n$. The larger the dimension, the larger the scale of quantum coherence at corresponding layer of magnetic body (MB) associated with the system: n would be analogous to IQ. One can assign a value of h_{eff} characterizing the evolutionary level also to genes. The genes with larger h_{eff} would serve as control genes and the increase of h_{eff} would mean an evolutionary step. Perhaps a dramatic increase of h_{eff} occurred to FOXP2 and some other genes as human language emerged.

Part I

TGD INSPIRED MODELS FOR GENETIC CODE

Chapter 2

About dark fermion realizations of the genetic code

2.1 Introduction

This chapter represents an attempt to integrate three different models of genetic code [K4, K85] with each other and with DNA as topological quantum computer (TQC) hypothesis [K4] as well as the general ideas behind the model of protein folding and bio-catalysis [K8]. The considerations lead to a modification of the earlier model of protein folding.

2.1.1 The Notions Of Dark Matter And Magnetic Body

The generalization of the embedding space to a book like structure (see Appendix) with pages labeled by two non-negative integers (n_a, n_b) characterizing the singular coverings of M^4 (or actually of causal diamond of M^4 defined as intersection of future and past directed light-cones) and of CP_2 together with pages representing singular coverings and represented similarly by a pair of integers (or equivalently inverses of non-negative integers) provides a possible mathematical realization of dark matter hierarchy. Dark matter is interpreted as phases of ordinary matter at various pages of the book like structure. The pages of the book are partially characterized by a hierarchy of Planck constants. The notion of darkness is only a relative concept in this picture. The phase having $(n_a, n_b) = (1, 1)$ can be identified as ordinary visible matter.

Magnetic body is second key concept in TGD based model of quantum biology. Magnetic body has onion like structure with layers characterized by a spectrum of values of (n_a, n_b) identifiable as orders of the cyclic groups Z_{n_a} *resp.* Z_{n_b} acting in the fiber of singular covering space or factor space assignable M^4 *resp.* CP_2 degrees of freedom. Also the extensions of these groups obtained by adding reflection can be considered. Phase transitions changing the values of (n_a, n_b) and thus also the length of magnetic tubes correspond to a tunnelling between two pages of the book and in general change the value of Planck constant. The basic selection rule is familiar from the sub-group rule for phase transitions and means that either n_{a_1} (n_{b_1}) divides n_{a_2} (n_{b_2}) or vice versa. These phase transitions are in a key role in TGD inspired model of bio-catalysis.

The reconnections of flux tubes represents second basic mechanism of bio-catalysis. Together these two mechanisms could be at least partially responsible for the amazing aspects of bio-catalysis such as extreme selectivity and the ability of distant bio-molecules to find each other in the dense soup of bio-molecules.

2.1.2 Realizations Of Genetic Code

I have proposed several realization of the genetic code during past 15 years. There are three realizations which are especially interesting physically.

1. The first realization is based on the map of G,C *resp.* A,T codons to quarks u,d *resp.* their anti-quarks. This code was proposed to realize DNA as TQC with braid strands represented as flux tubes connecting nucleotides with the lipids of cell membrane [K4]. The quantum

states at the ends of braid strands -would be represented by many particle states of quarks and anti-quarks in this model and entanglement of quarks and anti-quarks would be essential for TQC and affected by the braiding induced by the 2-D liquid flow of the lipids.

2. Second realization is based on the observation that the neutral states of dark baryons consisting of u and d quarks in nuclear string model can be regarded as counterparts of DNA, RNA, amino-acids and perhaps even tRNA [K41, K85]. Nuclear strings would represent DNA and other polymers at the level of dark matter.

3. Third realization is based on the interpretation of divisor code discovered by Khrennikov and Nilsson [A36] in terms of the sub-group rule for phase transitions [K85]. Second realization and this one are in 1-1 correspondence under certain prerequisites. The magnetic- interaction energy of the dark baryon depends on the projections of the total quark spin and total color flux tube spin to the direction of the magnetic field labeling both DNA codons and amino-acids. This interaction energy is a function of (n_a, n_b) and minimized for some pair (n_a, n_b). This gives 1-1 correspondence the states of dark baryon and page of the book and since the page numbering allows to interpret physically the divisor code, one might hope that this correspondence is consistent with both codes.

4. Proposals for two further realizations are inspired by the observation that the number of vertices of icosahedron is 12 - the number of notes in 12-note scale - and that of vertices is 20 - the number of amino-acids. This suggests a connection between music and genetic code. The second model allows to "understand" the degeneracies of the genetic code in terms of representations for discrete subgroups if icosahedral group and involves imbedding of 12-note scale as a Hamiltonian cycle to icosahedron.

5. I have also proposed number theory based thermodynamical models for the genetic code [K21, K89] discussed also by others [A25, A18]. and a suitable modification of this kind of model could allow to model the thermodynamics based on magnetic interaction energy.

I have also suggested realizations of the genetic code in terms of electromagnetic field patterns and computer metaphor encourages to think that standard genetic code is just one possible realization among many.

2.1.3 Questions

These ideas raise a bundle of questions.

1. There are severa candidates for the realization of the genetic code. Are all these realizations needed? Are the realizations based on dark baryons and divisor code equivalent?

2. The realization based on correspondence with DNA nucleotides and quarks and anti-quarks works nicely for DNA as TQC hypothesis. Can one consider also a realization of DNA as TQC in terms of dark baryons?

3. How dark baryon realization relates with ordinary chemical realizations and to evolution of pre-biotic life forms? Could it be that the life based on nuclear string genetic code gradually moved from the dark pages of the book to the page containing visible matter as chemical realizations of the analogs of DNA, RNA, amino-acids and even tRNA gradually developed? Note that the process bears formal similarity to the transition of life from sea to land. Is it possible to transcribe the counterparts of DNA,RNA, and amino-acids to their real counterparts? Is pre-biotic era continuing still inside dark magnetic flux tubes and could it make possible genetic engineering?

The appendix of the book gives a summary about basic concepts of TGD with illustrations. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L10].

2.2 A Vision About Evolution And Codes

The fact is that the only thing we really know about dark matter is that 95 percent of matter is dark (matter or dark matter and energy depending on theoretical framework used). Therefore the ideas about dark baryon code are necessarily speculative. One can however base the speculations to some vision in order achieve internal consistency if nothing else.

2.2.1 Basic Insights

The idea that biological life was preceded by dark life with subset for the counterparts of DNA, RNA, amino-acids and tRNA dominating the scene looks like a plausible starting point. Second attractive assumption is that this era still continues at magnetic bodies and makes possible genetic engineering based on experimentation and transcription of at least dark baryon analog of DNA to ordinary DNA.

The transformations for RNA and amino-acids to dark matter and vice versa seems necessary if the experimentation with new variants of genes is to be carried out unless one is satisfied with the testing of the modified genes in a small scale. Reconnection and $\hbar$ changing phase transitions of flux tubes would serve as the basic mechanism of bio-catalysis in TGD Universe. One can imagine two basic mechanisms involving reconnection of flux tube and transforming dark nuclear strings to polymers (see **Figs.** `http://tgdtheory.fi/appfigures/manysheetd.jpg`, `http://tgdtheory.fi/appfigures/field.jpg`, `http://tgdtheory.fi/appfigures/fluxquant.jpg`, `http://tgdtheory.fi/appfigures/reconnect1.jpg`, `http://tgdtheory.fi/appfigures/reconnect2.jpg`, `http://tgdtheory.fi/appfigures/fluxtubedynamics.jpg`, which can be also found in the appendix of this book).

1. Given bio-molecule could be accompanied by a closed flux tube of the magnetic field containing dark matter and extending to some page of the book characterized by two numbers x_a *resp.* x_b, which are integers for singular coverings of M^4 *resp.* CP_2 and inverse integers for singular factor spaces of M^4 *resp.* CP_2. For bio-molecules for which x_a and x_b are identical these closed loops could reconnect to form a pair of flux tubes connecting bio-molecules (see **Fig. ??**). A phase transition reducing Planck constant would bring the molecules close to each other. This would provide a general recognition mechanism central in the reactions of bio-molecules.

2. These flux tube connections between two molecules could also involve only single *permanently* existing flux tube (this is a rather strong prediction which might be used to kill this option). In this case the reconnection for the flux tubes connecting molecules X and Y *resp.* U and V would give rise to connections $X - U$ and $Y - V$ for instance. The general recipe for achieving these transformations is based on the assumption that molecule and its dark conjugate connected by flux tubes can be present and that reconnection process given exchange of particles describable in terms of diagrams analogous to stringy diagrams is possible. This means that pairings $X - dY$ and $U - dV$ can be transformed to pairings $X - U$ and $dY - dV$ and $X - dV$ and $U - dY$ (see **Fig. ??**). This process would extend the variety of possible transcription like processes to allow also transcription of dark variants of DNA, RNA and amino-acids to visible ones and vice versa.

Genetic engineering would be possible by the fact that the dark nuclear string variants of genes could be easily transferred around the biological body unlike modified DNAs. In particular, modified dark genes could be transferred to the nuclei of germ cells. Essentially the TGD inspired mechanism of homeopathy would be in question [K41].

There is analogy with the evolution of language. Both DNA codons and representation of nucleotides in terms of quarks and anti quarks (perhaps accompanying the intronic portions of DNA) mean a representation of codons as three-letter sequences. Since dark baryons represent genetic codons as indecomposable structures in terms of quantum entanglement, the emergence of both representations would be analogous to the emergence of written language when spoken words forming indecomposable units decomposed into letters having no meaning as such. The findings that there are major differences between the genomes of blood and tissue cells [I44] and that the

genetic variation due to jumping genes is highest in brain and germ cells [I22] is consistent with the view about dark evolution modifying at least intron portion of the genome.

RNA world [I59, I85, I27] represents a dominating vision about pre-biotic evolution. The idea is RNA era was first and that somehow DNA and amino-acids emerged in some later stage. It has not been possible yet to reproduce replicating RNA sequences in laboratory so that there is still room for alternatives. Dark baryon realization of the genetic code predicts that the analogs of DNA, RNA, amino-acids and even tRNA anticodons might have been there all the time. This might apply also to the primitive chemical representations of DNA, RNA, tRNA, and amino-acids. It is of course possible that the chemical representation of RNA evolved first. This era could still continue inside cell nuclei and make possible genetic engineering as experimentation with dark baryon genes producing amino-acids and RNA and then possibly transforming the resulting RNAs to DNA by reverse transcription. Also a direct transcription to DNA could take place.

2.2.2 The Simplest Scenario

The evolution could might have proceed as a gradual transition of life from dark pages to the visible page allowing chemical realization of the genetic code.

1. Dark matter era would replace RNA and already this era involved at least the dark counterparts of DNA, RNA, amino-acids and perhaps even $64-40 \to 40-20$ two-step realization of the genetic code with tRNA anticodons representing a particular example of 40-D realization intermediate between DNA and amino-acids. Maximum number of different tRNA codons is indeed around 40 [I20]. Without further assumptions the pairing of all dark DNA and RNA codons coding for the same amino-acid was possible. The situation changes if one assumes 1-1 correspondence between dark baryon realization and the realization of the divisor code in terms of dark magnetic flux tubes to be discussed later. This era could still continue at magnetic bodies and make genetic experimentation and genetic engineering possible.

2. Dark nuclear strings became gradually associated with the magnetic bodies of DNA, RNA and amino-acids and a machinery transforming DNA to mRNA to tRNA to amino-acids developed. Flux tube connections could have formed between nuclear strings and the magnetic bodies of the bio-molecules. A stronger condition is that dark nuclear strings became part of the magnetic bodies of DNA, RNA and amino-acids forming helical structures running parallel to the corresponding molecular structures. For this option base pairing could have made the dark counterparts of DNA-DNA and DNA-mRNA pairings unique (also the equivalence of dark baryon and divisor codes could have guaranteed this). mRNA-tRNA base is pairing is not unique but wobble base pairing made possible for all mRNA codons except stopping codons to pair to tRNA anticodons. Whether RNA appeared first or whether the counterparts of the basic bio-molecules were present from the beginning remains an open question.

3. Topological quantum computation based on the map of A, G *resp.* T, C to quarks *resp.* anti-quarks emerged later as something analogous to written language and would naturally correspond to the intron portions of genome for which the decomposition into triplets is not essential and the nucleotide composition is not too essential since it is braiding which defines topological quantum computation (the 4 different colors of the braid strands are not necessary).

2.2.3 How Dark Baryon Code Could Be Involved With Transcription And Translation Mechanisms?

In the following it is assumed that one can talk about magnetic flux tubes containing dark nucleon strings as independent objects and therefore not identified as a helical string parallel to DNA, RNA or amino-acid sequence as one might also imagine. Therefore it is not necessary to assume that dark baryons have the same size scale as corresponding molecular units. One can also assume that one can connect flux tubes associated with nuclear strings by magnetic flux tubes.

Genetic engineering makes sense if the transcription of nuclear string counterparts of DNA, RNA, tRNA, and amino-acids to their chemical counterparts is possible.

1. One can classify flux tube connections by introducing the notion of order of flux tube connection expected to characterize the probability of flux tube connection. First order means a flux tube entirely in given page of the book like structure defined by the generalized embedding space, second order to a flux tube between two different pages, third order a flux tube traversing through an intermediate page between two pages, and so on. Reconnection of the magnetic flux tubes provides a general mechanism for this transformations and as already explained there are two general recipes for the formation of reconnection.

2. **Option I** - the simpler one - involves a reconnection of the closed flux tubes associated with the molecules to be paired. This mechanism would make it possible for a bio-molecule X to catch a partner Y if the corresponding closed flux tubes reside at same page of the book s(see **Fig. ??**). This mechanism provides a straightforward description of replication, transcription and translation as well as their generalizations allowing to transform dark nuclear strings to their molecular counterparts and vice.

3. **Option II** is more complex (see **Fig. ??**) and can be formulated in terms of two stringy diagrams with two strings connecting objects X and Y *resp.* U and V at their ends touch and transform to strings with X and V *resp.* U and V or X and U *resp.* Y and V at their ends. The process can be visualized as exchange of half strings and stringy diagrams represent various processes. Denote by dX the dark matter counterpart of X which can be DNA, RNA, or amino-acid and assume that all combinations obtained by the reconnection process are possible so that one would has pairings $X-Y, X-dY, dX-Y$, and $dX-dY$ defined by flux tube connections. All these variants present and $X-Y$ and $dX-dY$ can be first order connections whereas $X-dY$ and $dX-Y$ are second or higher order connections. This option requires permanent flux tube connections.

4. These are the simplest options. One can wonder whether the hydrogen bonds associated with base pairs correspond to a pair $(A-T)$ or triplet $(G-C)$ of contracted flux tubes. It is of course possible to have more than two flux tubes. If the third hydrogen bond for $G-C$ corresponds to a flux tube a permanent flux tube connection between G and C nucleotides would exist.

One could think that only few bio-molecules can have flux tubes at the page at which the particular dark nuclear string typically resides (minimization of the magnetic interaction energy could fix the most probable candidate for this page and imply connection between dark baryon code and divisor code) and that bio-molecules are gradually selected from these particular molecules. The process would be still in progress. Vertebrate nuclear code would be however identical with the dark baryon code. For tRNA anti-codons the situation would be far from ideal.

Replication

In the following "$\circ$" means one or two bonds depending on whether Option I or II is in question.

Option I: Let $(X\circ Y)$ denote DNA double helix with two flux tubes connecting them and U a V DNA nucleotides. The opening of DNA double strand means reconnection of these flux tubes so that two closed loops are obtained. These flux tubes transform to dark flux tubes and reconnect with dark flux tubes associated with U and V respectively and a phase transition reducing $\hbar$ brings U and V near sequences X and Y where they combine with already existing new sequence.

Option II: Let $(X\circ Y)$ denote DNA double helix and $(U\circ V)$ to a pair of codon and anticodon assumed to be connected by a long flux tube (this should be a testable prediction). Replication of DNA would correspond to $(X\circ Y)+(U\circ V)\rightarrow X\circ U\rightarrow Y\circ V$ with reconnection taking place for the flux tubes.

With the same conventions the transcription of dark DNA to ordinary DNA and vice versa would correspond to a process $dX\circ dY+U+V\rightarrow dX\circ U\rightarrow V\circ dY$ giving rise to ordinary-dark DNA double strand. This process would be followed by $(dX\circ U)+(dV\circ Y)\rightarrow dX\circ dV\rightarrow U\circ Y$ proceeding like DNA replication.

$DNA \to mRNA$ transcription

Let $X \circ Y$ denote DNA double helix in the sequel. For Option I the transcription process would occur in straightforward manner by the transformation of double connection between X and Y to loops and the reconnection of loop associated with Y with that assignable to $mRNA$ codon followed by $\hbar$ reducing phase transition leading to a generation of DNA and mRNA sequences with nucleotides connected by flux tube pairs. The third step would be reconnection transforming double flux tube bonds between DNA and mRNA nucleotides to loops.

Consider next Option II:

1. Let $U \circ V$ denote mRNA-cmRNA that is pair of mRNA codon and its conjugate assumed to be connected by a long flux tube. Ordinary transcription $DNA \to mRNA$ could correspond to the $(X \circ Y) + (U \circ V) \to X \circ U \to Y \circ V$ followed by its reversal but mRNAs arranged to a sequence. Note that every mRNA would have long flux tube connection with the conjugate mRNA.

2. Let $U \circ V$ could denote mRNA-dcmRNA. The same process would give mRNA sequence with each codon connected by a long flux tube to dcmRNA codon.

3. For a third realization $U - V$ would denote the pair $mRNA - dtRNA$. The same process as above would give mRNA sequence with each mRNA codon connected by a long flux tube to $dtRNA$ anticodon.

   This process has also variants allowing to assign mRNA to dDNA and to DNA dmRNA.

Translation as a sequence of reconnections

For Option I the description of translation should be obvious on basis of previous examples. For Option II translation could be realized as a sequence of reconnections in several ways. The basic idea is that the reconnections and their reversals transform the tRNA_1-AA pairs with $tRNA_1$ denotes $tRNA$ without amino-acid AA to a sequence of them but $tRNA_1$ connected to amino-acid by a long flux tube. In the decay of the amino-acid this long tRNA would reduce to ordinary tRNA: this serves as a killer prediction.

For instance, let $X - Y = mRNA - dmRNA$ mRNA sequence with dark mRNA codons connected to mRNA codons and let $U - V = tRNA_1 - AA$ denote tRNA. Reconnection would allow to arrange tRNAs to sequence of "long" tRNAs while keeping $X - Y$ as such. One could also replace Y by $dtRNA$. Obviously the process has several variants. When amino-acid sequence decays ordinary "short" tRNAs are formed again. Also the translation of dark mRNA to ordinary amino-acid sequence with long flux tubes to either dark tRNA or ordinary tRNA.

2.3 DNA As Topological Quantum Computer: Realization Of The Genetic Code In Terms Of Quarks And Anti-Quarks

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Large values of Planck constant allow to imagine all kinds of quantum computations [B1, B19, B5, B17]. What makes topological quantum computation (TQC) [B10, B16, B13, B2], [C2] so attractive is that the computational operations are very robust and there are hopes that external perturbations do not spoil the quantum coherence in this case. The basic problem is how to create, detect, and control the dark matter with large $\hbar$. The natural looking strategy would be to assume that living matter, say a system consisting of DNA and cell membranes, performs TQC and to look for consequences.

There are many questions. How the TQC could be performed? Could TQC hypothesis might allow to understand the structure of living cell at a deeper level? What does this hypothesis predict about DNA itself? One of the challenges is to fuse the vision about living system as a conscious hologram with the DNA as TQC vision. The experimental findings of Peter Gariaev [I39, I55] might provide a breakthrough in this respect. In particular, the very simple experiment in which

one irradiates DNA sample using ordinary light in UV-IR range and photographs the scattered light seems to allow an interpretation as providing a photograph of magnetic flux tubes containing dark matter. If this is really the case, then the bottle neck problem of how to make dark matter visible and how to manipulate it would have been resolved in principle. The experiment of Gariaev and collaborators [I55] also show that the photographs are obtained only in the presence of DNA sample. This leaves open the question whether the magnetic flux tubes associated with instruments are there in absence of DNA and only made visible by DNA or generated by the presence of DNA.

2.3.1 Basic Ideas Of TQC

The basic idea of topological quantum computation (TQC) is to code TQC programs to braiding patterns (analogous to linking and knotting). A nice metaphor for TQC is as dance. Dancing pattern in time direction defines the TQC program. This kind of patterns are defined by any objects moving around so that the Universe might be performing topological quantum computation like activities in all scales.

One assigns to the strands of the braid elementary particles. The S-matrix coding for TQC is determined by purely topological consideration as a representation for braiding operation. It is essential that the particles are in anyonic phase: this means in TGD framework that the value of Planck constant differs from its standard value. Tqc as any quantum computation halts in state function reduction which corresponds to the measurement of say spins of the particles involved.

As in the case of ordinary computers one can reduce the hardware to basic gates. The basic 2-gate is represented by a purely topological operation in which two neighboring braid strands are twisted by π. 1-particle gate corresponds to a phase multiplication of the quantum state associated with braid strand. This operation is not purely topological and requires large Planck constant to overcome the effects of thermal noise.

In TGD framework TQC differs somewhat from the ordinary one.

1. Zero energy ontology means that physical states decompose into pairs of positive and negative energy states at boundaries of causal diamond formed by future and past directed light-cones containing the particles at their light-like boundaries. In positive energy ontology the interpretation is as an event, say particle scattering. The time like entanglement coefficients define S-matrix, or more precisely M-matrix, and this matrix can be interpreted as coding for physical laws in the structure of physical state as quantum superposition of statements "A implies B" with A and B represented as positive and negative energy parts of quantum state. The halting of topological quantum computation would select this kind of statement.

2. The new view about quantum state as essentially 4-D notion implies that the outcome of TQC is expressed as a four-dimensional pattern at space-time sheet rather than as time=constant final state. All kinds of patterns would provide a representation of this kind. In particular, holograms formed by large $\hbar$ photons emitted by Josephson currents, including EEG as a special case, would define particular kind of representation of outcome.

2.3.2 Identification Of Hardware Of TQC And TQC Programs

One challenge is to identify the hardware of TQC and realization of TQC programs.

1. Living cell is an excellent candidate in this respect. The lipid layers of the cell membrane is 2-D liquid crystal and the 2-D motion of lipids would define naturally the braiding if the lipids are connected to DNA nucleotides. This motion might be induced by the self organization patterns of metabolically driven liquid flow in the vicinity of lipid layer both in interior and exterior of cell membrane and thus self-organization patterns of the water flow would define the TQC programs.

2. This identification of braiding implies that TQC as dancing pattern is coded automatically to memory in the sense that lipids connected to nucleotides are like dancers whose feet are connected to the wall of the dancing hall define automatically space-like braiding as the threads connected to their feet get braided. This braiding would define universal memory realized not only as tissue memory but related also to water memory [K34, K35].

3. It is natural to require that the genetic code is somehow represented as property of braids strands. This is achieved if strands are "colored" so that A, T, C, G correspond to four different "colors". This leads to the hypothesis that flux tubes assignable to nucleotides are wormhole magnetic flux tubes such that the ends of the two sheets carry quark and anti-quark *resp.* anti-quark and quark) quantum numbers. This gives mapping A, T, C, G to u, u_c, d, d_c. These quarks are not ordinary quarks but their scaled variants predicted by the fractal hierarchy of color and electro-weak physics. Chiral selection in living matter could be explained by the hierarchy of weak physics. The findings of topologist Barbara Shipman about mathematical structure of honeybee dance led her to proposed that the color symmetries of quarks are in some mysterious manner involved with honeybee cognition and this model would justify her intuition [A20].

4. One should identify the representation of qubit. Ordinary spin is not optimal since the representation of 1-gates would require a modification of direction of magnetic field in turn requiring modification of direction of flux tubes. A more elegant representation is based on quark color which means effectively 3-valued logic: true, false, and undefined, also used in ordinary computers and is natural in a situation in which information is only partial. In this case 1-gates would correspond to color rotations for space-time sheets requiring no rotation of the magnetic field.

In this framework genes define the hardware of TQC rather than genetic programs. This means that the evolution takes place also at the level of TQC programs meaning that strict genetic determinism fails. There are also good reasons to believe that these TQC programs can be inherited to some degree. This could explain the huge differences between us and our cousins in spite of almost the identical genetic codes and explains also cultural evolution and the observation that our children seem to learn more easily those things that we have already learned [I78]. It must be added that DNA as TQC paradigm seems to generalizedDNA, lipids, proteins, water molecules, ... can have flux tubes connecting them together and this is enough to generate braidings and TQC programs. Even water could be performing simple TQC or at least building memory representations based on braiding of flux tubes connecting water molecules.

Comment:

1. Some years after writing this it became clear that elementary particles correspond to wormhole magnetic fields carrying monopole flux. By stability requirement the wormhole magnetic flux tubes associated with TQC could therefore correspond to elementary particles with large value of Planck constant or more generally, to meson like states having at both ends of the wormhole magnetic flux tube fermion or fermion pair. Both leptons and quarks could be associated with the ends, and the condition that braid colors realize genetic code poses additional conditions on the model.

2. It has also turned that genetic code allows a realisation in terms of dark nucleons [K41, L1]. Note that the assignment of genetic code with braid coloring is not necessary for TQC.

2.3.3 How Much TQC Resembles Ordinary Computation?

If God made us to his own image one can ask whether we made computers images of ourselves in some respects. Taking this seriously one ends up asking whether facts familiar to us from ordinary computers and world wide web might have counterparts in DNA as TQC paradigm.

1. Can one identify program files as space-like braiding patterns. Can one differentiate between program files and data files?

2. In ordinary computers electromagnetic signalling is in key role. The vision about living matter as conscious holograms suggests that this is the case also now. In particular, the idea that entire biosphere forms a TQC web communicating electromagnetically information and control signals, looks natural. Topological light rays (MEs) make possible precisely targeted communications with light velocity without any change in pulse shape. Gariaev's findings [I39] that the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind

$$\begin{aligned} Q_a &= [n(A)-n(T)]\tfrac{2}{3}-[n(G)-n(C)]\tfrac{1}{3} \ , \\ Q_a &= -[n(A)-n(T)]\tfrac{1}{3}+[n(G)-n(C)]\tfrac{2}{3} \ , \\ Q_a &= -[n(A)-n(T)]\tfrac{2}{3}+[n(G)-n(C)]\tfrac{1}{3} \ , \\ Q_a &= [n(A)-n(T)]\tfrac{1}{3}-[n(G)-n(C)]\tfrac{2}{3} \ . \end{aligned} \tag{2.3.2}$$

Table 2.1: Table show four possible options for em charge as sum of quark charges.

of picture. Also the model of EEG in which the magnetic body controls the biological body also from astrophysical distances conforms with this picture.

3. The calling of computer programs by simply clicking the icon or typing the name of program followed by return is an extremely economic manner to initiate complex computer programs. This also means that one can construct arbitrarily complex combinations from given basic modules and call this complex by a single name if the modules are able to call each other. This kind of program call mechanism could be realized at the level of TQC by DNA. Since the intronic portion of genome increases with the evolutionary level and is about 98 per cent for humans, one can ask whether introns would contain representations for names of program modules. If so, introns would express themselves electromagnetically by transcribing the nucleotide to a temporal pattern of electromagnetic radiation activating desired subprogram call, presumably the conjugate of intronic portion as DNA sequence. A hierarchical sequence of subprogram calls proceeding downwards at intronic level and eventually activating the TQC program leading to gene expression is suggestive. Note that the repetitive nature of introns is not a problem from the point of TQC.

   Gariaev [I39] has found that laser radiation scattering from given DNA activates only genomes which contain an address coded as temporal pattern for the direction of polarization plane. If flux tubes are super-conducting and there is strong parity breaking (chiral selection) then Faraday rotation for photons traveling through the wormhole flux tube code nucleotide to an angle characterizing the rotation of polarization plane. User id and password would define kind of immune system against externally induced gene expression.

4. Could nerve pulses establish only the connection between receiver and sender neurons as long magnetic flux tubes? Real communication would take place by electromagnetic signals along the flux tube, using topological light ray (ME) attached to flux tube, and by entanglement. Could neural transmitters specify which parts of genomes are in contact and thus serve as a kind of directory address inside the receiving genome?

2.3.4 Some Predictions Related To The Representation Of Braid Color

Even in the rudimentary form discussed above the model makes predictions. In particular, the hypothesis that neutral quark pairs represent braid color is easily testable.

Anomalous em charge of DNA as a basic prediction

The basic prediction is anomalous charge of DNA. Also integer valued anomalous charge for the structural units of genome is highly suggestive.

The selection of the working option - if any such exists - is indeed experimentally possible. The anomalous charge coupling to the *difference* of the gauge potentials at the two space-time sheets defines the signature of the wormhole contact at the DNA end of braid strand. The effective (or anomalous) em charge is given as sum of quark charges associated with DNA space-time sheet:

$$Q_a \quad = \quad [n(A)-n(T)]Q(q_A)+[n(G)-n(C)]Q(q_G) \tag{2.3.1}$$

is predicted. The four possible options for charge are given explicitly in **Table 2.1**.

Second option is obtained from the first option $(A,T,G,C) \to (u,\overline{u},d,\overline{d})$ by permuting u and d quark in the correspondence and the last two options by performing charge conjugation for quarks in the first two options.

The anomalous charge is experimentally visible only if the external electromagnetic fields at the two sheets are different. The negative charge of DNA due to the presence of phosphate groups implies that the first sheet carries different em field so that this is indeed the case.

The presence effective em charge depending on the details of DNA sequence means that electromagnetism differentiates between different DNA: s strands and some strands might be more favored dynamically than others. It is interesting to look basic features of DNA from this view point. Vertebral mitochondrial code has full $A \leftrightarrow G$ and $C \leftrightarrow T$ symmetries with respect to the third nucleotide of the codon and for the nuclear code the symmetry is almost exact. In the above scenario A and C *resp.* G and T would have different signs and magnitudes of em charge but they would correspond to different weak isospin states for the third quark so that this symmetry would be mathematically equivalent to the isospin symmetry of strong interactions.

The average gauge potential due to the anomalous charge per length at space-time sheet containing ordinary em field of a straight portion of DNA strand is predicted to be proportional to

$$\frac{dQ_a}{dl} = [p(A)-p(T)]Q(q_A) + [p(G)-p(C)]Q(q_G)\frac{1}{\Delta L} \quad ,$$

where ΔL corresponds to the length increment corresponding to single nucleotide and $p(X)$ represents the frequency for nucleotide X to appear in the sequence. Hence the strength of the anomalous scalar potential would depend on DNA and vanish for DNA for which A and T *resp.* G and C appear with the same frequency.

Chargaff's second parity rule and the vanishing of net anomalous charge

Chargaff's second parity rule states that the frequencies of nucleotides for single DNA strand satisfy the conditions $p(A) \simeq p(T)$ and $p(C) \simeq p(G)$ (I am grateful for Faramarz Faghihi for mentioning this rule and the related [H1] [I87] to me). This rule holds true in a good approximation. In the recent context the interpretation would be as the vanishing of the net anomalous charge of the DNA strand and thus charge conjugation invariance. Stability of DNA might explain the rule and the poly-A tail in the untranslated mRNA could relate stabilization of DNA and mRNA strands.

Together with $p(A)+p(T)+p(G)+p(C)=1$ Chargaff's rule implies the conditions

$$\begin{array}{ll} p(A)+p(C) \simeq 1/2 \ , & p(A)+p(G) \simeq 1/2 \ , \\ p(T)+p(C) \simeq 1/2 \ , & p(T)+p(G) \simeq 1/2 \ . \end{array} \tag{2.3.3}$$

An interesting empirical finding [I87] is that only some points at the line $p(A)+p(C) \simeq 1/2$ are realized in the case of human genome and that these points are in a good accuracy expressible in terms of Fibonacci numbers resulting as a prediction of optimization problem in which Fibonacci numbers are however put in by hand. $p(A)=p(G)=p(C)=p(T)=1/4$ results as a limiting case. The poly-A tail of mRNA (not coded by DNA) could reflect to the compensation of this asymmetry for translated mRNA.

The physical interpretation would be as a breaking of isospin symmetry in the sense that isospin up and down states for quarks (A and G *resp.* T and C) do not appear with identical probabilities. This need not have any effect on protein distributions if the asymmetry corresponds to asymmetry for the third nucleotide of the codon having $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries as almost exact symmetries. This of course if protein distribution is invariant under this symmetry for the first two codons.

The challenge would be to understand the probabilities $p_3(X)$ for the third codon from a physical model for the breaking of isospin symmetry for the third codon in the sense that u and $\overline{u}$ at DNA space-time sheet are more favored than d and $\overline{d}$ or vice versa. There is an obvious analogy with spontaneous breaking of vacuum symmetry.

Are genes and other genetic sub-structures singlets with respect to QCD color?

Genes are defined usually as transcribed portions of DNA. Genes are however accompanied by promoter regions and other regions affecting the transcription so that the definition of what one really means with gene is far from clear. In the recent case gene would be naturally TQC program module and gene in standard sense would only correspond to its sub-module responsible for the translated mRNA output of TQC.

Whatever the definition of gene is, genes as TQC program modules could be dynamical units with respect to color interaction and thus QCD color singlets (QCD color should not be confused with braid color) or equivalently - possess integer valued anomalous em charge.

One can consider two alternative working hypothesis - in a well-defined sense diametrical opposites of each other.

1. The division of the gene into structural sub-units correlates with the separation into color singlets. Thus various structural sub-units of gene (say transcribed part, translated part, intronic portions, etc...) would be color singlets.

2. Also different genetic codes that I have discussed in [K34, K35] could distinguish between different structural sub-units. For this option only gene - understood as TQC unit with un-transcribed regions included - would be color singlet.

Color singletness condition is unavoidable for mRNA and leads to a testable prediction about the length of poly-A tail added to the transcribed mRNA after translation.

1. The condition of integer valued anomalous charge for coding regions

In the case of coding region of gene the condition for integer charge is replaced by the conditions

$$n(A)+n(G) \ \ mod \ \ 3=0 \ , \quad n(C)+n(T) \ \ mod \ \ 3=0 \ . \tag{2.3.4}$$

These conditions are not independent and it suffices to check whether either of them is satisfied. The conditions are consistent with $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries of the third nucleotide. Note that the contribution of the stop codon (TAA, TGA or TAG) and initiating codon ATG to the A+G count is one unit.

2. General condition for integer valued anomalous charge

The anomalous charge of gene or even that of an appropriate sub-unit of gene is integer valued implies in the general case

$$n(A)-n(T)+n(G)-n(C) \ \ mod \ \ 3=0 \ . \tag{2.3.5}$$

Note that this condition does not assume that gene corresponds to $3n$ nucleotides (as I had accustomed to think). The surprising (to me) finding was that gene and also mRNA coding region of the gene in general fails to satisfy $3n$ rule. This rule is of course by no means requiredonly the regions coding for proteins can be thought of as consisting of DNA triplets.

A possible interpretation is in terms of TGD based model for pre-biotic evolution [K34, K35] according to which genetic code (or 3-code) was formed as a fusion of 2-code and 1-code. 2-code and 1-code could still be present in genome and be associated with non-translated regions of mRNA preceding and following the translated region. The genes of 2-code and coding for RNA would have $2n$ nucleotides and the genes of 1-code could also consist of odd number of nucleotides.

There might be analogy with drawings for a building. These contain both figures providing information about building and text giving meta-level information about how to interpret figures. Figures could correspond to 3-code coding for proteins and text could be written with other codes and give instructions for the transcription and translation processes. Prokaryotic code would contain mostly figures (CDS). In eukaryotic code intronic portions could carry rich amounts of this kind of metalevel information. In the case of mRNA untranslated region preceding $5'$ end could provide similar information.

1. Repeating sequences consisting of n copies of same repeating unit could obey 1-code or 2-code. The simplest building blocks of repeating sequences are AT and CG having vanishing anomalous em charge. TATATA.... and CGCGCG... indeed appear often. Also combinations of CG and AT could repeat: so called mini-satellites are CG rich repeating sequences. Interpretation in terms of 2-code suggests itself.

2. Triplet of the unit ATTCG with integer charge repeats also often: in this case 3-code suggests itself. Telomeres of vertebrates consist of a repeating unit TTAGGG which does not have integer charge: this unit appears also as 8-nucleotide variant which suggests 2-code. Color singletness would require that this unit appears $3n$ times.

3. I have also proposed that intronic regions could obey memetic code [K38] predicting that intronic codon can be represented as a sequence of 21 3-codons (implying 2^{63} 63-codons!). Individual intronic segments need not satisfy this rule, only their union if even that. Direct experimentation with gene bank data show that neither introns nor their union correspond to integer multiples of 63 nor 3 or 2 in general.

3. Color singletness conditions for gene

Gene is usually defined as the sequence of DNA coding for mRNA. mRNA involves also two untranslated regions (UTRs) [I1].

1. The $5'$ end of mRNA contains $5'$ cap (methylated G) and $5'$ untranslated region (UTR). The latter can be several kb long for eukaryotes. Methylated G is not coded by DNA but added so that it does not contribute to A+G-T-C count at DNA level.

2. mRNA continues after the stop codon as $3'$ UTR. Translation assigns to UTR also a poly-A tail (up to several hundreds A: s) not coded by DNA and not contributing to A+G-T-C count in the case of DNA. This region contains also AAUAAA which does not contribute to A+G-T-C count of mRNA.

   One could argue that any amino-acid sequence must allow coding and that one function of UTRs is to guarantee integer valued charge for the part of gene beginning from the initiating codon. Of course, also the non-transcribed regions of DNA not included in the standard definition of gene could take care of this.

4. Color singletness conditions for mRNA

Both poly-A tail and G gap are known to relate to the stabilization of mRNA. The mechanism could be addition of an anomalous charge compensating for the anomalous charge of mRNA to guarantee that second Chargaff's rule is satisfied in a good approximation: this hypothesis is testable.

Second function would be to guarantee color-singletness property. Color singletness would mean that transcribed mRNA + cap G + poly-A tail as a separate unit must be QCD color singlet at DNA space-time sheet. mRNA stability requires the condition

$$n(A) - n(T) + n(G) - n(C) + n_{tail}(A) + 1 \ \ mod \ \ 3 = 0 \tag{2.3.6}$$

to be satisfied. The knowledge of gene would thus predict $n_{tail}(A) \ \ mod \ \ 3$. This hypothesis is testable.

5.Chargaff's rule for mRNA

If Chargaff's rule applies also to mRNA strands one obtains one of the following predictions

$$
\begin{aligned}
&2\,[n(A)+n_{tail}(A)-n(T)]-[n(G)+1-n(C)]\simeq 0\ ,\\
&-[n(A)+n_{tail}(A)-n(T)]+2\,[n(G)+1-n(C)]\simeq 0\ ,\\
&-2\,[n(A)+n_{tail}(A)-n(T)]+[n(G)+1-n(C)]\simeq 0\ ,\\
&[n(A)+n_{tail}(A)-n(T)]-2\,[n(G)+1-n(C)]\simeq 0\ .
\end{aligned}
\tag{2.3.7}
$$

Here $n_{tail}(A)$ includes also AAUAA contributing 3 units to it plus possible other structures appearing in the tail added to the translated mRNA. The presence of poly-A tail which could also compensate for the ordinary negative charge of translated part of mRNA would suggest that A corresponds to u or $\overline{d}$ corresponding to options 1 and 4.

6. Moving genes and repeating elements

Transposons [I19], [J8] are moving or self-copying genes. Moving genes cut from initial position and past to another position of double strand. Copying genes copy themselves first to RNA and them to a full DNA sequence which is then glued to the double strand by cut and paste procedure. They were earlier regarded as mere parasites but now it is known that their transcription is activated under stress situations so that they help DNA to evolve. In TQC picture their function would be to modify TQC hardware. For copying transposons the cutting of DNA strand occurs usually at different points for DNA and cDNA so that "sticky ends" result ("overhang" and its complement) [I16]. Often the overhang has four nucleotides. The copied transposon have ends which are reversed conjugates of each other so that transposons are palindromes as are also DNA hairpins. This is suggestive of the origin of transposons.

In order to avoid boring repetitions let us denote by "satisfy P" for having having integer valued (or even vanishing) Q_a. The predictions are following:

1) The double strand parts associated with the segments of DNA produced by cutting should satisfy P.

2) The cutting of DNA should take place only at positions separated by segments satisfying P.

3) The overhangs should satisfy P.

4) Transposons should satisfy P: their reverse ends certainly satisfy P.

In the example mentioned in [I15] the overhang is $CTAG$ and has vanishing Q_a. The cut site $CCTAGG$ has also vanishing Q_a. It is known [J8] that transposons - repeating regions themselves - tend to attach to the repeating regions of DNA [I6].

1. There are several kinds of repeating regions. 6-10 base pair long sequences can be repeated in untranslated regions up to 10^5 times and whole genes can repeat themselves $50-10^4$ times.

2. Repeats are classified into tandems (say TTAGGG associated with telomeres), interspersed repetitive DNA (nuclear elements), and transposable repeat elements. Interspersed nuclear elements (INEs) are classified LINEs (long), SINEs (short), TLTRs (Transposable elements with Long Terminal Repeats), and DNA transposons themselves.

3. LINEs contain AT rich regions. SINEs known as alus (about 280 bps) contain GC rich regions whereas mariner elements (about 80 bps) are flanked by TA pairs. LTRs have length 300-1000 bps. DNA transposons are flanked with two short inverted repeat sequences flanking the reading frame: "inverted" refers to the palindrome property already mentioned.

AT and CG have vanishing Q_a so that their presence in LINEs and SINEs would make the cutting and pasting easy allowing to understand why transposons favor these regions. Viruses are known to contain long repeating terminal sequences (LTR). One could also check whether DNA decomposes to regions satisfying P and surrounded by repeating sequences which satisfy P separately or as whole as in the case DNA transposons.

7. Tests

Some checks of the color singletness hypothesis were made for human genome [I8].

1. For the coding sequences (CDSs) the strong prediction in general fails as expected (condition would pose restrictions on possible amino-acid contents).

2. Color singletness condition fails for genes defined in terms of translated part of mRNA (with gap and poly-A tail excluded). The un-transcribed regions of DNA involved with the gene expression (promoter region, etc...) could guarantee the color singletness. They could also stabilize DNA by bringing in compensating anomalous charge to guarantee second Chargaff's rule. Different genetic codes could distinguish between the subunits of gene.

3. To test color singletness conditions for mRNA one should know the length of poly-A tail. Unfortunately, I do not have access to this information.

4. The computation of total anomalous charges for a handful of genes, introns, and repeat units for some gene bank examples in the case of human genome indicates that both of them tend to carry net em charge which is largest for $(a, g) \leftrightarrow (\overline{d}, \overline{u})$ correspondence. The charge is in the range 5-10 per cent from the charge associated with the phosphates (-2 units per nucleotide). For second option giving negative charge (permute u and d) the anomalous charge is few per cent smaller.

   By Chargaff's law the regions outside genes responsible for the control of gene expression must contain a compensating charge of opposite sign. Kind of spontaneous symmetry breaking of charge conjugation symmetry $A \leftrightarrow T, G \leftrightarrow C$ and analogous to matter antimatter symmetry seems to take place. That control regions and translated regions have opposite densities of anomalous charge might also help in the control gene expression.

5. The poly-A tail of mRNA would carry compensating positive anomalous charge: the RNA-quark assignment could be conjugate to the DNA-quark assignment as suggested by what takes place in transcription. For instance, for the option $A \to \overline{d}$, the prediction for the length of polytail for $A \to \overline{d}$ option would be about $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)$ where $N(mRNa)$ is the number of nucleotides in transcribed mRNA and $p_a(mRNA)$ is the per cent of anomalous charge which is typically 5-10 per cent. For $p_a(mRNA) = 10$ per cent this gives as much as 30 per cent. For $A \to \overline{u}$ option one has $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)/2$. In this case also p_a is considerably smaller, typically by a factor of of order 2-3 per cent and even below per cent in some cases. Hence the relative length of tail would around 3-5 per cent. This option is perhaps more since it minimizes anomalous charge and maximizes the effectiveness of charge compensation by poly-A tail.

6. The predictions for transposons and their cut and past process should be easily testable.

Summary of possible symmetries of DNA

The following gives a list of possible symmetries of DNA inspired by the identification of braid color.

1. Color confinement in strong form

The states of quarks and anti-quarks associated with DNA both wormhole wormhole throats of braided (living) DNA strand can be color singlets and have thus integer valued anomalous em charge. The resulting prediction depends on the assignment of quarks and antiquarks to A, T, C, G which in principle should be determined by the minimization of em interaction energy between quark and nucleotide. For instance $2(A-T)-(G-C) \ \ mod \ \ 3 = 0$ for a piece of living DNA which could make possible color singletness. As a matter fact, color singletness conditions are equivalent for all possible for braid color assignments. This hypothesis might be weakened. For instance, it could hold true only for braided parts of DNA and this braiding are dynamical. It could also hold for entire braid with both ends included only: in this case it does not pose any conditions on DNA.

Questions: Do all living DNA strands satisfy this rule? Are only the double stranded parts of DNA braided and satisfy the rule. What about loops of hairpins?

2. Matter antimatter asymmetry at quark level

$A \leftrightarrow T$ and $G \leftrightarrow C$ corresponds to charge conjugation at the level of quarks (quark $\leftrightarrow$ antiquark). Chargaff's rules states $A \simeq T$ and $C \simeq G$ for long DNA strands and mean matter-antimatter symmetry in the scale of DNA strand. Double strand as a whole is matter anti-matter symmetric.

Matter-antimatter asymmetry is realized functionally at the level of DNA double strand in the sense that only DNA strand is transcribed. The study of some examples shows that genes defined as transcribed parts of DNA do not satisfy Chargaff's rule. This inspires the hypothesis about the breaking of matter antimatter symmetry. Genes have non-vanishing net $A - T$ and $C - G$ and therefore also net Q_a with sign opposite to that in control regions. Just as the Universe is matter-antimatter asymmetric, also genes would be matter-antimatter asymmetric.

3. Isospin symmetry at quark level

$A \leftrightarrow G$ and $T \leftrightarrow A$ correspond change of anomalous em charge by 1 unit and these operations respect color confinement condition. Local modifications of DNA inducing these changes should be preferred. The identification for the symmetries $A \leftrightarrow G$ and $T \leftrightarrow A$ for the third nucleotide of code is as isospin symmetries. For the vertebrate mitochondrial code the symmetry exact and for nuclear code slightly broken.

4. Matter antimatter asymmetry and isospin symmetries for the first two nucleotides

The first two nucleotides of the codon dictate to a high degree which amino-acid is coded. This inspires the idea that 3-code has emerged as fusion of 1- and 2-codes in some sense. There are two kinds of 2-codons. The codons of type A have fractional em charge and net quark number (consisting of either matter or antimatter at quark level) and are not able to form color singlets. The codons of type B have integer em charge and vanishing quark number (consisting of matter and antimatter) and are able to form color singlets. The 2-codons of type A (resp. B) are related by isospin rotations and there should be some property distinguishing between types A and B. There indeed is: if 2-codon is matter-antimatter symmetric, 1-codon is not and vice versa.

1. For almost all type A codons the amino-acid coded by the codon does not depend on the last nucleotide. There are two exceptions in the case of the nuclear code: (leu, leu, phe, phe) and (ile, ile, ile, met). For human mitochondrial code one has (ile, ile, ile, ile) and thus only one exception to the rule. The breaking of matter-antimatter symmetry for the third nucleotide is thus very small.

2. For codons of type B the 4-columns code always for two doublets in the case of vertebrate mitochondrial code so that for codons with vanishing net quark number the breaking of matter-antimatter symmetry for the third nucleotide is always present.

5. Em stability

Anomalous em charge Q_a vanishes for DNA and perhaps also mRNA strand containing also the G cap and poly-A tail which could compensate for the Q_a of the transcribed region so that

$$2(A - T) - (G - C) \simeq 0$$

or some variant of it holds true. Chargaff's rules for long DNA strands imply the smallness of Q_a.

6. Summary of testable working hypothesis

Following gives a summary of testable working hypothesis related to the isospin symmetry and color singletness. The property of having integer valued/vanishing Q_a is referred to as property P.

1. Gene plus control region and also DNA repeats should have property P. Transcribed and control regions of gene have Q_a with opposite signs.

2. Transposons, repeating regions, the overhangs associated with the cut and paste of transposon, and the DNA strands resulting in cutting should have property P. This could explain why transposons can paste themselves to AT and GC ($Q_a = 0$) rich repeating regions of DNA. The points at which DNA can be cut should differ by a DNA section having property

P. This gives precise predictions for the points at which transposons and pieces of viral DNA can join and could have implications for genetic engineering.

3. If also mRNA is braided, it has property P. This can be only true if the poly-A tail compensates for the non-vanishing Q_a associated with the translated region.

4. Living hairpins should have property P. If only double helix parts of hairpins are braided, the prediction is trivially true by the palindrome property. tRNA or at least parts of it could be braided. Braids could end to the nuclear membrane or mRNA or to the amino-acid attachable to tRNA. For stem regions Q_a is integer valued. The fact that the nucleotide of the anticodon corresponding to the third nucleotide of codon can base pair with several nucleotides of mRNA suggests that $I(nositol)$ can have Q_a opposite to that of A, T, C and U opposite to that of A, G. For 2-anticodon the pairing would be unique. This would give a lot of freedom to achieve property P in weak sense for tRNA. Braid structure for tRNA + amino-acid could be different that for tRNA alone and also in the translation the braid structure could change.

5. Telomeres [I18] are of special interests as far as anomalous em charge is considered. Chromosomes are not copied completely in cell replication, and one function of telomeres is to guarantee that the translated part of genome replicates completely for sufficiently many cell divisions. Telomeres consists of 3-20 kilobases long repetitions of TTAGGG, and there is a 100-300 kilobases long repeating sequence between telomere and the rest of the chromosome. Telomeres can form can also 4-stranded structures. Telomere end contains a hair-pin loop as a single stranded part, which prevents the action of DNA repair enzymes on the chromosome end. Telomerase is a reverse transcriptase enzyme involved with the synthesis of telomeres using RNA strand as a template but since its expression is repressed in many types of human cells, telomere length shortens in each cell replication. In the case of germ cells, stem cells and white blood cells telomerase is expressed and telomere length preserved. Telomere shortening is known to relate to ageing related diseases. On the other hand, overactive telomere expression seems to correlate with cancer.

   If telomeres possess braid strands, the compensation of Q_a might provide an additional reason for their presence. If this the case and if telomeres are strict multiples of TTAGGG, the shortening of telomeres generates a non-vanishing Q_a unless something happens for the active part of DNA too. Color singletness condition should however remain true: the disappearance of $3n$ multiples of TTAGGG in each replication is the simplest guess for what might happen. In any case, DNA strands would become unstable in cell replication. Q_a could be reduced by a partial death of DNA in the sense that some portions of braiding disappear. Also this would induce ill functioning of TQC harware perhaps related to ageing related diseases. Perhaps evolution has purposefully developed this ageing mechanism since eternal life would stop evolution.

6. Also amino-acids could be braided. Q_a could vary and correspond to Q_a for one of the codons coding for it. The amino-acid sequences of catalysts attaching to DNA strand should have opposite Q_a for each codon-amino-acid pair so that amino-acid would attach only to the codons coding for it. The TGD based model for nerve pulse [K68] inspires the proposal that magnetic flux tubes connecting microtubules to the axonal membrane allow TQC during nerve pulse propagation when axonal membrane makes transition from gel like phase to liquid crystal phase. Amino-acids of tubulin dimers would be connected by 3-braids, smallest interesting braid, to groups of 3-lipids in axonal membrane and tubulin dimers would define fundamental TQC modules.

Empirical rules about DNA and mRNA supporting the symmetry breaking picture

Somewhat surprisingly, basic facts which can be found from Wikipedia, support the proposed vision about symmetry breaking although, the mechanism of matter antimatter symmetry breaking is more complex than the first guess. I am grateful for Dale Trenary for references which made possible to realize this. Before continuing some comments about the physical picture are in order.

1. The vanishing of the induced Kähler field means that the space-time sheet of DNA is a highly unstable vacuum extremal. The non-vanishing of the induced Kähler electric field is thus a natural correlate for both the stability and the non-vanishing quark number density (matter antimatter asymmetry). The generation of matter antimatter asymmetry induces a net density of anomalous em charge, isospin, and quark number in the portion of DNA considered. This in turn generates not only longitudinal electric field but also a longitudinal Kähler electric field along DNA.

2. Weak electric fields play a key role in living matter. There are electric fields associated with embryos, central nervous system, individual neurons, and microtubules and their direction determines the direction of a process involved (head-to-tail direction, direction of propagation of nerve pulse, ...).

3. Same mechanism is expected to be at work also in the case of DNA and RNA. In the case of gene the direction of transcription could be determined by the direction of the electric field created by gene and telomeres at the ends of chromosomes carrying a net anomalous quark number could be partially responsible for the generation of this field. In the case of mRNA the direction of translation would be determined in the similar manner. The net anomalous em charges of poly-A tail and the transcribed part of mRNA would have opposite signs so that a longitudinal electric field would result.

It will be found that this picture is consistent with empirical findings about properties of DNA.

7. Breaking of matter antimatter symmetry and isospin symmetry for entire genome

Chargaff's rules are not exact and the breaking gives important information about small breakings of isospin and matter-antimatter symmetries at the level of entire genome. The basic parameters are em charge per nucleotide, isospin per nucleotide, the amount of quark number per nucleotide, and the ratio of u and d type matters coded by $(G+C)/(A+T)$ ratio. Recall that there are four options for the map of A, T, C, G to quarks and antiquarks and for option 3) *resp.* 4) the anomalous em charge is opposite to that for 1) *resp.* 2).

Table 2.2 gives A, T, C, G contents (these data are from Wikipedia [I3]) provides interesting data about DNA It will be found that so called Szybalski's rules can be interpreted as saying that for coding regions there is breaking of the approximate matter antimatter asymmetry.

Note that matter antimatter asymmetry in the scale of entire genome has largest positive value for human genome and negative value only for yeast genome: this case the magnitude of the asymmetry is largest.

For option 2) the amount of anomalous charge is about.0057e per nucleotide and thus about $3 \times 10^7 e$ for entire human DNA having length of about 1.8 meters. The inspection of tables of [I18] shows that the anomalous em charge for the repeating sequence defining the telomere is always non-vanishing and has always the same sign. Telomeres for human chromosomes consist of TTAGGG repetitions with anomalous em charge with magnitude $5e/3$ for all options and have a length measured in few kbases. Human genome as has 24 chromosomes so that the total anomalous em charge of telomeres is roughly $24 \times (5/18) \times x10^3 e \sim .8 \times 10^3 xe$, $1 < x < 10$. The anomalous em charge of telomeres is three orders of magnitude smaller than that of entire DNA but if DNA is quantum critical system the change the total anomalous em charge and quark number due to the shortening of telomeres could induce instabilities of DNA (due to the approach to vacuum extremal) contributing to ageing. Note that the small net value of quark number in all the cases considered might be necessary for overall stability of DNA. Telomeres are also known to prevent the ends of chromosomes to stick to each other. This could be partially due to the Coulomb repulsion due to the anomalous em charge.

According to [I3] Chargaff's rules do not apply to viral organellar genomes (mitochondria [I12], plastids) or single stranded viral DNA and RNA genomes. Thus approximate matter antimatter symmetry fails for DNA: s of organelles involved with metabolism. This might relate to the fact that the coding portion of DNA is very high and repeats are absent. Chargaff's rule applies not only to nucleotides but also for oligonucleotides which corresponds to DNA or RNA sequences with not more than 20 bases. This means that for single strand oligonucleotides and their conjugates appear in pairs. Matter antimatter asymmetry would be realized as presence

	Human	*Chicken*	*Grass−hopper*	*Sea Urchin*	*Wheat*	*Yeast*	*E.Coli*
$p(A)$	0.3090	0.2880	0.2930	0.3280	0.2730	0.3130	0.2470
$p(T)$	0.2940	0.2920	0.2930	0.3210	0.2710	0.3290	0.2360
$p(C)$	0.1990	0.2050	0.2050	0.1770	0.2270	0.1870	0.2600
$p(G)$	0.1980	0.2170	0.2070	0.1730	0.2280	0.1710	0.2570
$\frac{dq_1}{dn}$	0.0103	−0.0067	−0.0007	0.0060	0.0010	−0.0053	0.0083
$\frac{dq_2}{dn}$	0.0057	−0.0093	−0.0013	0.0050	−0.0000	0.0053	0.0057
$\frac{dI_3}{dn}$	0.0080	−0.0080	−0.0010	0.0055	0.0005	0.0000	0.0070
$\frac{d(q-\overline{q})}{dn}$	0.0140	0.0080	0.0020	0.0030	0.0030	−0.0320	0.0080
$\frac{p(A+T)}{p(G+C)}$	1.5189	1.3744	1.4223	1.8543	1.1956	1.7933	0.9342

(2.3.8)

Table 2.2: The table gives A, T, C, G contents (these data are from Wikipedia [I3]), the amount of quark charge per nucleotide for the options 1) *resp.* 2) given by $dq_1/dn = p[2(A-T)-G-C)]/3$ *resp.* $dq_2/dn = p[A-T-2(G-C)]/3$, the amount $dI_3/dn = p(A-G+C-T]/2$ of isospin per nucleotide, the amount $d(q-\overline{q})/dn = p(A-T+G-C)$ of quark number per nucleotide, and $(A+T)/(C+G)$ ratio for *entire genomes* in some cases.

of matter blobs and their conjugates. This might relate to the mechanism how the sequences of oligonucleotides are generated from DNA and its conjugate.

8. Breaking of matter antimatter symmetry for coding regions

As noticed, one can consider three type of symmetry breaking parameters for DNA in DNA as TQC model. There are indeed three empirical parameters of this kind. Chargaff rules have been already discussed and correspond to approximate matter antimatter symmetry. The second asymmetry parameter would measure the asymmetry between $u\overline{u}$ and $d\overline{d}$ type matter. $p(G+C)$ corresponds to the fraction of $d\overline{d}$ type quark matter for option 1) and $u\overline{u}$ matter for option 2). It is known that G+C fraction $p(G+C)$ characterizes genes [I64] and the value of $p(G+C)$ is proportional to the length of the coding sequence [I10, I64].

Besides Chargaff rules holding true for entire genome also Szybalski's rules [I3] hold true but only for coding coding regions. The biological basis of neither rules is not understood. The interpretation of Chargaff's rules would be in terms of approximate matter antimatter symmetry and the vanishing of net isospin at the level of quarks whereas Szybalski's rule would state the breaking of these symmetries non-coding regions. Hence all the three basic empirical rules would have a nice interpretation in DNA as TQC picture.

Consider now Szybalski's rules in more detail.

1. In most bacterial genomes (which are generally 80-90 % coding) genes are arranged in such a fashion that approximately 50 % of the coding sequence lies on either strand. Note that either strand can act as a template (this came as a surprise for me). Szybalski, in the 1960s, showed that in bacteriophage coding sequences purines (A and G) exceed pyrimidines (C and T). This rule has since been confirmed in other organisms and known as Szybalski's rule [I3, I65]. While Szybalski's rule generally holds, exceptions are known to exist.

   Interpretation. A breaking of matter antimatter symmetry occurs in coding regions such that the net breakings are opposite for regions using different templates and thus different directions of transcription (promoter to the right/left of coding region).

2. One can actually characterize Szybalski's rules more precisely. By Chargaff's rules one has $p(A+T) \simeq 1-p(G+C)$). In coding regions with low value of $p(G+C)$ $p(A)$ is known to be higher than on the average whereas for high value of $p(G+C)$ $p(G)$ tends to higher than on the average.

Interpretation. These data do not fix completely the pattern of breaking of the approximate matter antimatter symmetry.

i) It could take place for both kinds of quark matter ($u\overline{u}$ and $d\overline{d}$): both $p(A)$ and $p(G)$ would increase from its value for entire genome but the dominance of A over G or vice versa would explain the observation.

ii) The breaking could also occur only for the dominating type of quark matter ($u\overline{u}$ or $d\overline{d}$) in which case only $p(A)$ or $p(G)$ would increase from the value for entire genome.

Also a net isospin is generated which is of opposite sign for short and long coding sequences so that there must be some critical length of the coding sequences for which isospin per nucleotide vanishes. This length should have biological meaning.

3. For mRNA $A+G$ content is always high. This is possible only because the template part of the DNA which need not be always the same strand varies so that if it is strand it has higher $A+G$ content and if it is conjugate strand it has higher $T+C$ content.

Interpretation. mRNA breaks always matter antimatter symmetry and the sign of matter antimatter asymmetry is always the same. Thus mRNA is analogous to matter in observed universe. The poly-A tail added to the end of mRNA after transcription to stabilize it would reduce the too large values of isospin and anomalous em charge per nucleon due to the fact that mRNA does not contain regions satisfying Chargaff's rules. It would also generate the needed longitudinal electric field determining the direction of translation. In the case of DNA the breaking of matter antimatter symmetry is realized at the functional level by a varying direction of transcription and variation of template strand so that matter antimatter symmetry for the entire DNA is only slightly broken. Direction of transcription would be determined by the direction of the electric field. The stability of long DNA sequences might require approximate matter antimatter symmetry for single DNA strand if it is long. In the case of simple genomes (mitochondrial, plastid, and viral) the small size of the genome, the high fraction of coding regions, and the absence of repeating sequences might make approximate matter antimatter symmetry un-necessary. An interesting working hypothesis is that the direction of transcription is always the same for these genomes.

One can try to use this information to fix the most probable option for nucleotide quark correspondence.

1. In nuclear physics the neutron to proton ratio of nucleus increases as nucleus becomes heavier so that the nuclear isospin becomes negative: $I_3 < 0$. The increase of the nuclear mass corresponds to the increase for the length of the coding region. Since G/A fraction increases with the length of coding region, G should correspond to either d quark ($(Q_a < 0, I_3 = -1/2)$) or its charge conjugate d_c ($Q_a < 0$). Hence option 1) or its charge conjugate would be favored.

2. If one takes very seriously the analogy with cosmic matter antimatter asymmetry then matter should dominate and only $(A, G, T, C) \to (u, d, \overline{u}, \overline{d})$ option would remain.

Szybalski's findings leave open the question whether non-coding regions obey the Chargaff rules in good approximation or whether also they appear as pairs with opposite matter antimatter asymmetry. Introns are belong to coding regions in the sense that they are transcribed to mRNA. Splicing however cuts them off from mRNA. It is not clear whether introns break the approximate matter antimatter symmetry or not. If breaking takes place it might mean that introns code for something but not chemically. On the other hand, the absence of asymmetry might serve at least partially as a signal telling that introns must be cut off before translation. Many interesting questions represent itself. For instance, how the symmetry breaking parameters, in particular matter antimatter asymmetry parameter, depend on genes. The correlation with gene length is the most plausible guess.

Genetic codes and TQC

TGD suggests the existence of several genetic codes besides 3-codon code [K39, **?**]. The experience from ordinary computers and the fact that genes in general do not correspond to $3n$ nucleotides encourages to take this idea more seriously. The use of different codes would allow to tell what kind of information a given piece of DNA strand represents. DNA strand would be like a drawing

of building containing figures (3-code) and various kinds of text (other codes). A simple drawing for the building would become a complex manual containing mostly text as the evolution proceeds: for humans 96 per cent of code would corresponds to introns perhaps obeying some other code.

The hierarchy of genetic codes is obtained by starting from n basic statements and going to the meta level by forming all possible statements about them (higher order logics) and throwing away one which is not physically realizable (it would correspond to empty set in the set theoretic realization). This allows $2^n - 1$ statements and one can select 2^{n-1} statements consistent with a given atomic statement (1 bit fixed) (half of the full set of statements) and say that these are true and give kind of axiomatics about world. The remaining statements are false. DNA would realize only these statements.

The hierarchy of Mersenne primes $M_n = 2^n - 1$ with $M_{n(next)} = M_{M_n}$ starting from $n = 2$ with $M_2 = 3$ gives rise to 1-code with 4 codons, 3-code with 64 codons, and $3 \times 21 = 63$-code with 2^{126} codons [K39] realized as sequences of 63 nucleotides (the length of 63-codon is about $2L(151)$, roughly twice the cell membrane thickness. It is not known whether this Combinatorial Hierarchy continues ad infinitum. Hilbert conjectured that this is the case.

In the model of pre-biotic evolution also 2-codons appear and 3-code is formed as the fusion of 1- and 2-codes. The problem is that 2-code is not predicted by the basic Combinatorial Hierarchy associated with $n = 2$.

There are however also other Mersenne hierarchies and the next hierarchy allows the realization of the 2-code. This Combinatorial Hierarchy begins from Fermat prime $n = 2^k + 1 = 5$ with $M_5 = 2^5 - 1 = 31$ gives rise to a code with 16 codons realized as 2-codons (2 nucleotides). Second level corresponds to Mersenne prime $M_{31} = 2^{31} - 1$ and a code with $2^{30=15\times 2}$ codons realized by sequences of 15 3-codons containing 45 nucleotides. This corresponds to DNA length of 15 nm, or length scale $3L(149)$, where $L(149) = 5$ nm defines the thickness of the lipid layer of cell membrane. $L(151) = 10$ nm corresponds to 3 full 2π twists for DNA double strand. The model for 3-code as fusion of 1- and 2-codes suggests that also this hierarchy - which probably does not continue further - is realized.

There are also further short Combinatorial hierarchies corresponding to Mersenne primes [A9].

1. $n = 13$ defines Mersenne prime M_{13}. The code would have $2^{12=6\times 2}$ codons representable as sequences of 6 nucleotides or 2 3-codons. This code might be associated with microtubuli.

2. The Fermat prime $17 = 2^4 + 1$ defines Mersenne prime M_{17} and the code would have $2^{16=8\times 2}$ codons representable as sequences of 8 nucleotides.

3. $n = 19$ defines Mersenne prime M_{19} and code would have $2^{18=9\times 2}$ codons representable as sequences of 9 nucleotides or three DNA codons.

4. The next Mersennes are M_{31} belonging to $n = 5$ hierarchy, M_{61} with $2^{60=30\times 2}$ codons represented by 30-codons. This corresponds to DNA length $L(151) = 10$ nm (cell membrane thickness). M_{89} (44-codons), M_{107} (53-codons) and M_{127} (belonging to the basic hierarchy) are the next Mersennes. Next Mersenne corresponds to M_{521} (260-codon) and to completely super-astrophysical p-adic length scale and might not be present in the hierarchy.

   This hierarchy is realized at the level of elementary particle physics and might appear also at the level of DNA. The 1-, 2-, 3-, 6-, 8-, and 9-codons would define lowest Combinatorial Hierarchies.

2.4 Constraints On The Fermionic Realization Of Genetic Code From The Model For Color Qualia

The original model for DNA as topological quantum computer assigns to DNA nucleotides quarks at ends of flux tubes or quark pairs at the ends of wormhole flux tubes. This is only the realization that came first to my mind in TGD Universe where dark variants of quarks can define QCD like physics even in cellular length scales. One can actually imagine several realizations of the genetic code and the first realization is far from being the simplest one. It is enough to have four different particles or many-particle quantum states to build at least formally a map from A, T, C, G to

four states. It is obvious that the number of possible formal realizations is limited only by the imagination of the theoretician. Additional conditions are required to fix the model.

2.4.1 Fermionic Representation

Consider first the fermionic representations in the general case without specifying what fermions are.

1. The original proposal was that DNA nucleotides correspond to flux tubes with quark q and antiquark $\overline{q}$ at the ends of the parallel flux sheets extremely near to each other. Second options relies on wormhole magnetic flux tubes in which case quark pair $q\overline{q}$ is at both ends. Quarks u, d and their antiquarks would code for A, T, C, G. The spin of quarks is not taken into account at all in this coding: why not restrict the consideration to single quark. The total quark charge at given end of flux tube pair vanishes and flux tube ends carry opposite quark charges.

   The nice feature of this option is that one could understand the generation of color qualia in the model of sensory receptor in simple manner to be discussed below. Even if one accepts the arguments supporting the view that dark quarks in cell scale are natural outcome of the hierarchy of Planck constants, one could argue that the presence of both quarks and antiquarks does not conform with matter antimatter asymmetry (not that one can however identify the analog of matter antimatter asymmetry at DNA level).

2. Spin states for fermion pairs assigned with two parallel magnetic flux tubes with the magnetic field generated by spin provide much simpler representation for nucleotides. Similar fermion pair would reside at the second end of flux tube pair.

   (a) It is is essential that rotational symmetry is broken and reduces to rotational symmetry around the direction of flux tubes so that spin singlet and spin 0 state of triplet mix to form states for which each fermion is in spin eigenstate. The states must be antisymmetric under exchange of the protons and spin 1/0 states are antisymmetric/symmetric in spatial degrees of freedom (wave functions located to the ends of flux tubes). The states with definite spin for given flux tube are mixtures of s=1 states with vanishing spin projection and s=0 state.

   (b) It is not quite clear whether one should treat fermion pairs as identical bosons with 3+1 spin states since in TGD framework one considers disjoint partonic 2-surfaces and the situation is not that of QFT in M^4. This interpretation would require totally symmetry of the states under permutations of bosonic states defined by the 3+1 spin states. Coding by spin requires that each nucleotide corresponds to a state with a well defined spin. In field theory language the state would be obtained by applying bosonic oscillator operators generating states of given spin localized to a given nucleotide position.

   (c) The classical correlate for the permutations of coordinates of fermions has interpretation as braiding for the flux tubes of the flux tube pair. In the similar manner the permutation of the flux tube pairs associated with nucleotides has interpretation as braiding of the 3-braids formed form from flux tube pairs. Braiding therefore gives a representation of spin analogous to the well-known orientation entanglement relation invented by Dirac and providing geometric representation of spin 1/2 property.

2.4.2 Various Options For The Fermionic Representation Of A, T, C, G

Fermionic representations allows several options since fermion can be electron, u or d quark, or proton. Wormhole magnetic fields would not be needed in this case.

1. The problem of electron and proton options is that it does not allow realization of color qualia. There is also the well-known problem related to the stability of DNA caused by the phosphate charge of -2 units per nucleotide. Somehow this charge should be screened. In any case, the charge -2 should correspond to the electron pair at the DNA end of the flux tube

for electron option. For proton option the charge would be screened completely. One could of course consider also the large $\hbar$ color excitations of ordinary protons instead of quark at its nucleotide ends. This option would however require the modification of quark wave functions inside proton and this option will not be discussed here.

2. Quark option would give rise to both color and allow also to reduce the electronic charge of -2 units by 4/3 units to -2/3 units in the case of u quark pair. This would help to stabilize DNA. In the case of d quarks the charge would increase to -10/3 units and is not favored by stability argument. Flux tube pairs assigned to single nucleotide define diquarks with spin 1 or spin 0.

   (a) Diquarks behave ass identical bosons with 3+1 spin states and 3×3 color states. They form formally super-multiplet of $\mathcal{N} = 2$ SUSY. The states with well defined symmetry properties in spin degrees of freedom have such properties in spatial degrees of freedom. This means that one obtains a superposition of flux tube pairs with are either braided or unbraided. Triplet/singlet state is symmetric/antisymmetric and total asymmetry could be guaranteed by assuming symmetry/antisymmetry in spatial degrees of freedom and antisymmetry/symmetry in color degrees of freedom. This would give anti-triplet/6-plet in color degrees of freedom. Spatial symmetry would favor antitriplet and diquark would behave like antiquark with respect to color. Let us assume antitriplet state for definiteness.

   (b) DNA codon corresponds to three-di-quark state. This state must be totally symmetric under the exchange of bosons. One can have total symmetry in both spatial and color degrees of freedom or total antisymmetry/symmetry in spatial and total antisymmetry/symmetry in color degrees of freedom.The first option gives 10-dimensional color multiplet and the second one color singlet. Braiding is maximal and symmetric/antisymmetric in these case. One can consider also mixed symmetries. In this case one has color octet which is antisymmetric with respect to the first nucleotide pair and symmetric with respect to first nucleotide pair and third nucleotide. The braiding of the first two nucleotides must be antisymmetric and the braiding of this pair with third nucleotide. The conclusion would be that color multiplets correspond to well defined braidings and one would therefore have directed connection with topological quantum computation. Color octet is especially interesting concerning the representation of color qualia.

The challenge of all these options (note that the representability of color selects quark option) is to find a good justification for why the assignment of A, T, C, G to quark states or spin states is unique dynamically. Stability argument is expected to help here.

2.4.3 Realization Of Color Qualia For Quark Option

Consider now how one could understand the generation of qualia for quark option.

1. The generation of qualia involves interaction with external world giving rise to a sensory percept. In the case of visual colors it should correspond to a measurement of quark color and should give rise to eigenstages of color at the ends of flux tubes at DNA nucleotides for a nucleus or cell of photoreceptor. A modification of capacitor model is needed. Color polarization is still essential but now polarization in nucleus or cell scale is transformed in the generation of color quale to a polarization in longer length scale by the reconnection of flux tubes so that their ends attach to "external world". The nucleus/cell becomes color and state function reduction selects well defined quantum numbers. It is natural to assume that the entanglement in other degrees of freedom after color measurement is negentropic.

2. Does the "external world" corresponds to another cell or to the inner lipid layers of the cell membrane containing the nucleus. In the first case flux tubes would end to another cell. If the nuclei of receptor cells are integrate to a larger structure by magnetic flux sheets traversing through them one can also consider the possibility that the polarization in the scale of cell

nucleus (recall that the nucleus has also double lipid layer) is transformed to a polarization in cell scale so that similar process in cell scale gives rise to qualia.

The entire receptor unit must have net color charge before the state function reduction. This requires that there are flux tubes connecting the receptor unit to a unit representing "external world" and having vanishing color charge. If second cell is the "external world" these flux tubes must go through the pair of lipid layers of both cell membrane and end up to the nucleus of cell in the environment. If external world correspond to the complement of nucleus inside cell the inner layers of cell membrane represents external world. Cell membrane indeed serves as sensory receptor in cell length scale. One can of course have sensory qualia in various length scales so that both options are probably correct and a kind of fractal hierarchy is very natural giving rise also to our qualia at some higher level. Living matter as conscious hologram metaphor suggests a fractal hierarchy of qualia.

After state function reduction reducing the entanglement the flux tubes split and the receptor becomes un-entangled with external world and has vanishing color charges. At the level of conscious experience this means that there can be only memory about the quale experience. The sensation of quale lasts with respect to subjective time as long as the negentropic entanglement prevails. There is an obvious analogy with Orch-OR (see `http://tinyurl.com/ylfv6pp`) proposal of Hameroff and Penrose in which also conscious experience ends with state function reduction.

3. Consider now how the color qualia are generated.

   (a) There must be two flux tube states. In the first state there are two flux tube beginning from cell nucleus A and ending to the inner lipid layer a_1 and flux tube beginning from the outer lipid layer a_2 and ending cell nucleus B. Both flux tubes have vanishing net color so that cells have vanishing net colors. This could be regarded as the resting state of the receptor. The lipids in layers a_1 and a_2 are connected by another short flux tube. Same for b_1 and b_2.

   (b) The second flux tube state corresponds to long flux tubes connecting the nuclei of cells A and B. The ends carry opposite color charges. In this case the net color of both A and B is non-vanishing. This state would be an outcome of a reconnection process in which the flux tubes from A to a_1 and B to a_2 re-connect with the short flux tube connecting lipid layers a_1 and a_2.

   (c) When these flux tubes carry opposite colors numbers at their ends, the cell possess net color charge and can represent color quale. Or rather, creation of this kind of flux tube connections would give rise to the color charging of the receptor cell with external world carrying opposite color charge.

One can argue that this mechanism is not quite in spirit with color capacitor model. Polarization is still essential but now polarization in receptor scale is transformed to polarization in longer length scale by the reconnection of flux tubes. The analog of di-electric breakdown however still applies in the sense that its analog induces large polarization. Several mechanisms generating larger polarization are of course possible. One can ask how essential the electromagnetic polarization of cell membrane is for the generation of qualia at cell level. Note also that biomolecules are quite generally polar molecules.

The unexpected prediction of the model is that braiding would correlate directly with qualia. This would mean also a connection between quantum computation and qualia. This condition emerges from Fermi/Bose-Einstein statistics correlating braiding with symmetric properties of color states and spin states. Quite generally, the correlation of braiding with the symmetries of wave functions as functions of points of braid end points would allow to have direct geometric correlate between induced entanglement and braiding as naïve intuitive expectations have suggested.

This model is not consistent with the naïve expectation that the quale is generated after state function reduction. Rather, the beginning of sensation of quale means beginning of negentropic entanglement and fusion with external world and state function usually associated with the quantum measurement would mean the end of the sensation and separation from the external

world! Maybe one can say that state function reduction means that experience is replaced with a memory "I had the sensation of quale" ! Krishnamurti would certainly agree!

2.5 Realization Of Genetic Code In Terms Of Dark Baryons

Either dark baryon code or code based on u, d and their anti-quarks could be involved with various pairings. For dark baryon code DNA would not decompose into codons. For latter code this would be the case. One could also consider the possibility that the regions genes realized the dark baryon code and the regions between them are realized in terms of ududbardbar code. The latter code could be also involved with TQC.

2.5.1 Dark Nuclear Strings As Analogs Of DNA-, RNA- and Amino-Acid Sequences and Baryonic Realization Of Genetic Code?

Water memory is one of the ugly words in the vocabulary of a main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [L1, K41, K85], [L1] , [I47]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

The question is whether dark nuclear strings might provide a representation of the genetic code. In fact, I posed this question year before the results of the experiment came with motivation coming from attempts to understand water memory. The outcome was a totally unexpected finding: the states of dark nucleons formed from three quarks can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, and 20 amino-acids and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

The basic idea is simple. Since baryons consist of 3 quarks just as DNA codons consist of three nucleotides, one might ask whether codons could correspond to baryons obtained as open strings with quarks connected by two color flux tubes. This representation would be based on entanglement rather than letter sequences. The question is therefore whether the dark baryons constructed as string of 3 quarks using color flux tubes could realize 64 codons and whether 20 amino-acids could be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner.

The following model indeed reproduces the genetic code directly from a model of dark neutral baryons as strings of 3 quarks connected by color flux tubes.

1. Dark nuclear baryons are considered as a fundamental realization of DNA codons and constructed as open strings of 3 dark quarks connected by two colored flux tubes, which can be also charged. The baryonic strings cannot combine to form a strictly linear structure since strict rotational invariance would not allow the quark strings to have angular momentum with respect to the quantization axis defined by the nuclear string. The independent rotation of quark strings and breaking of rotational symmetry from SO(3) to SO(2) induced by the direction of the nuclear string is essential for the model.

   Baryonic strings could form a helical nuclear string (stability might require this) locally parallel to DNA, RNA, or amino-acid) helix with rotations acting either along the axis of the DNA or along the local axis of DNA along helix. The rotation of a flux tube portion around an axis parallel to the local axis along DNA helix requires that magnetic flux tube has a kink in this portion. An interesting question is whether this kink has correlate at the level of DNA too. Notice that color bonds appear in two scales corresponding to these two strings. The model of DNA as topological quantum computer [K4] allows a modification in

which dark nuclear string of this kind is parallel to DNA and each codon has a flux tube connection to the lipid of cell membrane or possibly to some other bio-molecule.

2. The new element as compared to the standard quark model is that between both dark quarks and dark baryons can be charged carrying charge $0, \pm 1$. This is assumed also in nuclear string model and there is empirical support for the existence of exotic nuclei containing charged color bonds between nuclei.

3. The net charge of the dark baryons in question is assumed to vanish to minimize Coulomb repulsion:

$$\sum_q Q_{em}(q) = - \sum_{flux\ tubes} Q_{em}(flux\ tube) \ . \tag{2.5.1}$$

This kind of selection is natural taking into account the breaking of isospin symmetry. In the recent case the breaking cannot however be as large as for ordinary baryons (implying large mass difference between Δ and nucleon states).

4. One can classify the states of the open 3-quark string by the total charges and spins associated with 3 quarks and to the two color bonds. Total em charges of quarks vary in the range $Z_B \in \{2, 1, 0, -1\}$ and total color bond charges in the range $Z_b \in \{2, 1, 0, -1, -2\}$. Only neutral states are allowed. Total quark spin projection varies in the range $J_B = 3/2, 1/2, -1/2, -3/2$ and the total flux tube spin projection in the range $J_b = 2, 1, -1, -2$. If one takes for a given total charge assumed to be vanishing one representative from each class (J_B, J_b), one obtains $4 \times 5 = 20$ states which is the number of amino-acids. Thus genetic code might be realized at the level of baryons by mapping the neutral states with a given spin projection to single representative state with the same spin projection. The problem is to find whether one can identify the analogs of DNA, RNA and amino-acids as baryon like states.

States in the quark degrees of freedom

One must construct many-particle states both in quark and flux tube degrees of freedom. These states can be constructed as representations of rotation group SU(2) and strong isospin group SU(2) by using the standard tensor product rule $j_1 \times j_2 = j_1 + j_2 \oplus j_1 + j_2 - 1 \oplus ... \oplus |j_1 - j_2|$ for the representation of SU(2) and Fermi statistics and Bose-Einstein statistics are used to deduce correlations between total spin and total isospin (for instance, $J = I$ rule holds true in quark degrees of freedom). Charge neutrality is assumed and the breaking of rotational symmetry in the direction of nuclear string is assumed.

Consider first the states of dark baryons in quark degrees of freedom.

1. The tensor product $2 \otimes 2 \otimes 2$ is involved in both cases. Without any additional constraints this tensor product decomposes as $(3 \oplus 1) \otimes 2 = 4 \oplus 2 \oplus 2$: 8 states altogether. This is what one should have for DNA and RNA candidates. If one has only identical quarks *uuu* or *ddd*, Pauli exclusion rule allows only the 4-D spin 3/2 representation corresponding to completely symmetric representation -just as in standard quark model. These 4 states correspond to a candidate for amino-acids. Thus RNA and DNA should correspond to states of type uud and ddu and amino-acids to states of type *uuu* or ddd. What this means physically will be considered later.

2. Due to spin-statistics constraint only the representations with $(J, I) = (3/2, 3/2)$ (Δ resonance) and the second $(J, I) = (1/2, 1/2)$ (proton and neutron) are realized as free baryons. Now of course a dark -possibly p-adically scaled up - variant of QCD is considered so that more general baryonic states are possible. By the way, the spin statistics problem which forced to introduce quark color strongly suggests that the construction of the codons as sequences of 3 nucleons - which one might also consider - is not a good idea.

3. Second nucleon like spin doublet - call it 2_{odd} - has wrong parity in the sense that it would require $L = 1$ ground state for two identical quarks (uu or dd pair). Dropping 2_{odd} and using only $4 \oplus 2$ for the rotation group would give degeneracies $(1, 2, 2, 1)$ and 6 states only. All the representations in $4 \oplus 2 \oplus 2_{odd}$ are needed to get 8 states with a given quark charge and one should transform the wrong parity doublet to positive parity doublet somehow. Since open string geometry breaks rotational symmetry to a subgroup SO(2) of rotations acting along the direction of the string and since the boundary conditions on baryonic strings force their ends to rotate with light velocity, the attractive possibility is to add a baryonic stringy excitation with angular momentum projection $L_z = -1$ to the wrong parity doublet so that the parity comes out correctly. $L_z = -1$ orbital angular momentum for the relative motion of uu or dd quark pair in the open 3-quark string would be in question. The degeneracies for spin projection value $J_z = 3/2, ..., -3/2$ are $(1, 2, 3, 2)$. Genetic code means spin projection mapping the states in $4 \oplus 2 \oplus 2_{odd}$ to 4.

States in the flux tube degrees of freedom

Consider next the states in flux tube degrees of freedom.

1. The situation is analogous to a construction of mesons from quarks and anti-quarks and one obtains the analogs of π meson (pion) with spin 0 and ρ meson with spin 1 since spin statistics forces $J = I$ condition also now. States of a given charge for a flux tube correspond to the tensor product $2 \otimes 2 = 3 \oplus 1$ for the rotation group.

2. Without any further constraints the tensor product $3 \otimes 3 = 5 \oplus 3 \oplus 1$ for the flux tubes states gives 8+1 states. By dropping the scalar state this gives 8 states required by DNA and RNA analogs. The degeneracies of the states for DNA/RNA type realization with a given spin projection for $5 \oplus 3$ are $(1, 2, 2, 2, 1)$. $8\times$ 8 states result altogether for both uud and udd for which color bonds have different charges. Also for ddd state with quark charge -1 one obtains $5 \oplus 3$ states giving 40 states altogether.

3. If the charges of the color bonds are identical as the are for uuu type states serving as candidates for the counterparts of amino-acids bosonic statistics allows only 5 states ($J = 2$ state). Hence 20 counterparts of amino-acids are obtained for uuu. Genetic code means the projection of the states of $5 \oplus 3$ to those of 5 with the same spin projection and same total charge.

Analogs of DNA, RNA, amino-acids, and of translation and transcription mechanisms

Consider next the identification of analogs of DNA, RNA and amino-acids and the baryonic realization of the genetic code, translation and transcription.

1. The analogs of DNA and RNA can be identified dark baryons with quark content uud, ddu with color bonds having different charges. There are 3 color bond pairs corresponding to charge pairs $(q_1, q_2) = (-1, 0), (-1, 1), (0, 1)$ (the order of charges does not matter). The condition that the total charge of dark baryon vanishes allows for uud only the bond pair $(-1, 0)$ and for udd only the pair $(-1, 1)$. These thus only single neutral dark baryon of type uud *resp.* udd: these would be the analogous of DNA and RNA codons. Amino-acids would correspond to uuu states with identical color bonds with charges $(-1, -1)$, $(0, 0)$, or $(1, 1)$. uuu with color bond charges (-1, -1) is the only neutral state. Hence only the analogs of DNA, RNA, and amino-acids are obtained, which is rather remarkable result.

2. The basic transcription and translation machinery could be realized as processes in which the analog of DNA can replicate, and can be transcribed to the analog of mRNA in turn translated to the analogs of amino-acids. In terms of flux tube connections the realization of genetic code, transcription, and translation, would mean that only dark baryons with same total quark spin and same total color bond spin can be connected by flux tubes. Charges are of course identical since they vanish.

3. Genetic code maps of $(4\oplus 2\oplus 2)\otimes(5\oplus 3)$ to the states of 4×5. The most natural map takes the states with a given spin to a state with the same spin so that the code is unique. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1,2,3,2\}$ and $D_b \in \{1,2,2,2,1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1,2,3,4,6$ are predicted. The numbers $N(k)$ of amino-acids coded by D codons would be

$$[N(1),N(2),N(3),N(4),N(6)] = [2,7,2,6,3] \ .$$

   The correct numbers for vertebrate nuclear code are $(N(1),N(2),N(3),N(4),N(6)) = (2,9,1,5,3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2,9,1,5,3)$!

4. Stopping codons would most naturally correspond to the codons, which involve the $L_z = -1$ relative rotational excitation of uu or dd type quark pair. For the 3-plet the two candidates for the stopping codon state are $|1/2,-1/2\rangle\otimes\{|2,k\rangle\}$, $k = 2,-2$. The total spins are $J_z = 3/2$ and $J_z = -7/2$. The three candidates for the 4-plet from which two states are thrown out are $|1/2,-3/2\rangle \otimes \{|2,k\rangle,|1,k\rangle\}$, $k = 1,0,-1$. The total spins are now $J_z = -1/2,-3/2,-5/2$. One guess is that the states with smallest value of J_z are dropped which would mean that $J_z = -7/2$ states in 3-plet and $J_z = -5/2$ states 4-plet become stopping codons.

5. One can ask why just vertebrate code? Why not vertebrate mitochondrial code, which has unbroken $A-G$ and $T-C$ symmetries with respect to the third nucleotide. And is it possible to understand the rarely occurring variants of the genetic code in this framework? One explanation is that the baryonic realization is the fundamental one and biochemical realization has gradually evolved from non-faithful realization to a faithful one as kind of emulation of dark nuclear physics. Also the role of tRNA in the realization of the code is crucial and could explain the fact that the code can be context sensitive for some codons.

If the pairing is based on the assumption that total quark spins and total flux tube spins are identical, the pairing of dark variants of DNA and its conjugate and DNA and mRNA are are not unique at the level of dark matter but respect the genetic code. Divisor code to be discussed later and equivalent with dark baryon code in realization based on magnetic flux tubes predicts similar non-uniqueness.

Is the genetic code a composite of $64 \to 40$ and $40 \to 20$ codes?

As found, dark baryon counterpart of tRNA could correspond to the multiplet of states containing 40 states. According to [I21] most organisms have fewer the 45 species of tRNA. Typical value of anticodons is around 30 and in some organisms the number is as low as 22. This means that the number of different anticodons in tRNA is not larger than 45 and could be at most 40. Unfortunately I do not know what the real situation is. The realization of mRNA-tRNA pairing is known to be based on wobble base pairing [I21]. This means that the pairing is not unique for the third nucleotide of the anticodon so that all mRNA codons can pair with tRNA in a way consistent with the genetic code.

This finding suggests that tRNA could correspond to a 40-plet of anticodons at the level of dark matter then for tRNA-amino-acid genetic code the numbers of codons $N(k)$ with given degeneracy k would be $(N(1),N(2),N(3)) = \{5,10,5\}$. The interpretation would be as $DNA \to tRNA$ dark baryon genetic code projection of states of $4\oplus 2\oplus 2$ to states of 4 with the same spin in color bond degrees of freedom to a state with same spin in $J = 2$ multiplet with 5 states. Numbers of dark aminocids with given degeneracy k would $(N(1),N(2)) = \{16,24\}$. Ordinary genetic code would result as a composite of the projections associated with these codes. If the identification in terms of 40-plet makes sense one might consider the possibility that the evolution for tRNA-dtRNA correspondence has not yet achieved the ideal situation in which tRNA anti-codons would be in 1-1 correspondence with their dark counterparts.

Objections

Consider next some particle physicist's objections against this picture.

1. The realization of the code requires the dark scaled variants of spin 3/2 baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one has a scaled up variant of hadron physics: possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states can be scaled up.

2. Both the absolute and relative mass differences between Δ and N *resp.* ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant 1/137 - so that the mass splittings could be so small as to make decays impossible.

3. Dark hadrons could have lower mass scale than the ordinary ones if scaled up variants of quarks in p-adic sense are in question. Note that the model for cold fusion that inspired the idea about genetic code requires that dark nuclear strings have the same mass scale as ordinary baryons. In any case, the most general option inspired by the vision about hierarchy of conscious entities extended to a hierarchy of life forms is that several dark and p-adic scaled up variants of baryons realizing genetic code are possible.

4. A heavy objection relates to the addition of $L_z = -1$ excitation to $S_z = |1/2, \pm 1/2\rangle_{odd}$ states which transforms the degeneracies of the quark spin states from $(1, 3, 3, 1)$ to $(1, 2, 3, 2)$. The most plausible answer is that the breaking of the full rotation symmetry induced by nuclear string reduces $SO(3)$ to $SO(2)$. Also the fact that the states of massless particles are labeled by the representation of $SO(2)$ might be of some relevance.

The conclusion is that genetic code can be understood as a map of stringy baryonic states induced by the projection of all states with same spin projection to a representative state with the same spin projection. Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin. Charge neutrality is essential for having only the analogs of DNA, RNA and amino-acids and would guarantee the em stability of the states.

2.5.2 DNA As Topological Quantum Computer Hypothesis And Dark Genetic Code

The coding of DNA codons by assigning to A, G *resp.* T, C of u and d quarks *resp.* their anti-quarks works nicely in the model of DNA as topological quantum computer. One can however consider also the option for which dark baryons code for entire DNA codons.

1. DNA as TQC using dark baryons to represent DNA codons would require that DNA strand is accompanied by a nuclear string parallel to it. If the pairing of baryons at the ends of string requires only opposite total quark spins and total flux tube spins the map would obey genetic code rather than being 1-1. The situation changes if dark baryon states are in 1-1 correspondence with the integers (n_a, n_b) labeling the page of book at which magnetic body of the codon resides.

2. The condition that the other end of flux tube beginning from the DNA codon contains nuclear string made from anti-baryons is natural but matter antimatter asymmetry if present also for dark matter does not favor this while mesonic strings with quarks at their ends are natural.

3. Rotating kinks assignable to 16 codons might be problematic from the point of TQC unless they represent codons with some special significance and play some special role - perhaps representing control commands in TQC program.

4. The flux tubes assignable to codons -instead of nucleotides as for earlier realization - would be basic units connected to lipids. The entanglement between dark baryon states of dark nuclear string would replaced the entanglement between quarks and anti-quarks at the ends of the flux tubes.

5. Only the portions of DNA having interpretation as gene have a natural decomposition to codons. Hence the dark baryon representation of codons is not attractive idea in intronic portions of the genome forming the most plausible candidates for quantum computing part of DNA since the portion of introns has been increasing during evolution and highest variation of this portion is encountered in human brain [I22]. Hence one might think that TQC as relatively late outcome of the evolution and that only this part of genome is responsible for TQC so that the mpa of nucleotides to quarks would realize genetic code. Furthermore, braiding matters in TQC much more than the colors of braid strands determined by nucleotides so that intronic portions could quite well be repeating sequences without any obvious as information carriers in standard sense and therefore interpreted as junk DNA. There would be also an analogy between emergence of written language meaning that words as holistic entities were replaced with sequences of letters having as such no meaning.

2.6 Could One Find A Geometric Realization For Genetic And Memetic Codes?

Many-sheeted space-time makes possible large deviations from gravitation predicted by GRT, which in TGD framework can be seen as a description of gravitation at the long length scale limit. A fundamental distinction between GRT and TGD is that in TGD framework gravitational constant and cosmological constant - actually space-time dependent cosmological "constants" emerge as predictions of the theory rather than as fundamental constants of Nature.

For almost two decades ago I deduced by purely dimensional considerations a formula for gravitational constant G in terms of p-adic length scale and exponent of Kähler action for CP_2 type vacuum extremal defining the line of generalized Feynman diagram representing graviton [K57]. The prediction was that G should have an entire spectrum of values and approach p-adic length scale squared $L_p^2 = pR_{CP_2}^2$ when the action of the deformed CP_2 type vacuum extremal becomes small: this happens at short length scale limit. In particular, hadronic strings would correspond to strong gravitation limit, and TGD predicts fractally scaled up variants of ordinary hadron physics so that a rich spectrum of strong gravities follows as a prediction. This means that in TGD Universe the the gravitational effects on space-time geometry can be rather dramatic even in condensed matter length scales whereas in GRT the effects are extremely small.

The cosmic honeycomb having voids with size of order 10^8 ly as basic building bricks is one possible quasi-lattice like structure suggested by these considerations. In condensed matter length scales strong gravitation could allow similar quasi-lattice like structures and icosahedral water clusters having tetrahedrons as building bricks could be examples of structures of this kind.

Cosmic honeycombs and their possible counterparts for water clusters modeled as consisting of icosahedral pieces of S^3 bring in mind foams (see `http://tinyurl.com/3a29pz`). Soap film foam is perhaps the most familiar example about foam. Plateau's laws (see `http://tinyurl.com/y7rrstej`) govern the structure of many foams. Mean curvature is constant for each film and physically derives from area minimization assuming constant pressure difference over the film. 3 films meet at angle of 120 degrees along a line known as Plateau border and 4 Plateau borders meet at each vertex at tetrahedral angle of $arcos(-1/3) \simeq 109.47$ degrees (tetrahedral angle is defined as the angle between radii drawn from the center of tetrahedron to its vertices). This suggests spherical tetrahedron as a basic building brick in a model as a honeycomb built from pieces of S^3. Plateau's laws can be derived mathematically for foams, for which films are minimal surfaces (pressure difference vanishes).

The idea that icosahedral structures assignable to water clusters could define a geometric representation of some kind of code is very intriguing. Genetic code is of course the code that comes first in mind. The observation that the number of faces of tetrahedron (icosahedron) is 4 (20) raises the question whether genetic code might have a geometric representation and the following piece of text is inspired by this question. In TGD framework also a second code emerges: I have christened

it memetic code [K39]. Also memetic code could have a geometric realization. Another purely TGD-based notion is that of dark DNA allowing to assign the states of dark protons with DNA, RNA, tRNA and amino-acids and to predict correctly the numbers of DNA codons coding for a given amino-acid in vertebrate genetic code [L1].

In the following some observations suggesting that this kind of geometric representation might exist are first discussed. After that a proposal for how genetic and memetic codes could be realized geometrically is considered.

2.6.1 The Notions Of Memetic Code And Dark Genetic Code

Before going to the topic two TGD inspired concepts must be introduced, namely the notions of memetic code and dark genetic code. From the perspective of standard biology the talk about codes in plural might sound highly speculative. If one takes serious the analogy of living matter with a computing system, it becomes easier to imagine that genetic code could have generalizations and that these codes could have several representations just as computers use an almost unlimited number of different languages. Living matter would in this picture consist of sub-systems emulating each other just as ordinary computers do.

The notion of memetic code

The notion of memetic code introduced for more than 20 years ago allows to interpret the sequences of 21 DNA codons as memetic codons [K39]. The starting point is so called Combinatorial Hierarchy [A30]. Mersenne integers are defined as numbers $M_n = 2^n - 1$. For some values of n, which belong to a subset of primes, one obtains Mersenne primes. In particular the lowest members in the hierarchy defined by the recursive formula $M(n+1) = M_{M(n)}$ with $M(1) = 1$, one obtains the sequence $M(1) = 1$, $M(2) = 3$, $M(3) = 7$, $M(4) = 127$, $M(5) = 2^{127} - 1$, ... All the explicitly listed Mersenne integers $M(n)$, $n > 1$, are Mersenne primes. An unproven conjecture by Hilbert is that all numbers $M(n)$, $n > 1$ in the sequence are Mersenne primes.

What makes this sequence so interesting is that the $M(n) + 1$ as a power of 2 defines the number of elements for a Boolean algebra. One can say that in a structure with $M(n)$ elements one has thrown single element out from the Boolean algebra. This procedure is natural if Boolean algebra is represented as subsets of a set: the subset which is empty is not realizable physically and must be thrown out. One can say that Combinatorial Hierarchy corresponds to an abstraction hierarchy with levels consisting of statements, statements about statements, statements about.... The geometric analog of this hierarchy would be a fractal structure consisting of geometric objects consisting of points, geometric objects consisting of points replaced with geometric objects, ... Something like this one might expect in living systems.

Furthermore, in Boolean algebra each element has negation and only half of the elements can represent statements, which are simultaneously true. Therefore for a Boolean algebra with 2^n elements only 2^{n-1} elements can represent mutually consistent truths, "axioms". For the Combinatorial Hierarchy the numbers of "axioms" would be $1, 2, 4, 64, 2^{126}, ...$ At the third level one obtains the number 4 of DNA nucleotides, at the next level the number 64 of DNA codons, and at the next level one obtains the number $(2^6)^{21} = 2^{126}$ of DNA sequences obtained from 21 DNA codons. This led to the proposal that there might exist a hierarchy of analogs of the genetic code and that the highest physically realized code in the sequence could be "memetic code" assignable to M_{127}.

The notions of dark nucleus and dark genetic code

The notions of dark nucleus and dark genetic code belong to the most speculative ideas of TGD inspired quantum biology. The original motivation for the notion of dark proton came from the observations suggesting that in atto-second time scale 1/4: th of protons of water molecules are dark in the sense that are not visible in electron scattering and neutron diffraction [D3, D2, D4].

The proposed TGD-based interpretation is that the protons are dark in the sense of having large value of effective Planck constant assignable to their magnetic body [L1]. The varying fraction of dark protons could explain the rich spectrum of anomalous temperature and pressure dependences of many observables related to water.

A model for dark nucleons as consisting of 3 dark quarks leads to a completely unexpected connection with genetic code. One can group the states of the dark nucleon (proton) to groups such that these groups correspond to DNA, mRNA, tRNA, and amino-acids and there is a natural map realizing vertebrate genetic code in the sense that the numbers of dark DNA codons mapped to a given dark amino-acid is the same as for vertebrate genetic code.

The recent work of Persinger's group [J14, J15, J16] combined with the observation of Hu and Wu [J19] that the magnetic interaction energy between protons assigned to the opposite sides of cell membrane corresponds to frequency in EEG range led to the conjecture that the pair of cell membrane lipid layers is accompanied by a pair of dark proton strings analogous to DNA double strand and indeed representing double DNA strand. There is also a close connection with the model of DNA as topological quantum computer [K4]: in this model magnetic flux tubes connecting nucleotide with lipids are responsible for braiding defining the quantum computer programs.

2.6.2 Could The Faces Of Tetrahedron Correspond To The Four DNA Nucleotides?

Consider first the intriguing observations suggesting that tetrahedral and icosahedral geometries relate to genetic code and its generalization to memetic code [K39]

1. The opening solid angle for each of the 20 tetrahedrons in S^3 icosahedron is $\Psi = 4\pi/20$. On the other hand, in DNA strand this angle corresponds in a good approximation to the twist angle for a single nucleotide from the fact that 30 DNA nucleotides (10 codons corresponds to twist angle of 6π (and to a length of 10 nm for DNA strand). For twist angle of 2π the number of nucleotides is not divisible by 3 (integer number of codons). This could be seen as a hint that S^3 icosahedral water clusters are biologically important.

2. Tetrahedron has 4 faces. Could they somehow correspond to the 4 DNA nucleotide? In order to distinguish between codons one must be able to distinguish between the faces of the tetrahedra - mark them - , to assign to given face a unique DNA, and to select one of the faces of tetrahedron - to "activate" it. In the case of DNA double strand this could mean that two of the faces of a given tetrahedron are glued to the precedessor and successor of the nucleotide in the DNA strand. The third face would be paired with conjugate strand by hydrogen bonds so that one open face would remain and would represent DNA nucleotide.

   The marking of the faces of the S^3 tetrahedron would require a breaking of $SO(3)$ symmetry. Symmetry breaking could take place when one looks the tetrahedron in E^3 geometry. One could say that $SO(4)$ symmetry of S^3 geometry breaks the $SO(3) \times T^3$ symmetry of E^3 (emergence of high space-time symmetry is not consistent with high embedding space symmetry). For instance, the faces of the tetrahedron could have different areas in E^3 metric. The breaking of symmetries could be due to the shift of the S^3 tetrahedron from North Pole of S^3 to some other point, and due to the breaking of translational invariance of E^3 for S^3 tetrahedron. The external face of an icosahedral tetrahedron can be distinguished from the other three faces which are internal even without the breaking of $SO(3)$ symmetry (only breaking of $SO(4)$ symmetry of S^3).

2.6.3 Could The 20 Outer Faces/Tetrahedrons Of The Icosahedron Correspond To Amino-Acids?

S^3 icosahedron has 20 faces. Could they somehow correspond to 20 different amino-acids? To achieve this two conditions must be satisfied.

1. One must be able to distinguish between the outer faces of the icosahedron so that one can associate to a given face only single amino-acid. As already explained, symmetry breaking allowing to distinguish between the faces is possible in E^3 geometry if the S^3 icosahedron is moved from the origin of S^3 to some other point.

   For instance, the areas of the faces could be different and if the amino-acid is glued only to the face which it "fits" (recall the analogy with lock and key mechanism) one would have the desired 1-1 correspondence with amino-acids and icosahedrons. The outcome could be that

only single amino-acid can be glued to a given face. Note that magnetic flux tubes could realize the correspondence between amino-acids and icosahedral outer faces in very concrete manner: this mechanism is proposed as a general mechanism of bio-catalysis making it possible for two reacting molecules to find each other in the thick molecular soup [K4, K28].

2. One must also be able to "activate" a given face, perhaps by gluing something to it. This "something" could be amino-acid but also something else, say additional tetrahedron representing a genetic codon.

Dark DNA codon corresponds to dark proton identified as 3-quark state. Could this 3-quark state have a geometric representation? The decomposition of icosahedral surface to triangles suggests that triangle is a natural geometric object for DNA, and in the sequel a geometric model for dark DNA codons based on a repeated division of equilateral triangle to equilateral triangles is considered. One must however keep in mind that this kind of representation might not be necessary. It is enough to assume single dark proton per each tetrahedral building brick of icosahedron. Dark protons would in turn be connected to nuclear string.

2.6.4 Icosahedral Realization Of The Memetic Code?

In the presence of symmetry breaking allowing to distinguish between the 20 icosahedral tetrahedrons the external faces of the icosahedron can be in 1-1 correspondence with amino-acids. One can consider even more ambitious option. The icosahedron + tetrahedron structures with 20 icosahedral tetrahedrons plus 1 tetrahedron glued to some icosahedral face could be perhaps interpreted as memetic codons if each tetrahedron represents a genetic codon. A crucially important constraint is that the icosahedral tetrahedrons have a unique linear ordering.

These memetic codons could be also associated with real amino-acids if a given amino-acid can attach only to single face of the icosahedron and there is a mechanism which selects which face is "active". This particular amino-acid would be naturally coded by the 21^{st} DNA codon at the surface of the icosahedron so that one would kill to flies with single blow obtaining both the a representation of memetic codons and assign to the 21^{st} DNA codon corresponding amino-acid. If so, water clusters could represent immense amount of dark biological information.

How could one realize dark memetic codons as dark nuclei? The obvious possibility is as strings of 21 dark protons: in this case the linear ordering of protons would be essential for the realization of the code. A realization inspired by the conventional nuclear physics framework leads naturally to the icosahedral structure.

1. A nucleus carrying 20 protons or neutrons is a magic nucleus (exceptionally stable). For instance, the biologically important ion Ca^{++} corresponds to double magic nucleus has 20 protons and 20 neutrons. Also neutrons are present in ordinary nuclei, and I have proposed that protons and neutrons could correspond to different space-time sheets: perhaps these space-time sheets could correspond to Northern and Southern hemispheres of S^3.

2. The information about the ordering of dark nucleons is not lost if icosahedral nucleus + single proton is obtained by a convolution of a dark proton nuclear string. The icosahedral core of S^3 icosahedral dark nucleus consisting of 20 dark protonic tetrahedra would be magic and analogous to a closed shell of an atom.

   From the net representation (see `http://tinyurl.com/yatsguy5`) of icosahedron obtained by cutting the icosahedron open, it is clear that there are at least two paths of this kind but differing only by orientation. Each of them can be regarded as a union of 5 4-triangle paths of the net combining to form a connected triangle path at the surface of icosahedron when appropriate identifications of the edges are made. The step between neighboring triangles corresponds to reflecting with respect to the common edge. Each 4-triangle path corresponds to a path containing vertices of "big" tetrahedron (not one of the twenty tetrahedrons with one vertex at the center of icosahedron) shared also by icosahedron. This sequence corresponds to the orbit of the icosahedral isometry group, which is the alternating group A_5 (60 even permutations of 5 letters) acting transitively so that the orbit visits all triangles at the isosahedral surface. A good guess is that these two oppositely oriented orbits and their images under A_5 define the only ways to fill the icosahedral surface by single path. The number

of images is 12 since each of the 12 vertices of icosahedron defines one tetrahedron. Note that this identification for the folded DNA sequence allows also to think that it traverses the surface of the icosahedron rather than filling the entire icosahedron.

3. In chemistry valence electrons dictate the chemistry and in complete analogy with this the 21^{st} dark proton at the surface of the icosahedron would code for the amino-acid attached to it. This icosahedral folding of the nuclear string would be analogous to the folding of protein to a globular shape in its resting state. This folding could indeed characterize the resting state of dark DNA and when dark DNA becomes active - say during a transcription like process - unfolding would occur. Similar unfolding takes place also for the ordinary DNA.

If each icosahedral tetrahedron corresponds to one particular amino-acid, one can argue that a given tetrahedron can be associated only to those DNA codons which code the amino-acid associated with the tetrahedron. As following arguments show, this correspondence leads to problems.

1. If the genetic code dictates the correspondence between tetrahedra and DNA codons, then the three stopping sign codons cannot be contained by the memetic codons so that memetic code would not be fully realised.

2. The allowed memetic codons would code for sequence of 20 different amino-acids and there would be strong correlations between neighboring amino-acids in the sequence since the DNA sequence would define a non-self-intersection path visiting every triangle at the surface of the icosahedron only once, and a given amino-adic would have as edge neighbors only three amino-acids. If only single sequence is possible as proposed above, then only single amino-adic sequence containing all amino-acids would be allowed and the number of memetic codons coding for it would be product of numbers of codons coding for the 20 amino-acids.

2.6.5 Geometric Representation Of Dark DNA Codons

Could one have a concrete geometric representation for DNA codons and nucleotides in the proposed model? The fact that dark DNA codon consisting of 3 quarks corresponds to triangle (or corresponding icosahedral tetrahedron) is highly suggestive.

1. Icosahedral surface triangle would naturally correspond to a triplet defining DNA codon and the vertices of the triangle to the letters A, T, C, G. This could be achieved geometrically by dividing a given icosahedral surface triangle, call it T, to 4 equilateral triangles T_i, $i = 1, 2, 3, 4$ and assigning the three letters of the codon to the resulting three triangles T_i, $i = 1, 2, 3$, sharing a vertex with T. The inner triangle T_4 would remain unpopulated.

2. How to represent codon geometrically for T and perhaps also the letter A, T, C, G for T_i? One manner to achieve the latter goal is to divide T_i to further equilateral triangles T_{ij}, $j = 1, 2, 3, 4$ and assign A, T, C, G to T_i by some kind of symmetry breaking distinguishing between them geometrically. The dark codon consisting of 3 quarks could select somehow this triangle. The simplest possibility is that the spatial wave function of i^{th} quark of proton is located inside one T_{ij}, $i = 1, 2, 3$, $j = 1, 2, 3, 4$. The connection with quark model of nucleon would be that the quarks are at the vertices of triangle T_i and are connected to the centre of T_i by color flux tubes. Inside T_i the location of quark is inside T_{ij}. An alternative option is that quarks are connected by color flux tubes directly to each other.

A couple of remarks are in order.

1. The model for dark DNA does *not* allow to represent the counterparts of DNA codons as unentangled products of 3-quark states: the states are quantum superpositions of 3-quark states and the decomposition of codon to letters is not possible. This means that DNA codons are "irreducible". One can however deduce correspondence between codons and amino-acids and it corresponds to the vertebrate genetic code. The geometric representation for the codons as mapping of DNA codons to geometric objects however still make sense if the positions of quarks obey the above rule for a given entangled quark triplet.

2. The model for dark DNA [L1] assumes that dark DNA strand is linear so that symmetry breaking of rotational symmetry to SO(2) consisting of rotations around the strand takes place. In the recent situation similar breaking of symmetry must take place and the natural axis is no the axes defined by the normal of the triangle defining dark DNA codon.

3. One can also wonder what might be the geometric counterparts of dark mRNA, tRNA, and amino-acids.

2.6.6 Could Water Clusters Represent Memetic Code?

Could the dark protons realizing dark genetic codons as nuclear strings be associated with water molecules or clusters of them? One can imagine two alternative realizations of the icosahedral memetic codons.

1. It is known that water molecules themselves have tetrahedral structure with 2 lone electron pairs and H_+ nuclei are at the vertices of the tetrahedron (maybe regular S^3 tetrahedron). There is chemical symmetry breaking since the faces come in two types: 2 faces of type $H_+H_+(2e)$ and 2 faces of type $H_+(2e)(2e)$. If the second proton is of the water molecule is dark, a further symmetry breaking takes place and one has faces of 3 types. The symmetry of $H_+H_+(2e)$ faces could be broken if they correspond the two lone electron pairs are located the center of icosahedron and it surface. The chemical symmetry breaking and perhaps also magnetic flux tubes would help to assign to unique amino-acid to one of the tetrahedrons.

   Icosahedron would consists of a folded linear sequence of tetrahedral water molecules - formed perhaps perhaps by hydrogen bonding. The representation of memetic codon as a single icosahedral cluster of 21 water molecules would predict single dark proton per water molecule. Recall that the average in atto-second time scale would be 1/4 dark protons per water molecule. I do not know whether icosahedral clusters of this kind exist.

2. It is however known that known (see `http://tinyurl.com/yb9waklg`) that 14 water molecules indeed combine to form tetrahedral structures (see `http://tinyurl.com/ybl9eqt9` [D3], and that these in turn combine to form icosahedral structures. The size scale of the 14 molecule cluster is nearer to the size scale of single DNA nucleotide so that perhaps this option is more realistic. If these structures provide a representation of memetic codons with tetrahedral structure of 14 water molecules representing single DNA codon or amino-acid, there are 14 water molecules per single dark proton representing dark DNA codon.

2.7 About Physical Representations of Genetic Code in Terms of Dark Nuclear Strings

The view about evolution as a random process suggests that genetic code is pure accident. My own view is that something so fundamental as life cannot be based on pure randomness. TGD has led to several proposals for genetic code, its emergence, and various realizations based on purely mathematical considerations or inspired by physical ideas. One can argue that genetic code is realized in several ways just like bits can be represented in very many ways. Two especially interesting proposals have emerged. The first one is based on geometric model of music harmony involving icosahedral and tetrahedral geometries. Second model has two variants based on dark nuclear strings: the original version maps codons do dark nucleons, the more recent version maps codons to dark 3-nucleon states. Both models predict correctly the numbers of DNA codons coding for a given amino-acid but the model based on dark 3-nucleon triplets is favoured by some recent findings suggesting a pairing between DNA nucleotides and dark nucleons. Also the counterparts of RNA,tRNA, and amino-acids are predicted. In the sequel the updated nuclear string variant is summarized and also its connection with the model of harmony is discussed.

2.7.1 Background

The view about evolution as a random process suggests that genetic code is pure accident. My own view is that something so fundamental as life cannot be based on pure randomness. TGD has

led to several proposals for genetic code, its emergence, and various realizations based on purely mathematical considerations or inspired by physical ideas (see chapters of [K38] and [L1, K41]). One can argue that genetic code is realized in several ways just like bits can be represented in very many ways.

Two especially interesting proposals have emerged. The first one is based on geometric model of music harmony [L11] involving icosahedral and tetrahedral geometries. Second one having two variants is based on dark nuclear strings. Both models predict correctly the numbers of DNA codons coding for a given amino-acid. In the sequel the nuclear string variant and also its connection with the model of harmony is discussed in detail.

It is good to start with an overall view about physical realization of genetic code that I have discussed during last twenty years.

Genetic code and Combinatorial Hierarchy

The first proposal [K39] was purely mathematics inspired and in terms of so called Combinatorial Hierarchy consisting of certain Mersenne primes $M_k = 2^k - 1$ via the formula $M(n+1) = M_{M(n)}$ having interpretation in terms of abstraction. The list beginning from $M(1) = 2$ is $2, M_2 = 3, M_3 = 7, M_7 = 127, M_{127} = 2^{127} - 1$: it is not known whether subsequent integers are Mersenne primes. The idea is that the $2^k - 1$ points define almost full Boolean algebra spanned by k bits- one visualization is as a polygon. The algebra defined $k - 1$ bits is maximal full Boolean sub-algebra having interpretation as maximal number of mutually independent statements, which can hold true simultaneously. For M_7 ($k = 3$) one would have 2 bits and 4 codons. For M_7 one would have $k = 7$ and 6 bits and genetic code. For M_{127} one would have 126 bits and one would have "memetic" code realizable in terms of sequences of 21 DNA codons.

Geometric theory of harmony and genetic code

The idea that the 12-note scale could allow mapping to a closed path going through all vertices of icosahedron having 12 vertices and not intersecting itself is attractive. Also the idea that the triangles defining the faces of the icosahedron could have interpretation as 3-chords defining the notion of harmony for a given chord deserves study. The paths in question are known as Hamiltonian cycles and there are 1024 of them [A7]. There paths can be classified topologically by the numbers of triangles containing 0, 1, or 2 edges belonging to the cycle representing the scale. Each topology corresponds to particular notion of harmony and there are several topological equivalence classes.

In the article [L16] I introduced the notion of Hamiltonian cycle as a mathematical model for musical harmony and also proposed a connection with biology: motivations came from two observations. The number of icosahedral vertices is 12 and corresponds to the number of notes in 12-note system and the number of triangular faces of icosahedron is 20, the number of amino-acids. This led to a group theoretical model of genetic code and replacement of icosahedron with tetra-icosahedron to explain also the 21st and 22nd amino-acid and solve the problem of simplest model due to the fact that the required Hamilton's cycle does not exist. The outcome was the notion of bioharmony.

All icosahedral Hamilton cycles with symmetries(Z_6,Z_4, Z_2^{rot} and $Z_2 refl$ turned out to define harmonies consistent with the genetic code. In particular, it turned out that the symmetries of the Hamiltonian cycles allow to to predict the basic numbers of the genetic code and its extension to include also 21st and 22nd amino-acids Pyl and Sec: there are actually two alternative codes - maybe DNA and its conjugate are talking different dialects! One also ends up with a proposal for what harmony is leading to non-trivial predictions both at DNA and amino-acid level.

The conjecture is that DNA codons correspond to 3-chords perhaps realized in terms of dark photons or even ordinary sound. There are 256 different bio-harmonies and these harmonies would give additional degrees of freedom not reducing to biochemistry. Music expresses and creates emotions and a natural conjecture is that these bio-harmonies are correlates of emotions/moods at bio-molecular level serving as building bricks of more complex moods. Representations of codons as chords with frequencies realized as those of dark photons and also sound is what suggests itself naturally. This together with adelic physics involving hierarchy of algebraic extensions of rationals

would explain the mysterious lookin connection between rational numbers defined by ratios of frequencies with emotions.

Letter-wise representations of genetic code in terms of single particle states

The model for DNA-cell membrane system as topological quantum computer with lipids and DNA nucleotide or codons connected by flux tubes led to a proposal for the correspondence of letters of genetic code with particle states.

1. The original proposal was that the 4 letters A,T,C,G correspond to dark u and d quark and their antiparticles $\overline{u}$ and $\overline{d}$. Quarks and their antiparticles would reside at the ends of the flux tube. Spin would not matter in this model. The obvious criticism is that introducing dark antiquarks is too far fetched.

2. One can also consider a variant for which one has u and d quarks and spin matters.

3. TGD based model of bio-superconductivity assumes that flux tubes appear as pairs with members of Cooper pair at parallell flux tubes [K65, K66]. This suggests that electron pairs at in spin 1 and spin 0 states could realize the code. The spin of the electrons would matter and one would obtain 4 states - two qubits in correspondence with A,T,C,G.

Also the model of dark nuclear strings allows to imagine letter-wise representations of the genetic code. The model for cold fusion based on the findings of Prof. Holmlid and his group [C1, L35] leads to the idea that Pollack's EZs [L15] are accompanied by dark nuclear strings consisting of dark protons connected by color flux tubes analogous to mesons [L22, L35]. Color bonds would have quark and antiquark at their ends [L1]. This leads to non-trivial predictions and nuclear anomalies giving support for the notion of nuclear string have emerged, the latest anomaly is so called X boson with mass of 17 MeV [L36, C3] having identification as p-adically scaled analog of pion.

Dark protons could also decay to neutrons by dark weak decays rapidly since dark weak bosons are effectively massless below dark Compton length. Furthermore, proton plus negatively charged color bond could behave like neutron as far as chemistry is considered. The X boson anomaly of nuclear physics [L36] suggests that the flux tubes in the ground state correspond to pion-like states which can be colored: this could bind the nucleons to form a nucleus. The evidence for the occurence of cold fusion in living matter gives support for the role of dark nuclear strings [K49] [L35].nOne can consider several representations of the genetic code in this framework.

Consider first models for which letters are represented separately.

1. Dark protons and neutrons have 4 spin states and could correspond to letter A,T,C,G. In this case dark color bonds would not matter. A rather convincing proposal for a pathway leading to a selection purines as DNA nucleotides has been proposed [I34]. TGD based model [L33] suggests that acidic solutions contain dark protons and purine results when the precursor amine combines with dark proton such that the proton remains dark. Could DNA nucleotide pair with dark protons and neutrons (resulting in dark beta decay from dark proton strings yielded by Pollack's mechanism)?

2. Also the 4 states of dark color bonds between dark nucleons (3 pion-like states and one eta meson like state: spin 1 bonds would be analogous to ρ and ω mesons and have higher mass) correspond to letters A,T,C,G. Now the dark protons and neutrons would not matter. This option would require that the character of the nucleotide correlates with the color flux tube attached to the dark proton. They would have at their ends charge conjugate color bonds. The states would be of form $u\overline{u}, d\overline{d}, u\overline{d}, d\overline{u}$ with the ordering of q and $\overline{q}$ correlating with the direction in which transcription and replication take place being thus same or opposite). For conjugate strand the direction of strand would be opposite in the sense that one would have $\overline{u}u, \overline{d}u, \overline{du}, \overline{u}u$.

   For this option one could consider the strands of dark DNA double strand being connected by flux tube pairs resulting when U-shaped color flux tube have reconnected. If color flux tubes are colored, color confinement could bind the dark protons to dark nucleus. Similar mechanism could be at work for the ordinary nuclei.

The basic problem of all the proposals based on letter-wise correspondence is that they do not even try to explain the numbers of DNA codons coding for a given amino-acid and are also silent about tRNA.

Codon-wise representations of genetic code realized in terms of dark strings

For this option entire codons rather than letters would be represented. The difference between two representations is analogous to that between spoken and written languages. In spoken languages words are not analyzed further to letters. These models are able to predict also the numbers of codons coding for a given amino-acid successfully.

1. The geometric theory of harmony represents codons as 3-chords without assigning fixed notes to A,T,C,G and explains also DNA-amino-acid correspondence.

2. The map of codons to the dark nucleon states of dark nucleon consisting of dark u and d type quarks does the same and also predicts the degeneracies successfully.

3. This model can be modified by replacing u and d by dark nucleon states p and n without any change in predictions related to genetic code. The evidence that DNA codons indeed couple to dark nucleon states [L33] supports this option.

In the sequel I consider the models mapping DNA codons to dark nucleons and then generalize the model so that it applies to triplets of dark nucleons.

2.7.2 Codons as dark quark-triplet strings

Water memory is one of the ugly words in the vocabulary of the main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [K41, K85], [I47]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

The question is whether dark nuclear strings might provide a representation of the genetic code. In fact, I posed this question year before the results of the experiment came with motivation coming from the attempts to understand water memory. The outcome was a totally unexpected finding: the states of dark nucleons formed from three quarks can be grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, and 20 amino-acids and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

Could DNA and amino-acids correspond to dark quark triplet strings

The dark model emerged from the attempts to understand water memory [K41]. The outcome was a totally unexpected finding [L1, K41]: the states of dark nucleons formed from three quarks connected by color bonds can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, 20 amino-acids, and tRNA and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

The basic idea is simple. The basic difference from the model of free nucleon is that the nucleons in question - maybe also nuclear nucleons - consist of 3 linearly ordered quarks - just as DNA codons consist of three nucleotides. One might therefore ask whether codons could correspond to dark nucleons obtained as open strings with 3 quarks connected by two color flux tubes or as closed triangles connected by 3 color flux tubes. Only the first option works without additional assumptions. The codons in turn would be connected by color flux tubes having quantum numbers of pion or η.

This representation of the genetic would be based on entanglement rather than letter sequences. Could dark nucleons constructed as string of 3 quarks using color flux tubes realize 64 DNA codons? Could 20 amino-acids be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner? The codons would be not be anymore separable to letters but entangled states of 3 quarks.

If this picture is correct, genetic code would be realized already at the level of dark nuclear physics and maybe even in ordinary nuclear physics if the nucleons of ordinary nuclear physics are linear nucleons. Chemical realization of genetic code would be induced from the fundamental realization in terms of dark nucleon sequences and vertebrate code would be the most perfect one. Chemistry would be kind of shadow of the dynamics of positively charged dark nucleon strings accompanying the DNA strands and this could explain the stability of DNA strand having 2 units of negative charge per nucleotide. Biochemistry might be controlled by the dark matter at flux tubes.

The ability of the model to explain genetic code in terms of spin pairing is an impressive achievement, which I still find difficult to take seriously.

1. The original model identifying codons to dark nucleon states assumed the overall charge neutrality of the dark proton strings: the idea was that the charges of color bonds cancel the total charge of dark nucleon so that all states uuu, uud, udd, ddd can be considered. The charge itself would not affect the representation of codons. Neutrality assumption is however not necessary. The interpretation as dark nucleus resulting from dark proton string could quite well lead to the formation the analog of ordinary nucleus via dark beta decays [L35] so that the dark nucleus could have charge. Isospin symmetry breaking is assumed so that neither quarks nor flux tubes are assigned to representations of strong $SU(2)$.

   There is a possible objection. For ordinary baryon the mass of Δ is much larger than that of proton. The mass splitting could be however much smaller for linear baryons if the mass scale of excitations scales as $1/h_{eff}$ as indeed assumed in the model of dark nuclear strings [L22, L35].

2. The model assumes that the states of DNA can be described as tensor products of the four 3-quark states with spin content $2 \otimes 2 \otimes 2 = 4 \oplus 2_1 \oplus 2_2$ with the states formed with the 3 spin triplet states $3 \otimes 3 = 5 \oplus 3 \oplus 1$ with *singlet state dropped*. The means that flux tubes are spin 1 objects and only spin 2 and spin 1 objects are accepted in the tensor product. One could consider interpretation in terms of ρ meson type bonding or gluon type bonding. With these assumptions the tensor product $(2 \otimes 2 \otimes 2) \otimes (5 \oplus 3)$ contains $8 \times 8 = 64$ states identified as analogs of DNA codons.

   The rejection of spin 0 pionic bonds looks strange. These could however occur as bonds connecting dark codons and could correspond to different p-adic length scale as suggested by the successful model of X boson [L36].

   One can also ask why not identify dark nucleon as as closed triangle so that there would be 3 color bonds. In this case $3 \otimes 3 \otimes 3$ would give 27 states instead of 8 ($\oplus 1$). This option does not look promising.

3. The model assumes that amino-acids correspond to the states 4×5 with $4 \in \{4 \oplus 2 \oplus 2\}$ and $5 \in \{5 \oplus 3\}$. One could tensor product of spin 3/2 quark states and spin 2 flux tube states giving 20 states, the number of amino-acids.

4. Genetic code would be defined by projecting DNA codons with the same total quark and color bond spin projections to the amino-acid with the same (or opposite) spin projections. The attractive force between parallel vortices rotating in opposite directions serves as a metaphor for the idea. This hypothesis allow immediately the calculation of the degeneracies of various spin states. The code projects the states in $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ to the states of 4×5 with same or opposite spin projection. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1, 2, 3, 2\}$ and $D_b \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of amino-acids coded by D codons would be

$$[N(1), N(2), N(3), N(4), N(6)] = [2, 7, 2, 6, 3] \ .$$

The correct numbers for vertebrate nuclear code are $(N(1), N(2), N(3), N(4), N(6)) = (2, 9, 1, 5, 3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2, 9, 1, 5, 3)$!

This simple observation would suggest that genetic code could be realized already at the level of dark or even ordinary nuclear physics and bio-chemistry is only a kind of shadow of dark matter physics.

Objections against the identification of codons as dark quark triplets

Consider next some particle physicist's objections against the option mapping codons to dark nucleon states.

1. The realization of the model of codon as dark quark triplet requires the dark scaled variants of spin 3/2 baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one would have a scaled up variant of hadron physics: possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states could be scaled up.

2. Both the absolute and relative mass differences between Δ and N *resp.* ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant 1/137 - so that the mass splittings could be so small as to make decays impossible.

   The color magnetic spin interaction energy give rise to hyperfine splitting of quark in perturbative QCD is of form $E_c \propto \hbar g B/m$, where m is mass parameter which is of the order of baryon mass. Magnetic flux scales as $\hbar$ by flux quantization and if flux tube thickness scales as $\hbar^2$, one has $B \propto 1/\hbar$. Mass splittings would not depend on $\hbar$, which does not make sense. Mass splitting becomes small for large $\hbar$ if the area of flux quantum scales as $\hbar^{2+n}$, $n > 0$ so that color magnetic hyper-fine splitting scales as $1/\hbar^n$ from flux conservation. The magnetic energy for a flux tube of length L scaling as $\hbar$ and thickness $S \propto \hbar^{2+n}$ has order of magnitude $g^2 B^2 L S$ and does not depend on $\hbar$ for $n = 1$. Maybe this could provide first principle explanation for the desired scaling.

   The size scale of DNA would suggest that single DNA triplet corresponds to 3 Angstrom length scale. Suppose this corresponds to the size of dark nucleon. If this size scales as $\sqrt{\hbar}$ as p-adic mass calculations suggest, one obtains a rough estimate $\hbar/\hbar_0 = 2^{38}$. The proton-Δ mass difference due to hyper-fine splitting would be scaled down to about $2^{-38} \times 300$ MeV $\sim 10^{-9}$ eV, which is completely negligible in the metabolic energy scale .5 eV. If the size of dark nucleon scales as $\hbar$ the mass difference is about 12 eV which corresponds to the energy scale for the ionization energy of hydrogen. Even this might be acceptable.

For these reasons the option mapping codons to dark nucleon triplets is clearly favored and will be discussed in the following.

2.7.3 Codons as dark nucleon-triplet strings?

The assumption that entire codon rather than letter corresponds to a state of dark proton does not conform with the model for the origin of purines as DNA nucleotides [L33] assuming that purines, and in fact all nucleotides, are combined with dark proton unless one assumes that 3 nucleotides combine with the same dark proton. This looks somewhat artificial but cannot be excluded.

The arguments of the model involve only the representations of rotation group and since p and n have same spin as u and d, the arguments generalize to 3- nucleon states (ppp, ppn, pnn, nnn)

connected by two color bounds and organized to linear structures. Concerning genetic code, exactly the same predictions follow in the recent formulation of the model. In this case quark color is not present. One could however use the 1-dimensionality and the ordering of dark nucleons as already described.

The model with linear quark triplets generalizes by replacing dark u and d quarks with dark nucleons p and n. The analogs of ρ mesons would correspond to 2 bonds also now. Irrespective of changes of nucleons, all states would have decomposition $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ corresponding to the degrees of freedom associated with 3 nucleon spins and 2 neutral ρ meson spins.

ppp could correspond to DNA and RNA and proton charges would neutralize the negative charges of ordinary DNA codons. The singlet formed by bonds would be neglected. nnn triplets could correspond to amino-acids and trNA. Amino-acids could correspond to $4 \times 5 = 20$ and the remaining states $4 \otimes 3 \oplus (2 \oplus 2) \otimes 5 \oplus 3$. could correspond to 44 tRNAs. Also other options are possible and have net charges 2 and 1.

This variant has several nice features. The model is consistent with the model for dark nucleon strings consisting of nucleons and color bonds between them. There is no need to introduce Δ type nucleon states and colored states are not needed in fermionic sector. Color bonds must be colored if one wants ordinary bosonic statistics for flux tubes but here braid statistics might help. Colored bonds could of course have some important function.

Could dark DNA, RNA, tRNA and amino-acids correspond to different charge states of codons?

If dark codons correspond to dark nucleon triplets as assumed in the following considerations there are 4 basic types of dark nucleon triplets: ppp, ppn, pnn, nnn. Also dark nucleons could represent codons as uuu, uud, udd, ddd: the following discussion generalizes as such also to this case. If strong isospin/em charge decouples from spin the spin content is same independently of the nucleon content. One can consider the possibility of charge neuralization by the charges assignable to color flux tubes but this is not necessarily. In any case, one would have 4 types of nucleon triplets depending on the values of total charges.

Could different dark nucleon total charges correspond to DNA,RNA, tRNA and amino-acids? Already the group representation content - perhaps correlating with quark charges - could allow to distinguish between DNA, RNA, tRNA, and amino-acids. For amino-acids one would have only 4×5 and ordinary statistics and color singlets. For DNA and RNA one would have full multiplet also color non-singlets and for tRNA one could consider $(4 \oplus 2_1 \oplus 2_2) \times 5$ containing 40 states. 31 is the minimum number of tRNAs for the realization of the genetic code. The number of tRNA molecules is known to be between 30-40 in bacterial cells. The number is larger in animal cells but this could be due to different chemical representations of dark tRNA codons.

If the net charge of dark codon distinguishes between DNA,RNA, tRNA, and amino-acid sequences, the natural hypothesis to be tested is that dark ppp, ppn, pnn, and nnn sequences are accompanied by DNA,RNA, tRNA, and amino-acid sequences. The dark beta decays of dark protons proposed to play essential role in the model of cold fusion [**?**]ould transform dark protons to dark neurons. Peptide backbones are neutral so that dark nnn sequence could be also absent but the dark nnn option is more natural if the general vision is accepted. There is also the chemically equivalent possibility that only dark protons are involved: dark proton + neutral color bond would represent proton and dark proton + negatively charged color bond would represent neutron. At this moment it is not possible to distinguish between these two options.

Is this picture consistent with what is known about charges of amino-acids DNA,RNA, tRNA, and amino-acids? Consider first the charges of these molecules.

1. DNA strand has one negative charge per nucleotide. Also RNA molecule has high negative charge. This conforms with the idea that dark nucleons accompany both DNA and RNA. DNA codons could be accompanied by dark ppp implying charge neutralization in some scale and RNA codons by dark ppn. The density of negative charge for RNA would be 2/3 for that for DNA.

2. Arg, His, and Lys have positively charged side chains and Asp,Glu negative side chains (see `http://tinyurl.com/jsphvgt`). The charge state of amino-acid is sensitive to the pH value of solution and its conformation is sensitive to the counter ions present. Total charge for

amino-acid in peptide however vanishes unless it is associated with the side chain: as in the case of DNA and RNA it is the backbone whose charge is expected to matter.

3. Amino-acid has central C atom to which side chain, NH_2, H and COOH are attached. For free amino-acids in solution water solution $NH_2 \to NH_3^+$ tends to occur pH=2.2 by receiving possibly dark proton whereas COOH tends to become negatively charged above pH= 9.4 by donating proton, which could become dark. In peptide OH attach to C and one H attached to N are replaced with peptide bond. In the pH range 2.2-9.4 amino-acid is zwitterion for which both COOH is negatively charged and NH_2 is replaced with NH_3^+ so that the net charge vanishes. The simplest interpretation is that the ordinary proton from negatively ionized COOH attaches to NH_2 - maybe via intermediate dark proton state.

4. The backbones of peptide chains are neutral. This conforms with the idea that dark amino-acid sequence consists of dark neutron triplets. Also free amino-acids would be accompanied by dark neutron triplets. If the statistics is ordinary only 4 dark nnn states are possible as also 5 dark color flux tube states.

5. tRNA could involve dark pnn triplet associated with the codon. An attractive idea is secondary genetic code assigning RNA codons to tRNA-amino-acid complex and projecting $8 \otimes (5 \oplus 3)$ containing 64 dark RNA spin states to $8 \otimes 5$ containing 40 dark tRNA spin states with same total nucleon and flux tube spins. Dark tRNA codons would in turn be attached to dark amino-acids by a tertiary genetic code projecting spin states $8 \otimes 5$ to $4 \otimes 5$ by spin projection. In the transcription dark tRNA would attach to dark mRNA inducing attachment of dark amino-acid to the growing amino-acid sequence and tRNA having only dark tRNA codon would be left. The free amino-acids in the water solution would be mostly charged zwitterions in the pH range 2.2-9.4 and the negative charge of COO^- would be help in the attachement of the free amino-acid to the dark proton of tRNA codon. Therefore also the chemistry of free amino-acids would be important.

   An interesting question is why pnn triplets for tRNA would only 5 in flux tube degrees of freedom entire 8 in nucleon degrees of freedom. For RNA consisting of ppn triplets also 3 would be possible. What distinguishes between ppn and pnn?

The model should explain the widely different properties of DNA, RNA, tRNA, and amino-acids. There are two options.

1. DNA/RNA/amino-acid codons could correspond to ppp/ppn/nnn and tRNA would correspond to pnn (order is not necessarily this). Different charge or dark codons explain why DNA (RNA) has H (OH) in $2'$ position. The repulsive Coulomb energy between dark codons would be stronger for DNA and the compensation of this forces by the magnetic tension associated with the flux tube pair connecting codon and anticodon this might have something to do with the stability of DNA double strand.

   (a) The instability of RNA as compared to DNA would result from the instability of the ribose in RNA (deoxiribose in DNA) as indeed believed. The absence of RNA double strands could be due to the instability of the flux tube pair assignable to n-n. This trivially implies absence of replication and transcription if it is based on same mechanism as in the case of DNA.

   (b) pnn structure could explain why tRNA does not form sequences and allow to understand wobble pairing, which states that the third mRNA codon does not correspond to unique tRNA anticodon but one has C,A,U $\to$ I and U$\to$ I. Due to the symmetries of the third letter of the codon, this is consistent with the genetic code. The physical explanation for wobble base pairing could relate to pnn structure of tRNA. If the charge ordering is random one would have nnp,npn,pnn and C,A,U $\to$ I could correspond to these 3 situations whereas for U$\to$ I the correspondence would not depend on the ordering. Also for RNA one would have ppn,pnp, npp degeneracy but in this case one would have charge independence.

A possible charge pairing between RNA and tRNA would be p↔n. The charge pairing between DNA and RNA could be p → n for the third least significant letter of DNA. This would minimize the coding errors possibly induced this pairing.

(c) One can criticize the charge assignment ppn (possibly allowing permutations) for RNA codons. Could dark weak beta decays give rise to 1-D lattice like structure? Could the repetitive structure be due to energy minimization.

2. Could the correspondence be letterwise? For DNA A,T,C,G would correspond to p, and for RNA A,C,G to p and U to n. Codons not containing U wold be ppp type codons and one can wonder why the oxiribose for them is not replaced with de-oxiribose. The possible presence of n in dark codons could explain why RNA sequences are highly unstable and why they do not replicate and transcribe.

Objections based on group theory and statistics

The quark-triplet model and its generalization replacing u, d with nucleon states p, n works nicely but is better to try to invent objections against the proposal and try to find inconsistencies. Fermi and Bose statistics are the most obvious providers of killer arguments.

1. The basic objection is that if the quarks are organized in linear structures, one cannot talk about representation of 3-D rotation group since symmetry breaking to SO(2) acting along common axis which could be either the local axis along dark DNA helix of the axis of the entire helix. The linear ordering of the quarks is not consistent with the full harmonics. Rather, harmonics restricted to half space $0 \leq \theta \leq \pi/2$ ($\pi \geq \theta \geq \pi/2$) should characterize the "upper" ("lower") flux tube direction at the position of quark in the middle.

   If reflection along quantization axis and SO(2) generate the symmetries one still has labelling of the states by angular momentum projection and states form doublets $(m, -m)$. The representations of SO(3) split into these representation and the numbers of states with given spin projection remain the same. Therefore the predictions for the numbers of DNA codons coding given aminoacid are not changed. It is quite possible that braid statistics made possible by 1-dimensionality is needed to realize the idea about ordering and this would allow to have full DNA multiplets.

2. In quark model one forms tensor product of tensor products of 3 quark spin states and 3 quark isospin states and by color singletness requires that the state is completely antisymmetric in quark degrees of freedom. The state is completely symmetric in the non-colored degrees of freedom. One obtains only two representations $\Delta \leftrightarrow (3/2, 3/2)$ and $N = (1/2, 1/2)$ with positive parity. In quark model context the presence of other tensor products in $(4 \oplus 2_1 \oplus 2_2)_S \otimes (4 \oplus 2_1 \oplus 2_2)_I$ is forbidden. One reason is that spatial wave function is assumed to be symmetric in ground state. This forbids 2_2 in spin degrees of freedom. Symmetrization leaves only the Δ and N (Note that the total number of these state is 20!). Now strong isospin is broken and it is natural to not include it to the tensor product.

3. The presence of 2_2 would be forbidden in quark model since it would require antisymmetric spatial wave function to compensate for the antisymmetry of 2_2. In the recent case the situation is 1-dimensional and the ordering along nuclear string forces localization of quarks and one cannot have identical wave functions for quarks.

   1-D situation also suggests strongly braid statistics. Perhaps the situation could be understood in terms of fermionic oscillator operators along nuclear string having anti-commutation relations corresponding to non-trivial braid statistics - maybe making the statistics commutative. This could naturally allow anti-symmetrization along nuclear string for 2_2 states.

4. If one assumes ordinary statistics, one could one take care of the statistics of the 16 states in $2_2 \otimes (5 \oplus 3)$ by assuming that for 2_2 the color state is symmetric and thus 10-D representation of $SU(3)$. The state associated with color flux tubes cannot compensate this color (triality is 1) since it must correspond to triality zero representation. If the colors of DNA strand and

conjugate correspond to 10 and $\overline{10}$ and color entanglement could guarantee color singletness for the codon pairs. This would however require anti-quarks for the conjugate strand.

3 10:s associated with 3 codons contains in their tensor product a singlet (see `http://tinyurl.com/zjxxqhj`). Minimal color singlet dark DNA sequence would requite 3 color codons. One can of course wonder whether the presence of 3 decouplet codons - 2 at the beginning and 2 at end and one in the middle could define genes as basic units.

5. The statistics problem is encountered also for the flux tubes. 5 (and 1) as symmetric representation is allowed by statistics but triplet is antisymmetric and thus not allowed. Again braid statistics might help. If one assumes that the flux tubes are colored - say color octets - and color wave function for flux tube pairs is antisymmetric, one can achieve Bose statistics for 3. Flux tube pair would correspond to $8 \in \{8 \times 8\}$ and minimum of two flux codons would be needed for color singletness in flux tube degrees of freedom.

6. For the counterparts of amino-acids one has only $4 \otimes 5$ allowed also by statistics considerations assuming color singlets. Could distinction between DNA/RNA and amino-acids related to statistics, perhaps braid statistics. The suggested role of braid strands possibly connecting DNA double strands and DNA double strands and lipid layers of cell membrane encourages the question whether the DNA strand and its conjugate entangle via via the reconnection of the color flux tubes defining U-shaped "tentacles" to a flux tube pair connecting the strands. For amino-acids they would not be needed. Same could happen in the transcription process of DNA to mRNA and in the translation process for mRNA tentacles and those associated with tRNA.

Ordinary or braid statistics?

There are four options to consider: ordinary/braid statistics (1/2) and dark nucleon as dark quark/nucleon triplet as representation of DNA codon (a/b). One has options 1a,1b,2a,2b. Options 1b and 2b are at this moment the only options, which can be taken seriously: the reason is that dark protons would neutralize the negative charges of ordinary DNA nucleotides.

1. Option 1a: codons as quark-triplets with ordinary statistics. For the ordinary statistics amino-acid like dark nucleons are color singlets. Part of DNA codons are represented as dark nucleons and would be colored and 10-D representation of SU(3). Dark amino-acids need not have color bonds with dark parts of other colored biomolecules like DNA,RNA, with exception possible formed by dark tRNA. DNA double strand could realize color confinement via the reconnection of color flux tubes.

2. Option 1b: codons as nucleon-triplets with ordinary statistics. Option 1b requires in ordinary statistics for antisymmetric doublet and antisymmetric wave function for the 3 nucleons not allowing constant valued wave function also disfavored by the linear ordering. This condition might have the same implications as braid statistics.

3. Options 1a and 1b. DNA is the only molecule that appears as double strands. A possible explanation is that codons and anticodons are paired by U-shaped flux tubes associated with the color bonds of dark DNA to form color singlets. Nucleonic colors would sum up to zero along the strand.

4. Option 2a. For braid statistics it could be possible to avoid colored states of nucleon and flux tubes.

5. Option 2b. The 3-nucleon codons would have no color and amino-acids could obey braid statistics reducing to ordinary statistics. This would not be the case for DNA/RNA.

It must be admitted that the situation is unsatisfactory as far as statistics is considered. For the option 1b) with codons identified as dark proton triplets one can however consider the following variant to satisfy statistics requirement.

1. Years after writing the above comments it has become clear that adelic physics [L50] brings in additional discrete degrees of freedom assignable to the group algebra of Galois group of extension of rationals inducing the extensions of p-adic number fields appearing in the adele.

2. Galois group acts on the space of space-time surfaces, and one can say that one has wave function at the orbit of the Galois group consisting of space-time sheets. At quantum level quantum states correspond to wave functions in the group algebra of Galois group of extension.

3. The role of color in helping to achieve correct statistics could be taken by Galois degrees of freedom. One can even consider the notion of Galois confinement as a generalization of color confinement [L110] binding codons as dark proton triplets to dynamical units. Even genes as sequences of codons could be bound to dynamical units as Galois singlets.

2.7.4 Further considerations

Replication, transcription, translation

The formation of flux tube pairs between molecules would be central in replication and transcription and in all bio-catalysis. Dark DNA would replicate first to dark DNA or mRNA. This requires that the building bricks of dark DNA and mRNA emerge from environment perhaps by mechanism involving reconnection for the magnetic tentacles and reduction of h_{eff} bringing the molecules near each other. Flux tube pairs between dark DNA codonsandtheir conjugates (individual dark RNA codons) would be formed during replication (transcription). The formation of flux tube pair between mRNA and dark tRNA part of tRNA would bring tRNA to mRNA, where amino-acid would associate with the growing amino-acid sequence.

For options 1a and 1b based on ordinary statistics color singletness condition could play an important role in the replication and transcription.

1. If the value of h_{eff} before reconnection and contraction of flux tube dictating the scale of color confinement is large enough, colored dark nucleons could float as free - possibly colored states - in the environment for option 1a). For option 1b dark nucleons could be present in environment - this could relate directly to the ionization in electrolyte. For options 1a and 1b dark codons representing dark tRNA molecules would accompany them.

2. For options 1a) and 1b) color confinement in flux tube degrees of freedom by forming dark color flux tube pairs between dark DNA and its conjugate in codon-wise manner could give rise to DNA double strands as chemical shadows of dark double strands. The coupling between codon and anticodon would be defined by the condition that the total color bond spins of paired codons are opposite. Quark color could be compensated for option 1a along DNA strand: 3 10:s give singlet. One can of course ask whether dark DNA RNA sequences exist rather than being built during replication and transcription.

Are sound-like bubbles whizzing around in DNA essential to life?

I got a link to a very interesting article [I43] about sound waves in DNA (see `http://tinyurl.com/z7hod9b`). The article tells about THz de-localized modes claimed to propagate forth and back along DNA double strand somewhat like bullets. These modes involve collective motion of many atoms. These modes are interpreted as a change in the stiffness of the DNA double strand leading to the splitting of hydrogen bonds in turn leading to a splitting into single strands. The resulting gap is known as transcriptional bubble propagating along double strand is the outcome. I do not how sound the interpretation as sound wave is.

It has been proposed that sound waves along DNA give rise to the bubble. The local physical properties of DNA double strand such as helical structure and elasticity affect the propagation of the waves. Specific local sequences are proposed to favor a resonance with low frequency vibrational modes, promoting the temperary splitting of the DNA double strand. Inside the bubble the bases are exposed to the surrounding solvent, which has two effects.

Bubbles expose the nucleic acid to reactions of the bases with mutagens in the environment whereas so called molecular intercalators may insert themselves between the strands of DNA. On the other hand, bubbles allow proteins known as helicases to attach to DNA to stabilize the bubble, followed by the splitting the strands to start the transcription and replication process. The splitting would occur at certain portions of DNA double strand. For this reason, it is believed that DNA directs its own transcription.

The problem is that the strong interactions with the surrounding water are expected to damp the sound wave very rapidly. Authors study experimentally the situation and report that propagating bubbles indeed exist for frequencies in few THz region. Therefore the damping deo not seem to be effective. How this is possible? As an innocent layman I also wonder how this kind of mechanism can be selective: it would seem that the bullet like sound wave initiates transcription at many positions along DNA. The transcription should be localized to a region assignable to single gene. What could guarantee this?

Can TGD say anything interesting about the mechanism behind transcription and replication?

1. In TGD magnetic body controls and coordinates the dynamics. The strongest hypothesis is that basic biochemical process are induced by those for dark variants of basic bio-molecules (dark variants of DNA, enzymes,...). The belief that DNA directs its own transcription translates to the statement that the dark DNA consisting most plausibly from sequences of dark proton triplets ppp at dark magnetic flux tubes controls the transcription: the transcription/replication at the level of dark DNA induces that at the level of ordinary DNA.

2. If the dark DNA codons represented as dark proton triplets (*ppp*) are connected by 3 flux tube pairs, the reverse of the reconnection should occur and transform flux tube pairs to two U-shaped flux tubes assignable to the two dark DNA strands. Dark proton sequences have positive charge +3e per dark codon giving rise to a repulsive Coulomb force between them. There would be also an attractive force due to magnetic tension of the flux tubes. These two forces would compensate each other in equilibrium (there also the classical forces due to the negatively charged phosphates associated with nucleotides but these would not be so important).

   If the flux tube pairs are split, the stabilizing magnetic force however vanishes and the dark flux tubes repel each other and force the negatively charged DNA strands to follow so that also ordinary DNA strand splits and bubble is formed. The primary wave could therefore be the splitting of the flux tube pairs: whether one can call it as a sound wave is not clear to me. Perhaps the induced propagating splitting of ordinary DNA double strand could be regarded as an analog of sound wave.

   The splitting of flux tube pairs for a segment of DNA would induces a further splitting of flux tubes since repulsive Coulomb force tends to drive the flux tubes further away. The process could be restricted to DNA if the "upper" end of the split DNA region has some dark DNA codons which are not connected by flux tubes pairs. This model reason why for dark proton sequences.

3. This model does not yet explain how the propagating splitting wave is initiated. Could a quantum phase transition increasing the value of h_{eff} associated with the flux tube pairs occur for some minimal portion of dark DNA "below" the region associated with gene and lead to the propagating wave induced by the above classical mechanism? That the wave propagates in one direction only could be due to chirality of DNA double helix.

An interesting question is how the RNA world vision (see `http://tinyurl.com/gpmxcmk`) relates to this general picture.

1. There are strong conditions on the precedessor of DNA and RNA satisfies many of them: reverse transcription to DNA making possible transition to DNA dominated era is possible. Double stranded RNA exists `http://tinyurl.com/y9mex4v7` in cells and makes possible RNA genome: this would however suggest that cell membrane came first. RNA is a catalyst. RNA has ability to conjugate an amino-acid to the $3'$ end of RNA and RNA catalyzes peptide bond formation essential for translation. RNA can self-replicate but only relatively short sequences are produced.

2. TGD picture allows to understand why only short sequences of RNA are obtained in replication. If the replication occurs at the level of dark ppn sequences as it would occur for DNA in TGD framework, long RNA sequences might be difficult to produce because of the stopping of the propagation of the primary wave splitting the flux tube pairs. This could be due to the neuron pairs to which there is associated no Coulomb repulsion essential for splitting.

3. In TGD framework RNA need not be the precedessor of DNA since the evolution would occur at the level of dark nucleon strings and DNA as the dark proton string is the simpest dark nucleon string and might have emerged first. Dark nuclear strings would have served as templates and biomolecules would have emerged naturally via the transcription of their dark counterparts to corresponding bio-polymers.

Is bio-catalysis a shadow of dark bio-catalysis based on generalization of genetic code?

Protein catalysis and reaction pathways look extremely complex (see `http://tinyurl.com/kp3sdlm`) as compared to replication, transcription, translation, and DNA repair. Could simplicity emerge if biomolecules are identified as chemical shadows of objects formed from dark nuclear strings consisting of dark nucleon triplets and their dynamics is shadow of dark stringy dynamics very much analogous to text processing?

What if bio-catalysis is induced by dark catalysis based on reconnection as recognition mechanism? What if contractions and expansions of U-shaped flux tubes by h_{eff} increasing phase transitions take that reactants find each other and change conformations as in the case of opening of DNA double strand? What if codes allowing only the dark nucleons with same dark nuclear spin and flux tubes spin to be connected by a pair of flux tubes?

This speculation might make sense! The recognition of reactants is one part of catalytic action. It has been found in vitro RNA selection experiments that RNA sequences are produced having high frequency for the codons which code for the amino-acid that these RNA molecules recognize (`http://tinyurl.com/kp3sdlm`. This is just what the proposal predicts!

Genetic codes DNA to RNA as $64 \to 64$ map, RNA to tRNA as $64 \to 40$, tRNA to amino-acids with $40 \to 20$ map are certainly not enough. One can however consider also additional codes allowed by projections of $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \oplus 3(\oplus 1))$ to lower-dimensional sub-spaces defined by projections preserving spins. One could also visualize bio-molecules as collections of pieces of text attaching to each other along conjugate texts. The properties of catalysts and reactants would also depend by what texts are "visible" to the catalysts. Could the most important biomolecules participating biochemical reactions (proteins, nucleic acids, carbohydrates, lipids, primary and secondary metabolites, and natural products, see `http://tinyurl.com/jlfxags`) have dark counterparts in these sub-spaces.

The selection of bio-active molecules is one of the big mysteries of biology. The model for the chemical pathway leading to the selection of purines as nucleotides [L33] assumes that the precedessor of purine molecule can bind to dark proton without transforming it to ordinary proton. A possible explanation is that the binding energy of the resulting bound state is higher for dark proton than the ordinary one. Minimization of the bound state energy could be a completely general criterion dictating which bio-active molecules can pair with dark protons. The selection of bio-active molecules would not be random after all although it looks so. The proposal for DNA-nuclear/cell membrane as topological quantum computer with quantum computations coded by the braiding of magnetic flux tubes connecting nucleotides to the lipids wlead to the idea that flux tubes being at O=-bonds [K4].

Comparing TGD view about quantum biology with McFadden's views

McFadden [I60] has very original view about quantum biology: I have written about his work for the first time for years ago, much before the emergence of ZEO, of the recent view about self as generalized Zeno effect, and of the understanding the role of magnetic body containing dark matter [K34, K35]. The pleasant surprise was that I now understand McFadden's views much better from TGD viewpoint.

1. McFadden sees decoherence as crucial in biological evolution: here TGD view is diametric opposite although decoherence is a basic phenomenon also in TGD.

2. McFadden assumes quantum superpositions of different DNAs. To me this looks an unrealistic assumption in the framework of PEO. In ZEO it is quite possible option.

3. McFadden emphasizes the importance of Zeno effect (in PEO). In TGD the ZEO variant of Zeno effect is central for TGD inspired theory of consciousness and quantum biology.

Mc Fadden suggests that quantum effects and Zeno effect are central in bio-catalysis: the repeated measurement keeping reactants in the same position can lead to an increase of reaction rate by factors of order billion. McFadden describe enzymes as quantum mousetraps catching the reactants and forcing them to stay in same position. The above description for how catalysis catches the reactants using U-shaped flux tube conforms with mousetrap picture.

McFadden discusses the action of enzymes in a nice manner and his view conforms with TGD view. In ZEO the system formed by catalyst plus reactants could be described as a negentropically entangled sub-self, and self indeed corresponds to a generalized Zeno effect. The reactions can proceed in shorter scales although the situation is fixed in longer scales (hierarchy of CDs): this would increase the length of the period of time during which reactions can proceed and lead to catalytic effect. Zeno effect in ZEO plus hierarchies of selves and CDs would be essentially for the local aspects of enzyme action.

4. Protons associated with hydrogen bonds and electronic Cooper pairs play a universal role in McFadden's view and the localization of proton in quantum measurement of its position to hydrogen bond is the key step of enzyme catalysis. Also TGD dark protons at magnetic flux tubes giving rise to dark nuclear strings play a key role. For instance, McFadden models enzyme catalysis as injection of proton to a very special hydrogen bond of substrate. In TGD one has dark protons at magnetic flux tubes and their injection to a properly chosen hydrogen bond and transformation to ordinary proton is crucial for the catalysis. Typical places for reactions to occur are C=O type bonds, where the transition to C-OH can occur and would involve transformation of dark proton to ordinary proton. The transformation of dark proton to ordinary one or vice versa in hydrogen bonds would serve as a biological quantum switch allowing magnetic body to control biochemistry very effectively.

   What about electronic Cooper pairs assumed also by McFadden. They would flow along the flux tube pairs. Can Cooper pairs of electrons and dark protons reside at same flux tubes? In principle this is possible although I have considered the possibility that particles with different masses (cyclotron frequencies) reside at different flux tubes.

McFadden [I60] has proposed quantum superposition for ordinary codons: This does not seem to make sense in PEO since the chemistries of codons are different) but could make sense in ZEO. In TGD one could indeed imagine quantum entanglement (necessary negentropic in p-adic degrees of freedom) between dark codons. This NE could be either between additional degrees of freedom or between spin degrees of freedom determining the dark codons. In the latter case complete correlation between dark and ordinary DNA codons would imply also the superposition of their tensor products with ordinary codons.

The NE between dark codons could also have a useful function: it could determine physically gene as a union of disjoint mutually entangled portions of DNA. Genes are known to be highly dynamical units, and after pre-transcription splicing selects the portions of the transcript translated to protein. The codons in the complement of the real transcript are called introns and are spliced out from mRNA after the pre-transcription (see `http://tinyurl.com/gmphzzy`).

What could be the physical criterion telling whether a given codon belongs to exonic or intronic portion of DNA? A possible criterion distinguish between exons and introns is that exons have NE between themselves and introns have no entanglement with exons (also exons could have NE between themselves). Introns would not be useless trash since the division into exonic and exonic region would be dynamical. The interpretation in terms of TGD inspired theory of consciousness is that exons correspond to single self.

Is there a connection between geometric model of harmony and nuclear string model of genetic code?

There should exists a connection between the geometric model of harmony and genetic code and the model of genetic code discussed.

1. Dark DNA strands could be connected by color flux tubes to form a double strand by reconnections of U-shaped color flux tubes. What would induce a codon-wise or letter-wise pairing

of DNA codons and their conjugates represented as dark quark triplets to form double DNA strand? Cyclotron resonance could accompany reconnection (magnetic field strength would be identical and reconnection could occur).

2. One has the correspondence codon $\leftrightarrow$ state of dark nucleon or codon $\leftrightarrow$ state of dark nucleon triplet. The geometric model of harmony and genetic code [L11] represents the codons as 3-chords. The 3-chord would be represented in terms of cyclotron frequencies of dark photons assignable to the 3 dark quarks (nucleons) in the state. Each quark-color bond pair (including the pion-like bond) could be in 12 states with corresponding cyclotron frequency mappable to the basic octave. The cyclotron frequency triplets would be same for codons and conjugates. The only manner to understand the scale is in terms of spectrum of magnetic field strengths for U-shaped flux tube pairs.

   This would require 3 pairs of flux tubes between the dark codons of DNA strands. If the quarks inside linear dark proton are connected by color flux tubes (like protons in the model of dark nucleus). Reconnection for U-shaped flux tube connecting quarks would give rise to the double strand formed by dark proton strings. The magnetic field strength of the 3-flux tubes would be determined by the state of dark proton and would be same for DNA and RNA codons and also for RNA codons and corresponding tRNA-amino-acid complexes. The cyclotron frequencies would define a scaled up variant of Pythagorean scale projected to the basic octave [L11]. This option does not favor the idea about separater 4-letter code.

3. The geometric model for harmony is formulated in terms of orbits of the subgroups of the isometry groups of tetrahedral and icosahedral geometries. The DNAs coding particular amino-acid correspond correspond to the orbit of the triangle of icosahedron corresponding to the amino-acid. The decomposition $60 \to 20 + 20 + 20$ suggests strongly decomposition of I to 20 Z_3 cosets containing 3 elements each other and in correspondences with the triangular faces of icosahedron.

4. The model of the genetic code just discussed relies on the model of dark nucleon based on group theory. The symmetric groups of Platonic solids are in turn associated with inclusion of hyper-finite factors and appear in Mc Kay correspondence, whose proof involves decompositions of SU(2) representations to the representations of the discrete subgroups of Platonic solids. A further observation is that the numbers of elements for isometries of icosahedron and tetrahedron are 60 and 4 respectively: the sum is 64. Could the action of Z_3 leaving face invariant could be posed as an additional condition on amino-acids and reduce the amino-acid representation to $4 \otimes 5$.

5. In the geometric model of harmony genetic icosahedral 20+20+20 part of the code involves a combination of three different Hamilton's cycles mapping 60 DNAs to 20 amino-acids: in terms of icosahedral group I and its coset space I/Z_3 these maps correspond to coset projections. Could the decomposition $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \otimes 3)$ be understood in terms of a reduction to icosahedral and tetrahedral subgroups of rotation group or of their spin coverings.

   In this process finite-dimensional representation of $SO(3)$ decomposes to a direct sum of representations of the discrete subgroup if its dimension is larger than any of the dimensions of representations of the finite sub-group (for basic facts about these see `http://tinyurl.com/ho4onbs`). One might hope that the decomposition of the representations of SO(3) appearing in the above formula under icosahedral group and or tetrahedral group could allow to understand the emergence of DNA, RNA, tRNA, and amino-acids as kind of symmetry breaking.

6. In the geometric model of harmony 64-codon code [L11] is obtained as a fusion 60-codon code assignable to icosahedron + 4 codon code assignable to tetrahedron. There are actually two codes corresponding to tetrahedron and icosahedron as disjoint entities and tetrahedron glued to icosahedron along one face. The model explains the two additional amino-acids Pyl and Sec coded for a variant of the genetic code.

How could these two successful models relate to each other? In p-adic physics of cognition Platonic solids and polygons can be seen as discrete approximation for sphere [L34] and

biomolecules could be understood as cognitive representation in the intersection of real and p-adic space-time surface consisting of algebraic points. Could one assign icosahedron and tetrahedron to a codon in some concrete manner? Could the attachment of tetrahedron to icosahedron along one face have concrete meaning? The answer seems to be negative.

1. One can about the interpretation of the 12 vertices of the icosahedron - how number 12 could be assigned with the genetic code? The vertices correspond to notes perhaps represented as magnetic field strength at the flux tubes assignable to color bonds. This field strength should be determined by the spin state of dark 3-nucleon. No concrete nuclear string counterpart seems to exist for the closed Hamiltonian cycle consisting of 12 notes and in case of tetrahedral extension of 13 notes. 12 vertices of icosahedron correspond to 12 notes and 20 faces to 3-chords so that there is not need for more concrete correspondence.

2. The attachment of tetrahedron to icosahedron would bring in further note very near to one of the notes of Pythagorean scale and corresponding 3-chords. This has concrete interpretation and there is no need to make this more concrete at the level of geometry of DNA. If icosahedron and tetrahedron are disjoint one obtains four additional codons. It seems that all these 4 3-chords be assigned with the 3 color bonds, one note for each of them. What distinguishes at the level of dark nucleon string the situations in which tetrahedron is attached and non-attached to the color bond? In presence of attachment there would be 1 shared 3-chord corresponding to stop codon assignable with the shared face. The 13:th note appearing in 4 3-chords differs very little from one of the notes of the icosahedral scale: this corresponds to the fact that 12 perfect quints do not quite give 7 octaves as already Pythagoras realized. Crazy question: Could this small difference relate to the small relative mass difference $(m_p - m_n)/m_p \simeq .0014$ making itself possible visible in cyclotron frequency scale? The idea does not seem plausible: $[(3/2)^{12} - 2^7]/2^7 \simeq .014$ is 10 times larger than $(m_p - m_n)/m_p \simeq .0014$.

The conclusion is that genetic code can be understand as a map of stringy nucleon states induced by the projection of all states with same spin projections to a representative state with the same spin projections (total quark spin and total flux tube spin). Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin.

Chapter 3

About the Correspondence of Dark Nuclear Genetic Code and Ordinary Genetic Code

3.1 Introduction

The idea about the realization of genetic code in terms of dark proton sequences giving rise to dark nuclei is one of the key ideas of TGD inspired quantum biology [L27]. This vision was inspired by the totally unexpected observation that the states of three dark protons (or quarks) can be classified to 4 classes in which the number of states are same as those of DNA, RNA, tRNA, and amino-acids. Even more, it is possible to identify genetic code as a natural correspondence between the dark counterparts of DNA/RNA codons and dark amino-acids and the numbers of DNAs/RNAs coding given amino-acid are same as in the vertebrate code [L27]. What is new is that the dark codons do not reduce to ordered products of letters.

During years I have considered several alternatives for the representations of genetic code. For instance, one can consider the possibility that the letters of the genetic code correspond to the four spin-isospin states of nucleon or quark or for spin states of electron pair. Ordering of the letters as states is required and this is problematic from the point of view of tensor product unless the ordering reflects spatial ordering for the positions of particles representing the letters. One representation in terms of 3-chords formed by 3-photon states formed from dark photons emerges from the model of music harmony [L11]. By octave equivalence the ordering of the notes is not needed.

3.1.1 Insights

The above observations inspire several speculative insights.

1. The emergence of dark nuclei identified as dark proton sequences would relate to Pollack's effect in which irradiation of water generates in presence of gel phase bounding the water what Pollack calls exclusion zones (EZs). EZs are negatively charged and water has effective stoichiometry $H_{1.5}O$. EZs deserve their name: somehow they manage to get rid of various impurities: this might be very important if EZs serve as regions carrying biologically important information. The protons of water molecules must go somewhere and the proposal is that they go to the magnetic body of some system consisting of flux tubes. The flux tubes contain the dark protons as sequences identifiable as dark nuclei.

2. Since nuclear physics precedes chemistry, one can argue that prebiotic life is based on these dark biomolecules serving as a template for ordinary biomolecules. To some degree biochemistry would be shadow dynamics and dark dynamics would be extremely simple as compared to the biochemistry induced by it. In particular, DNA replication, transcription, and translation would be induced by their dark variants. One can even extend this vision: perhaps

also ordinary nuclear physics and its scaled up counterpart explaining "cold fusion" are parts of evolutionary hierarchy of nuclear physics in various scales.

3. Nature could have a kind of R&D lab allowing to test various new candidates for genes by using transcription and translation at the level of dark counterparts of the ordinary basic biomolecules.

3.1.2 Conditions on the model

The model must satisfy stringent conditions.

1. Both the basis A, T, C, G and A, U, C, G as basic chemical building bricks of RNA and DNA must have emerged without the help of enzymes and ribozymes. It is known that the biochemical pathway known as pentose-phosphate pathway (see `http://tinyurl.com/y9akkwok`) generates both ribose and ribose-5-phosphate defining the basic building brick of RNA. In DNA ribose is replaced with de-oxiribose obtained by removing one oxygen.

   Pyrimidines U, T, and C with single aromatic ring are are reported by NASA to be generated under outer space conditions (see `http://tinyurl.com/y7sh9zk4`). Carell *et al* [I34] (see `http://tinyurl.com/z65kpyo`) have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons. TGD inspired model for the mechanism involves dark protons [L33] [**?**].

   Basic amino-acids are generated in the Miller-Urey type experiments (see `http://tinyurl.com/4q2arv`). Also nucleobases have been genererated in Miller-Urey type experiments [I38].

   Therefore the basic building bricks can emerge without help of enzymes and ribozymes so that the presence of dark nuclei could lead to the emergence of the basic biopolymers and tRNA.

2. Genetic code as a correspondence between RNA and corresponding dark proton sequences must emerge. Same true for DNA and also amino-acids and their dark counterparts. The basic idea is that metabolic energy transfer between biomolecules and their dark variants must be possible. This requires transitions with same transition energies so that resonance becomes possible. This is also essential for the pairing of DNA and dark DNA and also for the pairing of say dark DNA and dark RNA. The resonance condition could explain why just the known basic biomolecules are selected from a huge variety of candidates possible in ordinary biochemistry and there would be no need to assume that life as we know it emerges as a random accident.

3. Metabolic energy transfer between molecules and their dark variants must be possible by resonance condition. The dark nuclear energy scale associated with biomolecule could correspond to the metabolic energy scale of .5 eV. This condition fixes the model to a high extent but also other dark nuclear scales with their own metabolic energy quanta are possible. In fact, the dark nuclear binding energy for $k = 151$ scaled up from the typical value of the ordinary nuclear binding energy about 1 MeV is .5 eV.

3.1.3 Vision

The basic problem in the understanding of the prebiotic evolution is how DNA, RNA, amino-acids and tRNA and perhaps even cell membrane and microtubules . The individual nucleotides and amino-acids emerge without the help of enzymes or ribozymes but the mystery is how their polymers emerged. If the dark variants of these molecules served as templates for their generation one avoids this hen-and-egg problem. The problem how just the biomolecules were picked up from a huge variety of candidates allowed by chemistry could be solved by the resonance condition making possible metabolic energy transfer between biomolecules and dark nuclei.

The basic question is to what p-adic length scales $L(k)$ DNA, RNA and amino-acids correspond. The original hypothesis was that the p-adic length scale assignable to dark DNA is consistent with the radius of ordinary DNA. It however turned out that this implies that the

binding energy scale of corresponding dark nuclear physics is too high for the recent biology. Also the assumption that the dark variant of DNA double strand is horizontally scaled up variant of ordinary DNA strand excludes this identification since it requires that the horizontal size scale of dark DNA strand is larger than that of ordinary DNA strand.

DNA coil has radius $L(151) = 10$ nm and this suggests that dark DNA radius does not correspond to the radius of ordinary DNA (as assumed in the original version of this text) but to the p-adic length scale $L(151)$, where $k = 151$ corresponds to first Gaussian Mersenne prime belonging to the group $k = 151, 157, 163, 167$. The primes $k > 151$ would correspond to higher level coilings of DNA. From this hypothesis one ends up to the proposal that RNA, tRNA, and amino-acids correspond to $k = 149$. This picture follows essentially from the contraints posed by various biological anomalies.

Also the smaller primes $k = 127, 131, 137, 139$ can be present in pre-biotic evolutions. This hierarchy of dark nuclear physics leads to a vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compare it to PAH world hypothesis.

The vision about dark matter as a controller of biomatter leads to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures related to by radial scaling to their counterparts at the level of ordinary biomatter. This is supported by p-adic length scale hypothesis and thermodynamical considerations. These 2-D structures could represent 2-D variants of 1-D structures represented by DNA, RNA, and amino-acids with each node of lattice representing code letter.

Thermal constraints allow cell membrane of thickness about 5 nm as am additional realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. For $k = 149$ metabolic energy quantum is predicted to be .5 eV. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is just at the verge of thermal threshold. This could be understood in terms of minimization of metabolic resources. For bosonic singly charged ions the Josephson energy would be below the thermal threshold. The notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum.

Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is $E_{ex}(151) = .25eV$. Of course, the replacement of $E_{ex} = 1$ MeV for ordinary nuclei with $E_{ex} = 2$ MeV would give $E_{ex}(151) = .5$ eV so that one must take these estimates as order of magnitude estimates only. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

The great vision would be that hierarchy of dark variants of DNA, RNA, amino-acids and their replication, transcription, and translation would be behind biological replication in various scales. Ordinary bio-chemistry would be shadow dynamics doing its best to mimic what happens at the level of dark matter. The reduction of bio-physics to that of dark matter level would mean a huge simplification of the vision about living matter.

The picture that I discussed in the original version of this chapter involved several uncertainties and open questions. During the years, TGD itself has developed and I decided to add to end of the chapter the recent view about the genetic code as a section title "Genetic code in terms of dark nucleon triplets". This is the year 2022 view about dark nucleon realization of the genetic code.

3.2 About dark variants of DNA, RNA, and amino-acids

To make progress one must construct a concrete model for the dark nuclei. The recent picture relies strongly on various anomalies to which TGD provides a solution. The TGD inspired model for "cold fusion" leads to the notion of dark nuclear physics - actually hierarchy of them labelle by the values of $h_{eff}/h = n$ and corresponding p-adic length scales. Second basic idea [L15]

is that cylindrical variants of EZs discovered by Pollack [L15] give rise to the dark counterparts of DNA, RNA, and amino-acids as dark proton sequences. tRNAs would be analogs of tritium and ^{3}He. Pollack effect serves as a strong constraint for the model. Also the effects of ELF em fields on vertebrate brain [J6] combined with the rather recent finding about clustering of RNA II polymerase molecules [I35] exhibiting Comorosan effect [I81] provide valuable constraints on the model [L61]. The outcome of the arguments is that single strand of DNA, mRNA, tRNA and amino-acids most naturally correspond to $k = 149$ and double stranded DNA to $k = 151$.

Remark: The following argumentation is kind of Sherlock-Holmes-ing using all possible hints as constraints to select between imagined options rather than glorious march from axioms to theorems and thus not science in the usual sense.

3.2.1 Dark variant of DNA

Concerning the identification of the size scale of dark DNA one can consider several options. The first guess was that the scale is same as for ordinary DNA: L(141)=.34 nm obtained by scaling from the distance of protons in the $k = 127$ dark nucleus implicated by the findings of Holmlid *et al* [C1, L35] [L22]. It however turns out that the p-adic length scale assignable to dark DNA is most naturally $k = 151$ corresponding to the thickness 10 nm of DNA coil. The hypothesis that the integer k labelling p-adic length scale is prime is attractive working hypothesis leaving very few options under consideration. The options $k = 137$ and $k = 149$ are excluded since the pairing of dark DNA and ordinary DNA would not be possible without the coiling of ordinary RNA around dark DNA. This leaves only options for which $k \geq 149$ for prime values of k.

Remark: The p-adic length scale associated with a system is defined to be $L(k)$ if the size of the system is in the half open interval $[L(k), L(k+1))$. One can also consider the possibility that p-adic length scale corresponds to the upper end of $[L(k-1), L(k))$.

General considerations

Consider first some background.

1. The TGD based model leads to the proposal for a formation of this kind of dark nuclear strings such that the distance between protons is rather precisely electron Compton length $L_e \simeq .4 \times 10^{-12}$ meters explains "cold fusion" in terms of dark nucleosynthesis which should have preceded ordinary nucleosynthesis by heating the material to the temperature required by it [L41] [K17].

   Dark nucleosynthesis would have produced part of heavier nuclei outside stars. The binding energy scale for dark nuclear physics would be scaled down like 1/length and 2.6 MeV binding energy per nucleon for ^{3}He of the ordinary nuclei would be scaled down by a factor 2^{-11} to 1.3 keV. Note however that it is excitation energies of order 1 MeV what matters and would scale down to .5 keV. This level does not yet correspond to biology as we know it but could be one step in the evolutionary hierarchy leading from nuclear physics also based on nuclear strings to biology involving increase of Planck constant $h_{eff}/h = n$ identifiably as the dimension of algebraic extension of rationals characterizing the complexity of the dynamics.

2. These dark nuclei have $h_{eff}/h = n = 2^{11}$ (or near to it) and cannot be those responsible for the dark variants of biomolecules since the distances of dark protons given by electron Compton length are much shorter than the distance between DNA nucleotides about .34 nm, which is roughly 142 times the electron Compton length 2.4×10^{-3} nm.

3. The distance between the dark protons appearing as counterparts of DNA nucleotides should be larger than that between ordinary DNA nucleotides. The simplest assumption that dark DNA coil is a horizontally scaled variant of DNA coil with same twisting angle so that DNA nucleotides are projected horizontally to their dark counterparts at the surface of a cylinder. Once the p-adic length scale of this cylinder is given, the distance between dark protons is fixed by p-adic scaling from the distance between dark protons for $k = 127$ case - that is electron Compton length. In the case of uncoiled RNA/AA one could have also a coil rotating around the ordinary RNA/AA.

The distance between dark nucleotides must be longer than the distance $3 \times .34 \sim 1$ nm taken by single ordinary DNA codon. If k is prime this leaves only $k = 149$ or $k = 151$ into consideration.

4. The negative charge of DNA and RNA assignable to one oxygen of phosphate combining with ribose and DNA/RNA base could come from the tubular EZ formed in the formation of DNA. The negative charge of phosphates and the positive charge of dark protons could guarantee the stability of pairs of dark proton sequences and ordinary RNA and DNA.

   DNA strand has radius of $R = 1$ nm. The Debye length R_D of DNA gives rough idea about the scale above which the negative charge of DNA nucleotides associated with the phosphates screened. R_D should be longer than R: otherwise it is not possible to speak about charge of DNA only atomic length scales. One should have $R_D > R$: otherwise it does not make sense to assign negative DNA charge except in atomic length scales. The simplest option is that dark DNA has size scale $L(151)$.

   Remark: The rough estimates depend on how one identifies p-adic length scale. For the identification as $L(k) = \sqrt{5}L_e(k)$ motivated by the mass formula for electron, one would have $L(k) = \sqrt{5}L_e(k)$ giving $L(141) = 0.67$ nm. With this interpretation the estimate for the screening radius would be still shorter than R.

   Remark: Scaled up hadron physics would be associated with flux tubes of the magnetic body of the codon at which one would have nucleons as 3-quark color singlets. I have already earlier proposed that scaled variants of hadron physics [K37] appear in TGD inspired biology. One motivation comes from honeybee dance [A20]!

The pairing dark AAs with positive charge with ordinary AAs might lead to problems since 16 AAs are neutral. The only charged AA residues are Lys (+), Arg (+), Asp (-) and Glu (-).

1. The formation mechanism for dark proton sequences gives for dark AAs a large positive charge. AAs are however not accompanied by negatively charged phosphate ions. Does charge neutrality require that the dark bonds between dark proton has negative charge so that one has effectively neutron?

   Dark weak interactions correspond to large value of n [L41] so that in DNA length scale their proceed as fast as electromagnetic interactions (weak bosons would behave like massless particles below scaled up weak scale). This could make possible β decays changing the charges of the bonds between dark protons or dark neutrons [L41] and lead to a stability by β emission.

2. Proteins in water environment have a charge due to protons or electrons attaching to them. This charge depends on pH and becomes negative above certain critical pH. One might think that the limit of very large pH (no protons) corresponds to the situation in which the electrons of EZ attach to AAs.

Dark codons do not have decomposition to letters whereas ordinary codons have. In a well-defined sense one could say that dark code is "holistic" whereas the ordinary code is "reductionistic".

1. This brings in mind western written language in which words decompose to letters. In some eastern languages the symbols of written language correspond to entire words. Do these differences correspond at deeper level to ordinary and dark genes. Could the analytic and holistic aspects of cognition relate to the differences between ordinary and dark code.

2. One cannot exclude the entanglement between codons and evolution as emergence of entanglement even suggests this. Could this kind of entanglement give rise to basic units of DNA, in particular genes and introns. Could the decomposition of gene into coding regions and introns correspond to a decomposition to unentangled products of internally entangled pieces. This would increase exponentially the degrees of freedom involved and explain why organisms with practically the same code can be at so different evolutionary levels. In the splicing process when intronic portions are cut out from DNA sequence. Do the remaining

pieces of RNA get entangled or does the decomposition of dark RNA to unentangled pieces have some meaning? Note that also ordinary RNA would be entangled or entangled. Could introns provide the means for decomposing the coding RNA to unentangled pieces.

3. The most natural possibility is that entanglement contains superposition of codon sequences in which each sequence codes for the same AA. The chemical codons appearing in the superposition have different masses and chemical properties but in zero energy ontology (ZEO) this is possible. Situation would be like for a superconductor in which coherent state means superposition of states with different numbers of Cooper pairs and thus different fermion number in standard ontology but in ZEO this problem disappears.

Why one must have $k = 151$ for dark DNA

It was already found that for prime values of k the options $k < 149$ are not possible for dark DNA since ordinary DNA should coil around dark DNA. There is also second objection against prime $k < 149$ from energetics inspiring the hypothesis DNA corresponds to $k = 151$.

1. The scaling of the dark nuclear binding energy $E_b \sim 7$ MeV per nucleon as $L(107)/L(k)$ predicts very high binding energies for primes $k < 149$. For instance, $k = 139$ would correspond to the scaled binding energy $E_b(139) = E_b L(107)/L(139)$, $E_b \sim 7$ MeV, which is typical nuclear binding energy. This gives $E_b(139) = E_b/2^{(139-107)/2} = .14$ keV. For $k = 139$ the typical nuclear excitation energy $E_{ex} = 1$ MeV scales dow to 20 eV, which is still very high but could correspond to energies of atomic transitions. For $k = 151$ it E_b scales down to 3.5 eV. The typical dark excitation energy for $k = 151$ is $E_{ex}(151) = .5$ eV and the identification as a nominal value of metabolic energy quantum is attractive. Dark nuclear physics might therefore control biochemistry using dark nuclear transitions as a tool to provide desire energy currency.

2. The TGD based explanation of Pollack effect provides a consistency test for the idea [L15] [L15]. In Pollack effect IR light (besides either kinds of energy feeds) induces the formation of negative charged exclusion zones (EZs) in water bounded by gel phase. In TGD based model this would correspond to the formation of dark proton sequences at magnetic flux tubes. The scale of dark nuclear binding energy would be most naturally in eV scale. The binding energy scale of hydrogen atoms in water molecules is about 5 eV which suggests that the binding energy scale for dark protons sequences is smaller since otherwise energy would be liberated. This would suggest $k = 149$ as will be found.

3. One can imagine that an external perturbation induces

   (a) a transition in which the proton bound to water molecule transforms to its dark variant in higher energy state or

   (b) that the proton goes over a potential wall, whose height is measured in eV:s.

   If the dark nuclear binding energy is higher than the binding energy of proton in water molecule, the process should liberate energy and could occur spontaneously unless high potential wall prevents it. Hence the first option seems the only realistic one. Note that one could consider the cancellation of dark nuclear binding energy and repulsive Coulomb energy which scale in the same manner as function of p-adic length scale so that still the net energy would scale increase in shorter p-adic length scales.

Pollack effect suggests that if k is prime, one must have $k = 149$ for dark proton sequences formed in Pollack effect.

1. For $k = 149$ one has $E_b(151) \sim E_b/2^{(149-107)/2} = 3.5$ eV for $E_b = 7$ MeV, which is in UV range slightly above the visible range. The binding energy of hydrogen atom in water is about 5 eV which would require the incoming radiation to have energy 1.5 eV which is indeed in IR range. This option looks therefore realistic.

2. For $k = 151$ one would have $E_b(151) \sim 7MeV/2^{(151-107)/2} = 1.75$ eV, which just above the IR energy range. Now the energy needed to transform ordinary protons to dark protons in Pollack effect would be in UV range so that this options seems to be excluded.

This argument suggests that dark proton sequences generated in Pollack effect are analogs of single DNA strand, which would naturally correspond to $L(149) = L(151)/2$. Also RNA would naturally correspond to this scale.

1. $L(151) \simeq 10$ nm is the thickness of coiled DNA double strand. The size scale of dark nucleons would be $L(151)$ and the dark DNA strand should be horizontally scaled variant of ordinary DNA strand by a scaling factor $\lambda \sim L(151)/.33$ nm $= 30$. DNA double strand would be obtained by a transversal scaling from the ordinary DNA double strand.

2. The higher coilings of DNA could correspond to higher horizontally scaled variants of DNA corresponding to $k = 157, 163, 167$. $k = 167$ would correspond to nuclear membrane length scale of 2.5 μm. The emergence of nuclear membrane in $k = 151$ length scale would have been accompanied by the emergence of dark DNA in this scale. Cell membrane could correspond to $k = 173$ and p-adic length scale 17.6 μm. Neurons have size varying from 4-100 micrometers (the definition of size depends on whether one includes axons) and might correspond to $k = 179, 181$ and length scales of .16 mm and perhaps even .32 mm.

The only justification for this speculative picture is that it is consistent with the other basic ideas about TGD inspired quantum biology.

1. Cisse *et al* [I35] found that RNA II polymerase molecules cluster during transcription and their dynamics involves multiples of the time scale $\tau = 5$ seconds. Comorosan reported long time ago that just these time scales are universal bio-catalysis [I81]. The TGD inspired model [L61] for the findings of Cisse *et al* allows to sharpen the TGD based view about quantum biology considerably.

2. The basic parameter of the model is the value of gravitational Planck constant $\hbar_{gr} = GM_Dm/v_0$ assigned to magnetic flux tubes mediating gravitational interactions. Already earlier work gives estimates for the value M_D of dark mass and velocity parameter v_0 and the model leads to the same estimates. The identification of the values of τ as Josephson periods assuming the potential difference V along flux tubes connecting reacting molecules is universal and same as over neuronal membrane fixed the value of h_{gr}. The value of V along flux tube serving as Josephson junction would be universal and equal to membrane potential. Josephson radiation would have energies coming as multiples ot ZeV just above the thermal energy at physiological temperatures fixed by the membrane potential.

3. The model forces the conclusion that the endogenous magnetic field B_{end} has at its upper bound $B_{end} = .2$ Gauss deduced from the findings of Blackman about effects of ELF em fields on vertebrate brain [J6]. The earlier ad hoc hypothesis was that $B_{end} = .2$ Gauss is minimum value of B_{end}. Furthermore, for the required value of h_{gr} $B_{end} = .2$ Gauss corresponds to dark cyclotron energy of .12 keV, which is surprisingly large energy at the upper end of UV band: the earlier intuitive guess was that energy scale is in visible range.

   Also harmonics of cyclotron frequencies were found to have effects so that really large energy scales are involved with the interaction of ELF radiation and one can ask whether this picture really makes sense. This raises a question about the mechanism of the interaction of ELF em radiation with living matter. One also wonder why the ELF radiation has effects on both behavior and physiology.

   Assume

   (a) that dark photons with energies coming as multiples of .12 keV are in question,

   (b) that these dark photons excite dark cyclotron states in the cellular length scale deduced from flux quantization and

(c) that the dark cyclotron photons radiated as the excited cyclotron states return to the ground states perform some control action on ordinary DNA coil - this is in accordance with the basic vision about the role of magnetic body.

X rays have energy range varying from 100 eV to 100 keV and wavelengths varying from 10 nm to .01 nm. The wavelength of an ordinary photon resulting from dark photon with energy of .12 keV would be of order 10 nm, the radius of DNA coil for $k = 151$!

Could this energy induce an analog of standing em wave in transversal degrees of freedom of DNA perhaps transformable to many phonon state with very large number of photos and thus classical acoustic wave? This would allow to understand how cyclotron harmonics can have non-trivial effects. The effects of ELF radiation on behavior and physiology could be understood as gene expression induced by the irradiation.

Both dark cyclotron radiation and radiation generated in dark nuclear transitions could have biological effects

1. Can one relate energy scale of .12 keV associated with dark cyclotron radiation to atomic physics? The ionization energies behave as Z^2_{eff}/n^2, where Z_{eff} is nuclear charge minus the charge of the closed shells. Z_{eff} is also reduced by electronic screening by other valence electrons. The binding energies of valence electrons decrease with the principal quantum number n so that only $n = 2$ row of the periodic table might allow so high ionization energies for valence electrons.

   Oxygen is certainly the first candidate to consider. The ionization energy for oxygen is .12 eV from an estimate assuming that the effective nuclear charge is 6 (with the contribution of 2 valence electrons subtracted). The actual value is 68.9 eV: the reduction is due to electron screening. This value is smaller than the estimate estimate for $E_b = .12$ keV and since harmonics of this energy are involved, the interpretation in terms of ionization does not make sense.

2. Not only oxygen but also heavier elements are ionized in living matter and at least to me this has remained more or less a mystery. Could dark photons emitted by dark nuclei of MB perform control by inducing the transitions and even ionization of oxygen and other biologically important atoms. The process could proceed also in opposite direction. The energy scale would correspond to that of nuclear excitations scaled down by the above ratio of p-adic length scales. If the energy scale of ordinary nuclear excitations is taken to be about 1 MeV, the dark energy scale for $k = 127$ assignable to the dark nuclei created in "cold fusion" is keV. For $k = 131$ the scale would be 250 eV and above the ionization energy scales for valence electrons. For $k = 137$ the scale would be 17 keV. These dark nuclear transitions could generate dark photons inducing transitions of atoms and even ionizations.

3.2.2 What about dark variants of RNA, tRNA, and AAs?

Also RNA and AAs should have dark variants and one should understand their role. Suppose that the integer k characterizing the p-adic length scale is prime. The vision about RNA era preceding DNA era suggests that RNA accompanying dark RNA is at lower level in the evolution, and hence the value of h_{eff} is smaller for dark RNA than for dark DNA. Also the p-adic length scale for RNA would be shorter.

1. The most natural option is that RNA corresponds to $k = 149$ as also single DNA strand. This would conform with the above suggestion that the Pollack effect generates $k = 149$ dark proton sequence (dark RNA?). DNA double strand would correspond to $k = 151$.

   The emergence of $k = 151$ level would mean the emergence of structures with scale characterized by $L(151)$. This includes DNA double strand forming a coil with thickness $L(151)$ and nuclear and cell membranes. During RNA era these structures would have been absent.Both DNA double strand and cell membrane have binary structures. Therefore single DNA strand and lipid layer could correspond to $k = 149$. In transcription DNA opens and double strand becomes pair of strands having naturally $k = 149$. Therefore mRNA should have also $k = 149$.

2. If AAs correspond to $k = 149$ then also tRNA should correspond to $k = 149$. On the other hand, tRNA does not form strands and should be more elementary structure than RNA. Could tRNA corresponds to $k = 139$ or $k = 137$? This would require that also the attached AA would correspond to $k = 139$ or $k = 137$, which does not look plausible.

   Remark: TGD vision assumes tRNA was present already at RNA era and the role of AA in tRNA was to catalyze RNA replication. In fact, RNA could have been just tRNA at very early stages.

What about AAs? The following arguments suggest that one has $k = 149$ for both AAs and RNA.

1. For dark AAs one can imagine p-adic evolutionary hierarchy analogous to that for DNA. In TGD inspired vision AA sequences emerged together with DNA. Proteins can appear also as coils. Since mRNA pairs with single DNA strand and AAs with mRNA, it seems that AAs should correspond to $k \geq 149$?

2. One could however argue that AAs are building bricks rather than information molecules and k could be rather small for dark AAs. Dark AAs should pair with proteins. Pairing without coiling is possible only if the length per letter is same as the length per AA and thus same as for DNA letter, which is longer than the length taken by $k = 139$ dark proton. Also this suggests $k = 149$ for dark AAs and their coiling around the ordinary AAs.

3.2.3 Clustering of RNA polymerase molecules and Comorosan effect

Once again I had good luck: I received a link (see `http://tinyurl.com/y7bego83`) to a highly interesting popular article telling about the work by Ibrahim Cisse at MIT and his colleagues [I35] (see `http://tinyurl.com/y9wzt5yl`) about the clustering of RNA polymerase proteins in the transcription of RNA. Similar clustering has been observed already earlier and interpreted as a phase separation giving rise to protein droplets [L68]. Now this interpretation is not proposed by experiments but they say that it is quite possible but they cannot prove it.

I have already earlier discussed the coalescence of proteins into droplets as this kind of process in TGD framework [K22, K23, K24, K25] [L68]. The basic TGD based ideas is that proteins - and biomolecules in general - are connected by flux tubes characterized by the value of Planck constant $h_{eff} = n \times h_0$ for the dark particles at the flux tube. The higher the value of n is the larger the energy of given state. For instance, the binding energies of atoms decrease like $1/n^2$. Therefore the formation of the molecular cluster liberates energy usable as metabolic energy.

Remark: h_0 is the minimal value of h_{eff}. The best guess is that ordinary Planck constant equals to $h = 6h_0$ [L31, L63] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`.

TGD view about the findings

Gene control switches - such as RNA II polymerases in DNA transcription to RNA - are found to form clusters called super-enhancers. Also so called Mediator proteins form clusters. In both cases the number of members is in the range 200-400. The clusters are stable but individual molecules spend very brief time in them. Clusters have average lifetime of $5.1 \pm .4$ seconds.

Why the clustering should take place? Why large number of these proteins are present although single one would be enough in the standard picture. In TGD framework one can imagine several explanations. One can imagine at least following reasons.

1. If the initiation of transcription is quantum process involving state function reduction, clustering could allow to make this process process deterministic at the level of single gene in spite of the non-determinism of state function reduction. Suppose that the initiation of transcription is one particular outcome of state function reduction. If there is only single RNA II polymerase able to make only single trial, the changes to initiate the transcription are low. This could be the case if the protein provides metabolic energy to initiate the process and becomes too "tired" to try again immediately. In nerve pulse transmission there is analogous

situation: after the passing of the nerve pulse generation the neuron has dead time period. As a matter of fact, it turns out that the analogy could be much deeper.

How to achieve the initiation with certainty in this kind of situation? Suppose that the other outcomes do not affect the situation appreciably. If one particular RNA polymerase fails to initiate it, the others can try. If the number of RNA transcriptase molecule is large enough, the transcription is bound to begin eventually! This is much like in fairy tales about princess and suitors trying to kill the dragon to get the hand of princess. Eventually comes the penniless swineherd.

2. If the initiation of transcription requires large amount of metabolic energy then only some minimal number of N of RNA II polymerase molecules might be able to provide it collectively. The collective formed by N molecules could correspond to a formation of magnetic body (MB) with a large value of $h_{eff} = n \times h_0$ and controlling the molecules and inducing its coherent behavior. The molecules would be connected by magnetic flux tubes.

3. If the rate for occurrence is determined by an amplitude which is superposition of amplitudes assignable to individual proteins the rate is proportional to N^2, N the number of RNA II polymerase molecules. The process for the cluster is reported to be surprisingly fast as compared to the expectations - something like 20 seconds. The earlier studies have suggests that single RNA polymerase stays at the DNA for minutes to hours.

   Clustering could allow to speed up bio-catalysis besides the mechanism allowing to find molecules to find by a reduction of $h_{eff}/h = n$ for the bonds connecting the reactants and the associated liberation of metabolic energy allowing to kick the reactants over the potential wall hindering the reaction.

Concerning the process of clustering there are two alternative options both relying on the model of liquid phase explaining Maxwell's rule assuming the presence of flux tube bonds in liquid and of water explaining its numerous anomalies in terms of flux tubes which can be also dark (see `http://tinyurl.com/ydhknc2c`).

1. **Option I**: Molecules could form in the initial situation a phase analogous to vapour phase and there would be very few flux tube bonds between them. The phase transition would create liquid phase as flux tube loops assignable to molecules would reconnect form flux tube pairs connecting the molecules to a tensor network giving rise to quantum liquid phase. The larger then value of n, the longer the bonds between molecules would be. This kind of model [**?**] (see `http://tinyurl.com/yassnhzb`) is used to explain the strange findings that a system consisting of plastic balls seems to show primitive features of life such as metabolism.

2. **Option II**: The molecules are in the initial state connected by flux tubes and form a kind of liquid phase and the clustering reduces the value of $h_{eff}/h = n$ and therefore the lengths of flux tubes. This would liberate dark energy as metabolic energy going to the initiation of the transcription. One could indeed argue that connectedness in the initial state with large enough value of n is necessary since the protein cluster must have high enough "IQ" to perform intelligent intentional actions.

Protein blobs are said to be drawn together by the "floppy" bits (pieces) of intrinsically disordered proteins. What could this mean in the proposed picture? Disorder would mean absence of correlations between building bricks of floppy parts of the proteins in translational degrees of freedom.

1. Could floppiness correspond to low string tension assignable to long flux loops with large n assignable to the building bricks of "floppy" pieces of protein? Could reconnection for these loops give rise to pairs of flux tubes connecting the proteins in the transition to liquid phase (Option I)? Floppiness would also make possible to scan the environment by flux loops to get in touch with the flux loops of other molecules and in the case of hit (cyclotron resonance) induce reconnection.

2. In spite of floppiness in this sense, one could have quantum correlations between the internal quantum numbers of the building bricks of the floppy pieces. This would also increase the value of n serving as molecular IQ and provide molecule with higher metabolic energy liberated in the catalysis.

About Comorosan effect and clustering of RNA II polymerase proteins

What about the interpretation of the time scales τ equal 5, 10, and 20 seconds appearing in the clustering of RNA II polymerase proteins and Mediator proteins? What is intriguing that so called Comorosan effect [I81, I30] involves time scale of 5 seconds and its multiples claimed by Comorosan long time ago to be universal time scales in biology. The origin of these time scales has remained more or less a mystery although I have considered several TGD inspired explanations for this time scale is based on the notion of gravitational Planck constant [K92] (see `http://tinyurl.com/yb8fw3kq`).

One can consider several starting point ideas, which need not be mutually exclusive.

1. The time scales τ associated with RNA II polymerase and perhaps more general bio-catalytic systems as Comorosan's claims suggest could correspond to the durations of processes ending with "big" state function reduction. In zero energy ontology (ZEO) there are two kinds of state function reductions [L53]. "Small" state function reductions - analogs of weak measurements - leave the passive boundary of causal diamond (CD) unaffected and thus give rise to self as generalized Zeno effect. The states at the active boundary change by a sequence of unitary time evolutions followed by measurements inducing also time localization of the active boundary of CD but not affecting passive boundary. The size of CD increases and gives rise to flow of time defined as the temporal distance between the tips of CD. Large reductions change the roles of the passive and active boundaries and mean death of self. The process with duration of τ could correspond to a life-time of self assignable to CD.

   Remark: It is not quite clear whether CD can disappear and generated from vacuum. In principle this is possible and the generation of mental images as sub-selves and sub-CDs could correspond to this kind of process.

2. In [K92] I proposed that Josephson junctions are formed between reacting molecules in bio-catalysis. These could correspond to the shortened flux tubes. The difference $E_J = ZeV$ of Coulomb energy of Cooper pair over flux tube defining Josephson junction between molecules would correspond to Josephson frequency $f_J = 2eV/h_{eff}$. If this frequency corresponds to $\tau_J = 5$ seconds, h_{eff} should be rather large since E_J is expected to be above thermal energy at physiological temperature.

   Could Josephson radiation serve as a kind of of synchronizing clock for the state function reductions so that its role would be analogous to that of EEG in case of brain? A more plausible option is that Josephson radiation is a reaction to the presence of cyclotron radiation generated at MB and performing control actions at the biological body (BB) defined in very general sense. In the case of brain dark cyclotron radiation would generate EEG rhythms responsible for control via genome and dark generalized Josephson radiation modulated by nerve pulse patterns would mediate sensory input to the MB at EEG frequencies.

   A good guess motivated by the proposed universality of the Comorosan periods is that the energy in question does not depend on the catalytic system and corresponds to Josephson energy for protein through cell membrane acting as Josephson junction and giving to ionic channel or pump. The flux tubes themselves have universal properties.

3. The hypothesis $\hbar_{eff} = \hbar_{gr} = GMm/\beta_0 c$ of Nottale [E1] for the value of gravitational Planck constant [K75, K60, K61, K22, K23, K24, K25] gives large $\hbar$. Here $v_0 = \beta_0 c$ has dimensions of velocity. For dark cyclotron photons this gives large energy $E_c \propto \hbar_{gr}$ and for dark Josephson photons small frequency $f_J \propto 1/h_{gr}$. Josephson time scale τ_f would be proportional to the mass m of the charged particle and therefore to mass number A of ion involved: $f_J \propto A$ possibly explaining the appearance of multiples of 5 second time scale. Cyclotron time scale does not depend on the mass of the charged particle at all and now sub-harmonics of τ_c are natural.

The time scales assignable to CD or the lifetime-time of self in question could correspond to either cyclotron of Josephson time scale τ.

1. If one requires that the multiplies of the time scale 5 seconds are possible, Josephson radiation is favoured since the Josephson time scale proportional to $h_{gr} \propto m \propto A$, A mass number of ion.

   The problem is that the values $A = 2, 3, 4, 5$ are not plausible for ordinary nuclei in living matter. Dark nuclei at magnetic flux tubes consisting of dark proton sequences could however have arbitrary number of dark protons and if dark nuclei appear at flux tubes defining Josephson junctions, one would have the desired hierarchy.

2. Although cyclotron frequencies do not have sub-harmonics naturally, MB could adapt to the situation by changing the thickness of its flux tubes and by flux conservation the magnetic field strength to which f_c is proportional to. This would allow MB to produce cyclotron radiation with the same frequency as Josephson radiation and MB and BB would be in resonant coupling.

Consider now the model quantitatively.

1. For $\hbar_{eff} = \hbar_{gr}$ one has

$$r = \frac{\hbar_{gr}}{\hbar} = \frac{GM_D m}{c\beta_0} = 4.5 \times 10^{14} \times \frac{m}{m_p}\frac{y}{\beta_0} \quad .$$

   Here $y = M_D/M_E$ gives the ratio of dark mass M_D to the Earth mass M_E. One can consider 2 favoured values for m corresponding to proton mass m_p and electron mass m_e.

2. $E = h_{eff} f$ gives the concrete relationship $f = (E/eV) \times 2.4 \times 10^{14} \times (h/h_{eff})$ Hz between frequencies and energies. This gives

$$x = \frac{E}{eV} = 0.4 \times r \times \frac{f}{10^{14} Hz} \quad .$$

3. If the cyclotron frequency $f_c = 300$ Hz of proton for $B_{end} = .2$ Gauss corresponds to bio-photon energy of x eV, one obtains the condition

$$r = \frac{GM_D m_p}{\hbar\beta_0} \simeq .83 \times 10^{12} x \quad .$$

   Note that the cyclotron energy does not depend on the mass of the charged particle. One obtains for the relation between Josephson energy and Josephson frequency the condition

$$x = \frac{E_J}{eV} = 0.4 \times .83 \times 10^{-2} \times \frac{m}{m_p} \times x\frac{f_J}{Hz} \quad , \quad E_J = ZeV \quad .$$

   One should not confuse eV in ZeV with unit of energy. Note also that the value of Josephson energy does not depend on h_{eff} so that there is no actual mass dependence involved.

For proton one would give a hierarchy of time scales as A-multiples of $\tau(p)$ and is therefore more natural so that it is natural to consider this case first.

1. For $f_J = .2$ Hz corresponding to the Comorosan time scale of $\tau = 5$ seconds this would give $ZeV = .66x$ meV. This is above thermal energy $E_{th} = T = 27.5$ meV at $T = 25$ Celsius for $x > 42$. For *ordinary* photon ($h_{eff} = h$) proton cyclotron frequency $f_c(p)$ would correspond for $x > 42$ to EUV energy $E > 42$ eV and to wavelength of $\lambda < 31$ nm.

   The energy scale of Josephson junctions formed by proteins through cell membrane of thickness $L(151) = 10$ nm is slightly above thermal energy, which suggests $x \simeq 120$ allowing to identify $L(151) = 10$ nm as the length scale of the flux tube portion connecting the reactants. This would give $E \simeq 120$ eV - the upper bound of EUV range. For $x = 120$ one would have

$GM_E m_p y/v_0 \simeq 10^{14}$ requiring $\beta_0/y \simeq 2.2$. The earlier estimates [K22, K23, K24, K25] for the mass M_D give $y \sim 2\times 10^{-4}$ giving $\beta_0 \sim 4.4\times 10^{-4}$. This is rather near to $\beta_0 = 2^{-11} \sim m_e/m_p$ obtained also in the model for the orbits of the 4 inner planets as Bohr orbits.

For ion with mass number A this would predict $\tau_A = A \times \tau_p = A \times 5$ seconds so that also multiples of the 5 second time scale would appear. These multiples were indeed found by Comoran and appear also in the case of RNA II polymerase.

2. For proton one would thus have 2 biological extremes - EUV energy scale associated with cyclotron radiation and thermal energy scale assignable to Josephson radiation. Both would be assignable to dark photons with $h_{eff} = h_{gr}$ with very long wavelength. Dark and ordinary photons of both kind would be able to transform to each other meaning a coupling between very long lengths scales assignable to MB and short wavelengths/time scales assignable to BB.

   The energy scale of dark Josephson photons would be that assignable with Josephson junctions of length 10 nm with long wavelengths and energies slightly above E_{th} at physiological temperature. The EUV energy scale would be 120 eV for dark cyclotron photons of highest energy would be fixed by flux tube length of 10 nm.

   For lower cyclotron energies forced by the presence of bio-photons in the range containing visible [K13, K18] and UV and obtained for B_{end} below .2 Gauss, the Josephson photons would have energies below E_{th}. That the possible values of B_{end} are below the nominal value $B_{end} = .2$ Gauss deduced from the experiments of Blackman [J6] does not conform with the earlier ad hoc assumption that B_{end} represents lower bound. This does not change the earlier conclusions.

   Could the 120 eV energy scale have some physical meaning in TGD framework? The corresponding wavelength for ordinary photons corresponds to the scale $L(151) = 10$ nm which correspond to the thickness of DNA double strand. Dark DNA having dark proton triplets as codons could correspond to either $k = 149$ or $k = 151$. The energetics of Pollack effect suggests that $k = 149$ is realized in water even during prebiotic period [L58] (see `http://tinyurl.com/yalny39x`). In the effect discovered by Blackman the ELF photons would transform dark cyclotron photons having $h_{eff} = h_{gr}$ and energy about .12 keV. They would induce cyclotron transitions at flux tubes of B_{end} with thickness of order cell size scale. These states would decay back to previous states and the dark photons transformed to ordinary photons absorbed by ordinary DNA with coil structure with thickness of 10 nm. Kind of standing waves would be formed. These waves could transform to acoustic waves and induce the observed effects. Quite generally, dark cyclotron photons would control the dynamics of ordinary DNA by this mechanism.

   It is natural to assume that $B_{end} = .2$ Gauss corresponds to the upper bound for B_{end} since magnetic fields are expected to weaken farther from the Earth's surface: weakening could correspond to thickening of flux tubes reducing the field intensity by flux conservation. The model for hearing [K67] requires cyclotron frequencies considerably above proton's cyclotron frequency in $B_{end} = .2$ Gauss. This requires that audible frequencies are mapped to electron's cyclotron frequency having upper bound $f_c(e) = (m_p/m_e)f_c(p) \simeq 6\times 10^5$ Hz. This frequency is indeed above the range of audible frequencies even for bats.

For electron one has $h_{gr}(e) = (m_e/mp)\times h_{gr}(p) \simeq 5.3\times 10^{-4} h_{gr}(p)$, $\hbar_{gr}(p)/\hbar = 4.5\times 10^{14}/\beta_0$. Since Josephson energy remains invariant, the Josephson time scales up from $\tau(p) = 5$ seconds to $\tau(e) = (m_e/m_p)\tau(p) \simeq 2.5$ milliseconds, which is the time scale assignable to nerve pulses [K68, K29].

To sum up, the model suggests that the idealization of flux tubes as kind of universal Josephson junctions. The model is consistent with bio-photon hypothesis. The constraints on $h_{gr} = GM_D m/v_0$ are consistent with the earlier views and allows to assign Comorosan time scale 5 seconds to proton and nerve pulse time scale to electron as Josephson time scales. This inspires the question whether the dynamics of bio-catalysis and nerve pulse generation be seen as scaled variants of each other at quantum level? This would not be surprising if MB controls the dynamics. The earlier assumption that $B_{end} = 0.2$ Gauss is minimal value for B_{end} must be replaced with the assumption that it is maximal value of B_{end}.

3.3 TGD view about the emergence of chemical life

Consider first the basic assumptions.

1. Dark DNA, RNA,... emerged before chemistry and serve as templates for ordinary DNA, RNA,... The replication, transcription, and translation for ordinary DNA, RNA,... are induced by the corresponding processes for their dark counterparts.

2. Dark proton sequences are associated with tubular EZs in water generated by Pollack effect.

3. The amount of entanglement measured by entanglement negentropy (having a well-defined meaning in adelic physics [L51]) is expected to increase gradually during evolution. Hence one expects generation of more and more entangled sequences of dark nucleons. At the bottom - perhaps ordinary nuclear physics - one would have the product states of dark nucleons. Perhaps dark nuclear physics with $n = 2^{11}$ came next. After that came $n = 2^{18}$ dark nuclear physics. But which came first: dark variants amino-acids, tRNA, RNA, or DNA and their chemical counterparts? And could one see even genes as entangled codon sequences coding for the same protein?

3.3.1 The quantum vision about the prebiotic evolution

The following vision about quantal prebiotic evolution beginning from amino-acids suggests itself. The basic idea is that all processes took place at dark level and induced the processes for ordinary biomolecules in water environment. Even the enzyme and ribozyme actions essential in recent biology would be replaced with corresponding actions at dark level and biochemistry would reduce to shadow dynamics.

1. Amino-acids are easiest to produce (as Miller-Urey experiment demonstrated (see `http://tinyurl.com/4q2arv`)) requiring no enzymatic action and there is just single chemical amino-acid per dark RNAs coding for it. Therefore the pairs of amino-acids and their dark variants could have emerged first. Note that proteins were not yet present.

   Remark: Vivo-vitro difference could mean that dark partner of biomolecule is present in vivo and missing in vitro.

2. DNA requires cell membrane. This requires RNA emerged after amino-acids. This implies that dark variants of dark tRNA, their pairing with tRNA and the pairing of dark RNA with RNA emerged next?

   This picture supports that the old TGD inspired idea about the role of tRNA during RNA era. Dark tRNA would have made possible the replication of dark RNA sequences (rather than the translation of RNA to amino-acid sequence) during this era. The dark amino-acid of dark tRNA would have served as a catalyst inducing the addition of dark RNA codon to the growing RNA sequence. No chemical transcription machinery nor DNA was needed at this stage. This would solve one hen-or-egg problem.

3. After that a revolution would have occurred. For some reason dark amino-acids began to attach to the growing sequence of amino-acids and dark RNA codon was left alone. What prevented dark RNA codon to attach to the growing dark RNA sequence? Was it the emerging entanglement between dark codons giving rise to genes as entangled pieces of DNA that made this impossible.

   This means entanglement also between the ordinary codons, which makes sense only in ZEO. If possible at all this entanglement should respect genetic code so that entangled superposition would involve only codons coding for the same amino-acid so that the translation to a single amino-acid sequence rather than their quantum superposition is possible. If more general superpositions are allowed the translation process would be like state function reduction to amino-acid sequence.

4. At this step the replication of both dark and ordinary RNA was lost and it seems that dark DNA-DNA pairs replicating dark DNA and transcribing it to dark RNA and inducing corresponding process at the level of chemistry must have emerged at the same time.

The emergence of DNA requires also the emergence of cell membrane. Could the emergence of cell membrane relate to the emergence of dark nuclei in the p-adic length scale $L(k)$, $k = 149$ and could the double layered structure of cell membrane serve as an analog for that of DNA double strand? Could lipid layers correspond to 2-D analogs of DNA strand with lipids taking the role of codons?

5. Could the full genetic code emerged in step-wise manner as proposed earlier [K4, K87]? Genetic code can be seen in a good approximation as a fusion of 16-letter code and 4-letter code. This might be understood if the entanglement of dark codons emerges first as entanglement of only two first letters.

What gave rise to the correspondences between dark DNA, RNA, tRNA, amino-acids and their dark variants? How the amino-acids and nucleotide bases were selected?

1. The basic principle would be the condition that metabolic energy can be transferred between chemical and dark levels. This is possible if there identical transition energies in the spectra of biomolecules and their dark variants making possible resonance.

2. Metabolic energy quantum in the range .4-.5 eV should correspond to the excitation energy scale of dark dark nuclear physics if $E_{ex} = 1$ MeV is taken as the estimate for a typical nuclear excitation energy. Hydrogen bonds also correspond to this energy scale but this might be just what is needed to give rise to coherent metabolic activity.

   The original proposal was that dark DNA associated with ordinary DNA corresponds to $k = 141$ assignable to the ordinary DNA but this proposal predicts $E_{ex}(141) = 16$ eV. This proposal turned out to be unrealistic also in other respects. $k = 149$ assignable to dark RNA predicts $E_{ex}(149) = .5$ eV and is a more plausible option in many other aspects. Also lower values of k than $k = 149, 151$ might be present - at least during the prebiotic stage. Pollack's findings however support the view that the irradiation of water with IR light generates dark proton sequences with $k = 149$. Does this mean that the evolutionary level of water is raised to $k = 151$ in presence of gel phase binding the water sample? Note that "cold fusion" [L22, L41] might be interpreted as creation of $k = 127$ dark proton sequences.

To sum up: for DNA,RNA, and tRNA the emergence of entanglement would have created the chemical counterparts of quantum superpositions: ZEO is necessary since in positive energy ontology superpositions are highly implausible.

There are some questions to ponder.

1. Why the decomposition into triplets? Does resonance condition for the metabolic energy transfer select triplets as basic units and also the RNA-amino-acid correspondence? Do also intronic regions have triplets as basic units?

   One ends up to a prediction of vertebrate genetic code also from a model of music harmony [L11]. In fact, the model explains also its slight variation and the 2 additional amino-acids. Could this help to understand why the triplet code is so unique.

2. Could one imagine that also quarks and antiquarks were involved? Could dark nucleon pair with dark quark with same spin and isospin and color confinement forces dark proton triplets? Dark quarks indeed define a representation for A,T,C, G. In the model of topological computation [K4, K87]. I have actually speculated with the possibility that dark quarks and antiquarks are paired with ordinary DNA codons.

3. Could dark conjugate protons or their triplets of parallel dark DNA strands form Cooper pairs or does pairing of dark protons triplets (their conjugates) with dark quarks (anti-quarks) give rise to bosonic states?

3.3.2 Unidentified Infrared Bands as a test for the proposal

Unidentified Infrared Bands (UIBs) are an ill-understood phenomenon associated with radiation coming from interstellar space. There are also other analogous phenomena having no explanation in terms of molecular transitions [K11] and one can ask whether they could be seen as signatures of dark nuclear physics.

1. UIBs are observed around bands around IR energies $E \in \{.11, .20, .375\}$ eV.

2. Poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`) are known to generate UIBs [K11]. Therefore the UIBs from interstellar space could originate from PAHs.

TGD based models for UIBs

TGD suggests several explanations for UIBs involving new physics related to the p-adic length scale hypothesis and $h_{eff}/h = n$ hierarchy.

1. For years ago I discussed a model for UIBs based on p-adic length scale hypothesis [K11]. The idea was that protons "drop" from atomic space-time sheet with $k = 137$ to a larger space-time sheet to $k_1 > 137$ space-time sheet and the difference of zero point kinetic energies is liberated as radiation [K11]. The proposal was that the zero point kinetic energies give rise to a hierarchy of metabolic energy quanta.

   Second possibility is phase transition in which the size of the $k = 137$ space-time sheet increases to $k_1 > 137$ and liberates the difference of zero point kinetic energy. For the third option energy preserving phase transition increasing $h_{eff}/h = n$ by a factor $(k_1 - k)/2$ followed by a phase transition reducing the value of h_{eff} back to the initial one but without change of the size of the space-time sheet would liberate the difference of zero point kinetic energies.

2. Could dark nuclear transitions explain UIBs? For $k = 149$ as the p-adic length scale of DNA letters would give nuclear energy scale $E = .5$ eV equal to the metabolic energy quantum by scaling 1 MeV for the ordinary nuclei by factor $2^{149-107}/2 = 2^{21}$ (here the original version of text contained error: this claim was made for $k = 141$). This energy has correct order of magnitude but is too high an energy for UIBs but there are of course also smaller energies possible for the nuclear excitations possibly explaining the UIBs.

3. What about hydrogen bonds? The strength of hydrogen bond - essentially the bond energy - is in the range .4-.5 eV -, which as such does not correspond to the average UIB energy, which come approximately as three lowest powers of two. The range of bond energies is .1 eV is smaller than the smallest UIB energy .11 eV.

   UIBs can be associated with hydrogen bonds if there are states of bond with higher bond energy. They could correspond to higher values of $n = h_{eff}/h$ for the de-localized dark proton associated with the bond (analogous to de-localized valence electron). For instance, if the energy of the bond corresponds to the cyclotron energy of proton in a magnetic field associated with the bond, it is proportional to n.

   The photon energies come approximately as powers of 2. If the favored values of n are in bands around $n = 2^k$ favored by the p-adic length scale hypothesis, one has hopes of understanding the band structure in terms of transitions reducing the value of k.

Membrane potential (see `http://tinyurl.com/chylvs9`) plays a key role in metabolism and one can wonder whether UIBs might relate to the potential energies defining energies $E_J = ZeV$ of Josephson photons associated with membrane if it acts like Josephson junction like structures associated with the prebiotic lifeforms.

1. Membrane potential energy varies in the range (.04, .08) eV (cell interior is negatively charged). Excitable cells (able to generate action potentials) include neurons, muscle cells, endocrine cells, and some plant cells. The average value for them is around .06 eV and further depolarization makes these cell more excitable. This suggests that the instability is caused by thermal radiation with nearly the same energy. The threshold for the generation of the action potential E_{act} is in the range $(.050, .055)$ eV. Interestingly, during ageing neurons become more hyperpolarized and therefore less excitable. In photoreceptors the resting potential energy can be as low as .03 eV making them very sensitive to light.

2. In TGD inspired quantum biology axonal membrane can be seen as a generalized Josephson junction [K65, K66, K68] decomposing nanoscopically to Josephson junctions defined by cell

membrane proteins. The protein as junction would correspond to a magnetic flux tube along which various charged particles with $h_{eff} = n \times h$ flow possibly as supra currents. As a special case cell membrane acts like an ordinary Josephson junction. In this case the increment of the electrostatic energy of the Cooper pair over membrane given by $E_J = 2eV$ defines the energy of the smallest quantum of Josephson radiation.

The intensity of thermal radiation at temperature T as function of photon energy E has a peak at $E \simeq 3T$, which for room temperature about $T = .03$ eV gives $E_{max} = .09$ eV. The energy ZeV of Cooper pair should be larger than E_{max}. For critical action potential one has $E_{act} = 0.1$ eV, which is slightly above $E_{max} = .09$ eV so that the action potential has minimal value and thus minimizes metabolic energy costs and implies quantum criticality with temperature as a critical parameter.

Note however that for energies below E_{max} the intensity of thermal radiation decreases so that also these energies might serve as Josephson energies: this and the fact that incoming photons have intensity higher than termal background at this energy could explain why some photoreceptors can have $eV = .03$ eV.

3. Could also Josephson radiation relate to UIBs? The Josephson energy of Cooper pair for the membrane potential is around $E_J = 0.1$ eV, which corresponds to the lowest UIB band, which could thus correspond to action potential .05 eV of excitable membrane. The higher bands would correspond roughly to two octaves suggesting that the action potentials in these case are roughly .1 eV and .2 eV. Quantum criticality would suggest that temperatures scale like the energies of the bands slightly higher than $E_{max} \simeq 3T$.

Metabolic energy transfer between magnetic body and biological body (defined in very general sense for any system) is possible if the spectra of transition energies share common transition energies. Therefore the spectrum of transition energies assignable to hydrogen bonds could have many transition energies common with that assignable to dark nuclear transitions and second and third explanation could be consistent with each other.

Model for hydrogen bond

The explanations of UIBs in terms of hydrogen bonds encourages to consider a concrete model for the hydrogen bond as flux tube. This suggests a connection with metabolism at cellular level involving transfer of protons through cell membrane against potential gradient assumed to take place as dark protons carrying the metabolic energy and providing it to ADP-ATP process after their return.

1. The simplest model for the proton inside flux tube is as particle in 1-D flux tube with magnetic field. Unless the magnetic field strength and/or n is very large, the kinetic energy in the direction of flux tube dominates and phase transition would change the scale of kinetic energy proportional to n^2 for fixed flux tube length. For $n = 2^k$ this would give too strong dependence of photon energies on k.

2. On the other hand, if the flux tubes are flux loops of the magnetic body of molecule their lengths naturally scale as n and the longitudinal kinetic energy is not affected in the transition. The cyclotron energy proportional to n would change and for $n \sim 2^k$ one obtains qualitatively correct behavior.

   For proton in magnetic field of $B_{end} = .2$ Gauss the cyclotron frequency is 300 Hz and corresponds to $E_c(B_{end}) = 1.2 \times 10^{-12}$ eV. The identification of $E_c(B) = .5$ eVs would give $E_c(B) = n(B/B_{end}) \times E_c(B_{end}) = E_c(B) = .5$ eV. An estimate for B for the flux tube of hydrogen bond comes from flux quantization: $eBS = 1$ holds true for unit quantum of flux and for flux tube radius of one Angstrom this would give $B/B_{end} \sim 5 \times 10^8$. This gives the estimate $n \sim 10^8 \sim 2^{27}$. The rather large value conforms with the general vision for the values of n for dark protons whereas dark electrons of valence bonds would have much smaller values. The emergence of dark protons could be seen as the transition from chemistry already involving n as characterizer of valence bonds [L47] to bio-chemistry.

3. The identification of the metabolic energy quantum in terms of cyclotron energy could apply also in the case of cellular metabolism. The model for the generation of ATP from ADP assumes that protons are pumped by the energy coming from nutrient molecules against the membrane potential.

   The membrane potential correspond to energy of .05 eV but metabolic energy quantum is 10 times larger. This looks like an inconsistency, which in thermodynamical approach is resolved by introducing of chemical potentials. In genuine quantum approach the introduction of thermodynamics quantities is not allowed.

   The general vision about metabolic energy as a tool to increase $h_{eff}/h = n$ defining kind of molecular IQ suggests that the transformation to dark proton at magnetic flux tube along which proton can travel through the membrane is responsible for the most of the energy needed for pumping. After the dark proton has returned through cell membrane it transforms to ordinary proton and liberates the metabolic energy and makes possible ADP-APT transformation.

   The above model assumes that the lengths of hydrogen bonds as flux loops scale like n. This makes possible the reconnection of flux loops coming from opposite sides of the membrane to pair of flux tubes along which dark protons can flow. Similar picture applies also to other biologically important ions.

   The general view about superconductivity in TGD Universe [K65, K66] suggests that reconnection can give rise to a Cooper pairs of protons with members at separate flux tubes. Also Cooper pairs of electrons and biologically important ions could form by the same mechanism.

3.3.3 PAH world hypothesis from TGD point of view

The so called PAH world hypothesis (see `http://tinyurl.com/ycxm9zes`) has been proposed as a prebiotic era preceding RNA world. As a matter of fact, PAH world hypothesis inspired more a detailed development of TGD based model for dark nuclei.

Let us first list some properties of poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`).

1. PAHS consist of aromatic rings glued together along sides. By definition aromatic rings have delocalized electrons. In benzene, which is the classical and simplest example of PAH, the electronic state is quantum superposition of states in which bonds and double bonds alternate along the ring but are shifted by 60 degrees with respect to each other. Naphtalene has two aromatic rings and anthracene and pnenanthtrene have 3 rings.

2. PAHs are very stable non-charged non-polar molecules and are very common in Earth. They are found in coal and tar deposits and produced in an incomplete combustion of organic matter. PAHs are poisonous. For instance, tobacco smoke contains PAHs with carcinogenic effects. The stability of PAHs motivates the belief that a large fraction of carbon in the interstellar space consists of PAHs.

3. Benzene in difficult to detect in in the interstellar space since the rotational symmetry does not allow to detect rotational transitions. Recently however nitrobenzene was detected so that benzene and more complex PAHs presumably exist in interstellar space (see `http://tinyurl.com/yap9ksrg`).

Benzene and more complex PAHs can give rise to more complex aromatic by hydrogenation, oxidation, carboxylation, and nitrogenation and led also to the basic building bricks of DNA and amino-acids and PAHs are proposed to have played important role in prebiotic life.

1. PAH world hypothesis states that the polymer like sequences of PAHs serve as scaffoldings for the formation of RNA like polymers (see `http://tinyurl.com/ycxm9zes`). The key motivation is that the distances between PAHs are same as between RNA and DNA bases: 3.4 nm. The proposal is that during PAH era RNA nucleosides A, U, C, G were attached to PAHs by hydrogen bonds.

2. Second hypothesis is that formaldehyde molecules [(H_2C)=O] formed valence bonds with RNA bases and with each other giving rise to sequences analogous to the phosphate-ribose backbone of RNA. The sequence of disjoint CO=:s was replaced with the sequence ..(C-R)-O-(C-R)-O-.. with R denoting the RNA nucleoside. After this hydrogen bonds were split and the precedessor of RNA was detached from the PAH scaffolding. Later the pre-RNA strands were folded to form double pre-RNA strands similar to ribozymes. The problem is to understand how the formaldehyde backbone was replaces with more stable phosphate-ribose backbone.

In TGD framework dark nuclei would serve as scaffolding, which however does not detach from the corresponding biomolecules. The distances between dark variants of biomolecules would explain why the two distances are the same. Very many molecules, including PAHs, can attach around dark RNA/DNA and the periodic structure would be reflect the properties of dark nuclei. This could explain UIBs as emission bands of both dark nuclei and hydrogen bonds essential for the pairing and the transfer of metabolic energy between ordinary and dark biomolecules. Also in DNA double strand hydrogen bonds could serve similar function. If thermal radiation excites higher energy states of nuclei, the emission of UIBs depends on temperature. Perhaps this could be tested.

UIBs could therefore serve as a direct signature of dark nuclear physics. If dark nuclei are not associated with PAHs in vitro or in an environment not containing water, UIBs would be absent.

3.3.4 Did RNA replicate in codon-wise manner during RNA era?

3.3.5 Did RNA replicate in codon-wise manner during RNA era?

There was an interesting popular article in Spacedaily with title "*Scientists crack how primordial life on Earth might have replicated itself*" (see `http://tinyurl.com/y92ng5vd`). The research paper [I46] is titled "*Ribozyme-catalysed RNA synthesis using triplet building blocks*" and published in eLife (see `http://tinyurl.com/ya5qyjfn`).

It is possible to replicate unfolded RNA strands in Lab by using enzymes known as ribozymes, which are RNA counterparts of enzymes, which are amino-adic sequences. In the presence of folding the replication is however impossible. Since ribozymes are in general folded, they cannot thus catalyze their own replication in this manner. The researchers however discovered that the replication using RNA triplets - genetic codons - as basic unit can be carried out in laboratory even for the folded RNA strands and with rather low error rate. Also the ribozyme involved can thus replicate in codon-wise manner. For units longer than 3 nucleotides the replication becomes prone to errors.

These findings are highly interesting in TGD framework. In TGD the chemical realization of genetic code is not fundamental. Rather, dark matter level would provide the fundamental realizations of analogs of DNA, RNA, tRNA, and amino-acids as dark proton sequences giving rise to dark nuclei at magnetic flux tubes [L58] (see `http://tinyurl.com/yalny39x`). Also ordinary nuclei correspond in TGD Universe to sequences of protons and neutrons forming string like entities assignable to magnetic flux tubes.

The basic unit representing DNA, RNA and tRNA codon and amino-acid would consist of 3 entangled dark protons. The essential aspect is that by entanglement the dark codons do not decompose to products of letters. This is like words of some languages, which do not allow decomposition to letters. This representation is holistic. As we learn to read and write, we learn the more analytic western view about words as letter sequences. Could the same hold true in evolution so that RNA triplets would have come first as entities pairing with dark RNA codons from from dark proton triplets as a whole? Later DNA codons would have emerged and paired with dark DNA codons. Now the coupling would have have been letter by letter in DNA replication and transcription to mRNA.

It is intriguing that tRNA consists of RNA triplets combined from amino-acids and analogs of mRNA triplets! The translation of mRNA to amino-acids having no 3-letter decomposition alone forces the holistic view but one can ask whether something deeper is involved. This might be the case. I have been wondering whether during RNA era RNA replicated using a prebiotic

form of translational machinery, which replicated mRNA rather than translated RNA to protein formed from amino-acids (AAs) with AA serving as a catalyst.

1. During RNA era amino-acids associated with pre-tRNA molecules would served as catalysts for replication of RNA codons. The linguistic mode would have been "holistic" during RNA era in accordance with the findings of the above experiments. RNA codon would have been the basic unit.

2. This would have led to a smaller number of RNAs since RNA and RNA like molecules in tRNA are not in 1-1 correspondence. A more realistic option could have been replication of subset of RNA molecules appearing in tRNA in this manner.

3. Then a great evolutionary leap leading from RNA era to DNA era would have occurred. AA catalyzed replication of RNA would have transformed to a translation of RNA to proteins and the roles of RNA and AA in tRNA would have changed. [Perhaps the increase of h_{eff} in some relevant structure as quantum criticality was reached led to the revolution]

4. At this step also (subset of) DNA and its transcription to (a subset of) mRNA corresponding to tRNA had to emerge to produce mRNA in transcription. In the recent biology DNA replicates and is transcribed nucleotide by nucleotide rather than using codon as a unit so that helicases and DNA and RNA polymerases catalyzing replication and transcription should have emerged at this step. The ability of DNA to unwind with the help of helicase enzyme helping DNA to unwind is essential for the transcription and translation of DNA. Therefore helicase must have emerged together with the "analytic linguistic mode" as an analog of written language (DNA) decomposing codons to triplets of letters. This would been a crucial step in evolution comparable to the emergence of written language based on letters. Also the counterpart of RNA polymerase and separate RNA nucleotides for transcription should have emerged if not already present.

   An alternative option would involve "tDNA" as the analog of tRNA and the emergence of helicase and polymerases later as the transition from holistic to analytic mode took place.

   The minimal picture would be emergence of a subset of DNA codons corresponding to RNAs associated with pre-tRNA and the emergence of the analogs of helicase and DNA and RNA polymerases as the roles of amino-acid and RNA codon in tRNA were changed.

5. How DNA could have emerged from RNA? The chemical change would have been essentially the replacement of ribose with de-oxiribose to get DNA from RNA and U$\rightarrow$ T. Single O-H in ribose was replaced with H. O forms hydrogen bonds with water and this had to change the hydrogen bonding characteristics of RNA.

   If the change of $h_{eff} = n \times h_0$ was involved, could it have led to stabilization of DNA? Did cell membrane emerge and allow to achieve this? I have proposed [L58] (see `http://tinyurl.com/yalny39x`) that the emergence of cell membrane meant the emergence of new representation of dark genetic code based on dark nuclei with larger value of h_{eff}.

   Remark: One has $h = 6 \times h_0$ in the most plausible scenario [L31, L63] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`).

The communication between dark and ordinary variants of biomolecules involves resonance mechanism and would also involve genetic code represented as 3-chords, music of light, and it is interesting to see whether this model provides additional insights.

1. The proposal is that 3-chords assignable to nucleotides as music of light with allowed 64 chords defining what I have called bio-harmony is essential for the resonance [L64, L67, L63](see `http://tinyurl.com/ydhxen4g`, `http://tinyurl.com/yd5t82gq`, and `http://tinyurl.com/y9jxyjns`). The 3 frequencies must be identical in the resonance: this is like turning 3 knobs in radio. This 3-fold resonance would correspond to the analytic mode. The second mode could be holistic in the sense that it would involve only the sum only the sum of the 3 frequencies modulo octave equivalence assigning a melody to a sequence of 3-chords.

2. The proposal is that amino-acids having no triplet decomposition are holistic and couple to the sum of 3 frequencies assignable to tRNA and mRNA in this manner. Also the RNAs in tRNA could couple to mRNA in this manner. One could perhaps say that tRNA, mRNA and amino-acids codons sing whereas DNA provides the accompaniment proceeding as 3-chords. The couplings of DNA nucleotides to RNA nucleotides would rely on the frequencies assignable to nucleotides.

3. If the sum of any 3 frequencies associated with mRNA codons is not the same except when the codons code for the same amino-acids, the representation of 3-chords with the sum of the notes is faithful. The frequencies to DNA and RNA nucleotides cannot be however independent of codons since the codons differing only by a permutation of letters would correspond to the same frequency and therefore code for the same amino-acid. Hence the information about the entire codon would be needed also in transcription and translation and could be provided either by dark DNA strand associated with DNA strand or by the interactions between the nucleotides of the DNA codon.

4. The DNA codon itself would know that it is associated with dark codon and the frequencies assignable to nucleotides could be determined by the dark DNA codon. It would be enough that the frequency of the letter depends on its position in the codon so that there would be 3 frequencies for every letter: 12 frequencies altogether.

   What puts bells ringing is that this the number of notes in 12-note scale for which the model of bio-harmony [L11, L64] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/ydhxen4g`) based on the fusion of icosahedral (12 vertices and 20 triangular faces) and tetrahedral geometries by gluing icosahedron and tetrahedron along one face, provides a model as Hamiltonian cycle and produces genetic code as a by-product. Different Hamiltonian cycles define different harmonies identified as correlates for molecular moods.

   Does each DNA nucleotide respond to 3 different frequencies coding for its position in the codon and do the 4 nucleotides give rise to the 12 notes of 12-note scale? There are many choices for the triplets but a good guess is that the intervals between the notes of triplet are same and that fourth note added to the triplet would be the first one to realize octave equivalence. This gives uniquely $CEG\sharp$, $C\sharp FA$,$DF\sharp B\flat$, and $DG\sharp B$ as the triplets assignable to the nucleotides. The emergence of 12-note scale in this manner would be a new element in the model of bio-harmony.

   There are 4!=24 options for the correspondence between $\{A,T,C,G\}$ as the first letter and $\{C,C\sharp,D,D\sharp\}$. One can reduce this number by a simple argument.

   (a) Letters and their conjugates form pyrimidine-purine pairs T,A and C,G. The square of conjugation is identity transformation. The replacement of note with note defining at distance of half-octave satisfies this condition (half-octave - tritonus - was a cursed interval in ancient music and the sound of ambulance realizes it). Conjugation could correspond to a transformation of 3-chords defined as

   $$CEG\sharp \leftrightarrow DF\sharp B\flat \ , \quad C\sharp FA \leftrightarrow D\sharp GB \ .$$

   (b) One could have

   $$\begin{aligned} &\{T,C\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ , \quad \{A,G\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ , \\ &\qquad\qquad\qquad\qquad \text{or} \\ &\{T,C\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ , \quad \{A,G\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ . \end{aligned}$$

   .

   (c) One can permute T and C and A and G in these correspondences. This leaves 8 alternative options. Fixing the order of the image of (T,C) to say $(C,C\sharp)$ fixes the order of the image of (A,G) to $(D,D\sharp)$ by the half-octave conjugation. This leaves 4 choices. Given the bio-harmony and having chosen one of these 4 options one could therefore check what given DNA sequence sounds as a sequence of 3-chords [L11].

That the position the frequency associated with the nucleotide depends on its position in the codon would also reflect the biochemistry of the codon and this kind of dependence would be natural. In particular, different frequencies associated with the first and third codon would reflect the parity breaking defining orientation for DNA.

3.4 Improved reckless speculation about higher level variants of dark genetic code

In an earlier article I represented what I called reckless speculations about higher level variants of genetic code (see [L58] for the updated version of the original article). The speculations turned out to be not only reckless but to contain besides an unrealistic working hypothesis for p-adic length scale of dark DNA also a numerical error in the estimate of dark nuclear excitation energy scale leading to a wrong track.

The wrong working hypothesis was the assumption that ordinary DNA, RNA, etc correspond to same p-adic length scale as their dark variants. Simple argument shows that the dark scales must result via radial scaling of the typically linear structures such as DNA, RNA, etc and also 2-D structures such as membranes and microtubules giving rise to 2-D lattice like realizations of genetic code generalizing the ordinary 1-D realizations.

Also new improved picture conforms with the vision that dark realizations of genetic code at various p-adic length scales serve as controllers of the ordinary biochemistry, which is kind of shadow dynamics. Replication, certainly one of the most mysterious feats of living matter, would reduce to the replication at the level of dark DNA in various p-adic length scales involved. This would be a huge simplification.

A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h_0 = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier. A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier [K44].

3.4.1 Ideas

Consider first the general ideas.

1. The assumption of prime values for k in $L(k)$ would pose extremely tight constraints on the allowed p-adic length scales and values of h_{eff}/h_0. One would have $k \in \{127, 131, 137, 139, 149\}$ and $k \in \{151, 157, 163, 167\}$ and $k \in \{173, ..\}$ at least at the level of dark matter. So predictive an idea deserves to be killed, if not anything else.

   A further motivation for these speculations is that the Gaussian Mersenne primes $M_{G,k=}(1+i)^k - 1$ for $k \in \{151, 157, 163, 167\}$ define p-adic length scale $L(k) \propto 2^{k/2}$ between 10 nm assignable to the neuronal membrane and 2.5 μm assignable to cell nucleus: so many Gaussian Mersenne in so short length scale range is a number theoretical miracle.

2. Cell membrane consisting of two lipid layers (see `http://tinyurl.com/h9a2hsq`) is a binary structure as also DNA double strand. DNAs replicate as would do also RNAs during RNA era. Also cells and therefore also cell membranes replicate so that the analogy might make sense. Since processes like translation and transcription do not occur, cell membrane might serve as 2-D as analog of RNA: the counterpart of RNA era might prevail at these levels. Neuronal membrane might correspond to 2-D analog of DNA.

   So: could various 2-D structures such as nuclear membrane, cell membrane, neuronal membrane, and microtubuli correspond to a new level in the hierarchy of dark codes for which genes and their dark variants would be 2-D rather than 1-D structures? One would have 2-D lattices of codons. Could there be entire hierarchy of them assignable to certain p-adic length scales? As 2-D realizations could be paired with their dark variants so that one could speak of dark variants of various membrane like structures. This applies also to microtubuli.

The idea that dark variants of DNA, RNA, and AAs are their radially scaled up variants generalizes also. The processes like replication of cell could be induced by a much simpler replication of 2-D dark DNA. This kind of pairing hierarchy could be behind miraculous looking replication of entire organisms. p-Adic fractality and hierarchy of dark DNAs could lurk behind the curtains.

3. The structures of ordinary bio-matter and also their dark variants assumed to control them are characterized by p-adic length scales. How these p-adic length scales could relate? The natural idea inspired by scaling invariance is that the dark variants of 1-D linear structure and 2-D structures formed from ordinary bio-matter are obtained by radial scaling consistent with p-adic length scale hypothesis, and guaranteeing that the distances between building bricks are scaled to the size scales of dark variants of DNA and other basic molecules. This rule makes sense also for the 2-D structures. For instance, it would scale up the p-adic length scale $L(143)$ characterizing lipid to $L(149)$ assignable to single dark RNA strand or $L(151)$ assignable to dark double DNA strand.

4. One can argue that cell membrane - in particular neuronal membrane - is highly dynamical unlike RNA. In ZEO however dynamical evolutions of space-time surfaces as preferred extremals - correlates for behaviors - replace 3-D static patterns as basic entities so that the emergence of cell membrane might mean dark genetic code for dynamical patterns analogous to deterministic computer programs defining predetermined dynamical patterns. In central nervous system nerve pulse patterns coded by dark RNA could provide similar coding of behavioral patterns.

5. I have claimed in earlier publications that the lipid double layer defining cell membrane has thickness $L_e(151) = 10$ nm: actually the thickness is $L_e(149) = 5$ nm for ordinary cells and 8-10 nm - roughly $L_e(151)$ - only for neuronal membranes. Therefore the emergence of neuronal membranes could be seen as an evolutionary step in p-adic and thus number theoretic sense. Needless to say, this little difference might be absolutely crucial for undestanding why neurons are at higher evolutionary level than ordinary cells. It would be nice if this difference could correspond to an increase of $h_{eff}/h_0 = n$ and p-adic length scale of ordinary and dark membrane like structure by a factor 2.

   There is double cell membrane associated with mitochondria. The thickness of the two double membranes is about 7 nm so that they might correspond to $k = 149$. The double membrane would have roughly the thickness 22 nm. If this structure is a functionally coherent structure it would corresponds to $L_e(153)$ and could be controlled by its dark counterpart.

6. I have proposed that the flux tubes connecting the dark DNA sequences above lipid layer to those associated with DNA could make possible to realize topological quantum computation [K4, K87] in terms of braiding induced by the 2-D liquid flow induced by nerve pulse patterns at nuclear membrane. Flux tubes might be associated with cytoskeleton and define an analog of central nervous system at the level of cell. A rough estimate for the numbers of codons for human DNA of length about 1 m and the number of codons allowed by the surface of the nuclear membrane are of order 10^9 so that the proposal might make sense.

   This proposal generalizes and has many alternative forms. For instance, microtubules inside axons could be connected by flux tubes to the surface of axons.

   One could also consider braidings between ordinary and dark levels, say braiding of flux tubes connecting lipid layers of neuronal membrane to 2-D analog of dark DNA. This braiding would code quantum computer programs and be part of coding of nerve pulse patterns inducing 2-D flow of lipids to memories represented as braidings. Quite generally, the braidings could be very naturally between ordinary and dark variants of structures considered.

3.4.2 Could cell membrane and neuronal membrane realize genetic codons as 2-D structures?

In the sequel I discuss in more quantitative level the idea that cell membrane and neuronal membrane realize analogs of genes as 2-D structures.

The p-adic length scales associated with the dark variants of 2-D structures?

Consider next the p-adic length scales associated with the structures considered.

1. The thickness of ordinary cell membrane corresponds roughly to $L_e(149) = 5$ nm whereas the coiling associated with the cell membrane corresponds to $L_e(151)$. Also neurons correspond to $L_e(151)$. Could $k = 149$ *resp.* $k = 151$ define levels of ordinary cell *resp.* neuron in the hierarchy of dark nuclear physics?

2. Cell membrane consists of lipid bilayer. The lipid layer has three parts (see `http://tinyurl.com/h9a2hsq`).

   - The totally hydrated layer nearest to water is hydrophilic head group, which in the case of phospholipids contains negatively charged phosphate. This phosphate layer has thickness $.7 - 1.0$ nm.
   - Below it is a partially hydrated layer of thickness .3 nm, which corresponds to $L(141)$: this of course puts bells ringing!
   - Hydrophobic lipid tail layer below it is dehydrated. The thickness of single lipid layer is 1.25-1.75 nm and would correspond to the p-adic length scale $L_e(145) = 1.2$ nm. $k = 145$ is not prime.

3. The phosphate layer analogous to phosphate-ribose backbone and the thickness $L(141)$ of partially hydrated layer suggests that it corresponds to EZ created in Pollack effect so that there would be parallel dark RNA sequence along axon (possibly helical as for microtubules). In the case of cell membrane would have lattice like system formed from dark protons, and maybe even dark neutrons (as an analog for the neutron halo in some nuclei).

4. If the recent biology is the analog of RNA era for $k = 149$ codes, their manifestations could be seen as analogs of RNAs and the number of different lipids associated with the cell membrane could give some idea about their number. Cell membrane could perhaps be seen as a 2-D analog of RNA polymer. Cell division implying membrane replication would be induced by dark RNA replication. Even the analogs of tRNA and AAs but not proteins might be present if one takes the analogy very seriously. Could one identify pairs of lipids and some molecules analogous to proteins appearing in cell division?

What kind of general conditions can one pose on the dark variants of DNA, RNA, and AAs?

1. Dark variant of 2-D variants of DNA, RNA, or AAs realizing the hierarchy of dark codes should control their analogues or possibly some other molecules coded by them. The coupling would be by resonance. This suggest the hierarchy of codes uses as building bricks simpler structures by starting from 1-D structures and building from them more complex structures. Hence the natural hypothesis is that the 2-D variants of proteins consisting of a 2-D lattice like structure formed from proteins is in question.

2. The geometric aspect of membrane dynamics would be determined by basic dynamics of TGD determined by action, which is a generalization of charged point-like particle coupling to Maxwell field by replacing the particle orbit with 4-D surfaces. This allows as special case minimal surfaces such as deformations of cosmic strings giving magnetic flux tubes. Cell membranes should correspond to extremals for which coupling to Kähler force is non-trivial as it indeed is by membrane potential. This because static closed surfaces, in particular spherical layers, are not possible as minimal surfaces. Remarkably, these extremals are not analogs of external particles (geodesic lines) but correspond to interaction regions. This conforms with the fact that cell membrane is a self-organization pattern requiring a continual feed of metabolic energy.

   The 2-D dark variants of DNA, RNA, and AAs would be involved mostly with the control the electro-chemistry of membrane like structures. Of course their geometrodynamics would induce also morphogenesis of ordinary bio-matter.

Also enzymes and ribozymes would have dark variants controlling their behavior. Folded protein represents an interesting example about possibly 3-dimensional graph like structure in which the protein forms an analog of Hamilton's cycle going through all points of the graph defined as a lattice with nearest neighbors connected by edges without self-intersections. This hypothesis is rather powerful since for Hamiltonian cycle do not necessarily exist for an arbitrary graph.

3. In the case of cell membrane membrane proteins are the natural candidate for the building bricks. They indeed have an active role and serve as both channels and pumps and in the case of the neural membrane this role is especially important. Membrane proteins are identified in TGD framework as generalized Josephson junctions. In the case of cell membranes mebrane proteins having length of about 5 nm (5 AAs) or 10 nm (10 AAs) going through the membrane are an excellent candidate for the basic building brick. One could see the basic structure either as 2-D structure built from membrane proteins or 3-D structure build from AAs. Membrane proteins would form kind of generalized protein as a 2-D lattice of proteins and accompanied by their dark variants or of 2-D dark variants of RNA or DNA coding for them and identifiable as radial scalings of these proteins to $k = 149$ or $k = 151$.

   The model for topological quantum computation [K4] suggesting that DNA codons of are connected to lipids of cell membrane could be modified so that dark DNA, RNA, or AAs associated with membrane proteins are connected to them by flux tubes which can get braided. This would allow the quantum control of the 2-D protein like structure and make it effectively single quantum coherent Josephson junction as suggested in the quantum model for nerve pulse [K68].

The original proposal was that there might exist an analog of genetic code for lipids. The number of different lipids is however too high to allow any simple correspondence. Lipids have also rather passive role in the dynamics of the cell membrane: their serve as signal pathways, provide metabolic energy, and serve as signal pathways (see `http://tinyurl.com/z7d7osm`). The proposal however deserves to be explained.

1. Both sides of the lipid bilayer of cell membrane could pair with 2-D lattice of dark RNA whose size scale would be obtained by radial scaling giving rise to what might be called dark cell membrane. In the case of neuronal membrane the dark lattice would consist of pairs of dark DNA codon and its conjugate. In the case of axon one could have the analog of dark DNA strand extended to a cylinder containing bundles of these strands at its surface. Lipid layers would be 2-D analogs of 1-D DNA strands in this case.

2. Lipids would be analogs of ordinary RNA codons and dark RNA codons would code for them: this would predict 64 different lipids in cell membrane. Single dark RNA would correspond to the size scale of single lipid given by $L(143) = 2L(141) = .625$ nm. The dark nuclear physics would correspond to $k = 149$. The number N of parallel dark RNA strands would be roughly the circumference of the axonal lipid layer divided by the size of single lipid about $L(143) = .625$ nm given by $N \sim 2\pi \times L_e(167)/L_e(143) = \pi \times 2^{24} \sim 5 \times 10^6$.

Thermodynamical constraints

Could this totally irresponsible speculation about p-adic hierarchy of dark nuclear physics and genetic codes survive thermodynamical constraints?

1. The condition that metabolic energy quantum is not below thermal energy at physiological temperatures poses constrains on the model. I have considered several identifications of the metabolic energy quantum. These identification need not be mutually exlusive.

   - One interpretation is as 1-D zero point kinetic energy of proton at tubular space-time sheet of atomic size with transversal length scale $L(137)$. This energy is invariant under scalings induce by increase of h_{eff} since h_{eff}^2/L^2 is not changed.

   - Second identification of metabolic quanta would be as energies assignable to hydrogen bond and its dark variants.

- Third identification of the metabolic energy quantum would be as scaled variant of $E_b(k) = 2^{(k-107)/2}E_b$ of typical dark nuclear binding energy $E_b =\sim 1$ MeV. The value would be about .5 eV for $k = 149$ and .25 eV for $k = 151$.

2. Note that the action potential assignable to $k = 151$ neuronal membrane is around .05 eV (the membrane potential for some photoreceptors is .03 eV). In TGD Universe the cell membrane can be seen as Josephson junction decomposing in an improved resolution to membrane proteins acting as Josephson junctions [K65, K66]. Josephson energy of Cooper pair is twice this - that is $E_J = 0.1$ eV slightly above the maximum $E_{max} = 3T = .09$ eV of the thermal distribution at physiological temperature.

3. As far Josephson radiation are considered, for $k = 151$ membrane would be a quantum critical system. Quantum criticality could give rise to instability making possible the generation of nerve pulses. During nerve pulse the dark protons at the dark space-time sheet would return to the neuronal membrane and destroy the ionic equilibrium. Also the temperature criticality of consciousness manifesting itself as the generation of hallucinations during fever could be understood. For $k = 151$ the situation would be overcritical and will be discussed separately.

The Josephson energy of Cooper pair is scaled down to $E_J = .1$ eV near to $E_{max} = .09$ eV. This is slightly above the thermal energy but one could still argue that Josephson radiation cannot carry information. Or could Nature have found the means to overcome this potential problem? The notion of generalized Josephson junction central in TGD inspired theory of EEG as communications from brain to MB [K68, K29] could save the situation.

1. For the generalized Josephson junction the energy of quantum of Josephson radiation is $E = E_J + \Delta E_c$, where ΔE_c is the difference of cyclotron energies at the two sides of the membrane. E_c is proportional to $h_{eff} = n \times h$ and large enough value of n guarantees that E_c is above $E_{max} \simeq 3T$ irrespective of the value of the membrane potential. The variations of the membrane potential modulate Josephson frequency, and are proposed to provide a coding of sensory data defined by nerve pulse patterns communicated to MB.

2. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis [K61, K22, K23, K24, K25] guarantees the spectrum of cyclotron energies is universal and does not depend on the mass m of the charged particle being in the range of visible and UV energies of photons (this allows to deduce information about the values of mass M and velocity parameter $v_0 < c$): bio-photons would be produced in energy conserving phase transitions transforming dark photons to ordinary ones [K13, K18].

3. If MB itself (a structure which has size scale of Earth at EEG frequencies around 10 Hz) has low enough temperature, this would allow to overcome the limitations caused by the thermal masking of the ordinary Josephson radiation so that the frequency modulations by nerve pulse patterns could code for the sensory data. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis indeed allows very large values of h_{eff} for which ordinary cyclotron energies proportional to h_{eff} would be ridiculously small for the ordinary value of h.

What about the situation for massive particles like proton? Now Maxwell-Boltzmann (Gaussian) distribution is a good approximation and for effectively D-dimensional system the value of distribution is reduced by $1/e$ at thermal energy $E_{cr} = DT/2$. One could argue that above this energy thermal masking can be avoided. For $D = 1$ at magnetic flux tubes this would give $E_{cr} = T/2 = E_{max}/6$. At $T_{phys} = .03$ eV one would have $E_{cr} = 0.15$ eV. Metabolic energy quantum would be above E_{cr} for $k = 151$. Even $k = 153$ possibly assignable to mitochondrial double membrane can be considered but represents an upper bound at physiological temperatures.

Remark: In TGD view about information processing in brain [L40] active linear neuron groups relate to verbal cognition and 2-D neuronal groups relate to the geometric cognition associated with the decomposition of perceptive field to objects. At cellular level DNA and cell membrane could perhaps be seen as counterparts for these structures. In TGD framework neuronal membrane is proposed to be a constructor of sensory representations communicated to the magnetic body (MB) using generalized Josephson radiation whereas motor control by MB has been assumed to take place via DNA [K39].

3.4.3 DNA packing problem and p-adic length scales

DNA manages to pack huge amount of DNA to single cell nucleus. For instance, human DNA as length of about 1 meter. This is achieved by a hierarchical coiling structure involving 3 levels with highest level identifiable as chromatides and the lowest level defined by nucleosomes (see `http://tinyurl.com/yat5cm4y`) wound around histon isomers linked together by straight portions of DNA. One can find a detailed representation of the 4-levelled packing of DNA (see `http://tinyurl.com/ybxv6w4v`).

There are 4 levels involved. Could they relate to the Gaussian miracle primes $k = 151, 157, 163, 167$? The general proposal is that the products of powers of small primes define the scale hierarchy. There is evidence that at least the powers of 2 and 3 define p-adic length scales, which would correspond also to dark scales. The simple guess is that the dark scales are identical to the ordinary p-adic scales.

- The diameter of the nucleosome is 11 nm $= 1.1L(151)$, which suggests $k = 151$. Chromatosome consists of histone H_1 plus nucleosome.
- Nucleosomes coil to form a fiber of diameter $d = 30$ nm. This scale is $3L(151)$.
- At the next level loops of average length 300 nm $= 30L(151) \sim 32L(151)$. This level is only intermediate level in packing.
- These loops compress and fold to 250 nm $=25L(151) \simeq 3 \times L(157)$, $L(157) = 8L(151)$ wide fiber. Thus third harmonic of also the miracle length scale $L(157)$ would be involved.
- This fiber compresses a tight coil of radius 700 nm $= 70L(151) \simeq 64L(151) = L(163) = 640$ nm giving rise to the chromatid fiber of chromosome. $k = 163$ is the third miracle length scale.
- Chromosomes have width 1400 nm which corresponds to the scale $L(165)$.

The 3 levels $k = 131, 157, 163$ seem to be realized although not in the simplest manner. Nuclear membrane would correspond to $L(k = 167) = 2.5$ μm. For $n = h_{eff}/h_0$ these levels would correspond to the values n of form $n = 2^r 3^s$.

Consider next nucleosome.

1. DNA wraps of around histone octamers forming a cubical structure consisting of 8 smaller cubes (octamers). There are 2×4 histones forming two identical layers. The 4 histones H_{2A}, H_{2B}, H_3, H_4 of given layer are not identical. There is also histone H_1 attached to the entire structure. The incoming DNA double strand enters to the upper end of H_1 and leaves from its lower end. H_1 is related to the secondary coiling. The wrapping gives rise nucleosomes as helices with two turns and containing about 146 base pairs making 48 codons plus 2 base pairs.
2. According to the standard model of nucleosome double DNA strand wraps around the analog of a spool formed from an octamer consisting of two identical units above each other consisting of 4 different histones. The incoming DNA strand enters the upper 4-histone unit and winds once around it and then does the same for the lower unit before leaving the nucleosome.

One can construct a rough TGD inspired model for this structure (not completely realistic) to get a concrete idea about what is involved.

1. The size scale of the cube like structure is $L(151) = 10$ nm so that single histone corresponds to a cube with side roughly about $L(149) = 5$ nm. One can estimate the total length L of the wire from the equation $z = xR\phi/\pi$, $R \sim L(149)$, $\phi \in [0, 4\pi]$, as $L = \sqrt{1 + \pi^{-2}} 4\pi R$. For $R \sim L(149)$ and $h = L(151)$ this gives $L \sim 66$ nm, There are roughly 146 DNA base pairs and 48 whole codons ($144 = 3 \times 48$ base pairs) and each codon has length about 1 nm. This gives total length of 48 nm. The reduction of radius R by factor $r = 48/66 = 3/4$ to $R = 3L(149)/4$ would give a correct value of L

   According to the representation for the hierarchy of packings (see `http://tinyurl.com/ybxv6w4v`), the diameter of the structure is $d = 1.1L(151)$ rather than small and the height

of the structure is smaller in the illustration. This width is however not consistent with the helix structure for any value of the height.

2. If the double DNA strand is accompanied by a dark double strand of radius $L(149)$, the situation is like having a band of width $L(151)$ going around the spool. The dark double strand covers an area, which is 4/3 times the spool area. The horizontal thickness of the entire dark structure is about $d_D = (7/4)L(151)$. If the radius of DNA double strand is $r = L(151)$ the area covered by the double strand is roughly twice the area of the spool. This suggests that one should identify the p-adic length scale of DNA double strand as its diameter about $L(151)$ rather than its radius.

Remarks:

1. While trying to understand nucleosomes in TGD framework, I encountered an interesting side result related to Hamiltonian face paths and Hamiltonian cycles on octahedron, which to my best understanding must correspond to Hamiltonian paths and cycles on cube. The octahedral face paths can be identified as closed paths connecting the middle points of the centers of a cube. The 8 histones define a decomposition of the entire cube to 8 sub-cubes. The idea was that Hamiltonian face cycles in these cubes could give up to tight packing of 6 codons. The number of the Hamiltonian paths for cube is 64 (see `http://tinyurl.com/ybqw6zpt`) and the number of cycles is 6! Single genetic codon would dictate the choice of the Hamiltonian path on cue! Although the idea did not work (the length of, it led to ask whether the Hamiltonian cycles on octahedron or their duals at cube might have some biological relevance.

2. A further interesting finding is that the sequence of 8 quints defines a piece of 12-note scale proceeding by quints as steps between nearest neighbor vertices (using octave equivalence) in the icosahedral model of harmony [L11, L69] based on 12-note scale could be interpreted as cubic Hamiltonian cycle giving rise to the notes $F, C, G, D, A, E, H, F\sharp$. This gives the notes of C major scale with 7 notes plus tritonus $F\sharp$ defining half-octave as 8:th note. One could also identify the cycles as consisting of the notes of 8-note scale along cycle in the usual order $C, D, E, F, G, A, H, F\sharp$ based on standard notion of nearness for which neighboring vertices correspond to neighboring notes of the scale. Allowed 3-chords would correspond to triplets containing no neighboring notes. The Hamiltonian cycle for cube is unique apart from isometries as also for tetrahedron and dodecahedron.

3.4.4 Microtubules as quantum critical systems

Also microtubules (see `http://tinyurl.com/y8km9vve`) are 2-D structures having a strong resemblance with the lipid layers of cell membrane. Could a higher level representation of genetic code similar to the one proposed for cell membranes make sense for them. Also now one can imagine that the microtubular surface is accompanied by its dark variant realizing 2-D dark genes, dark RNA, or dark proteins with scaled up size. The p-adic prime should correspond to $k > 151$ so that higher level realization of genetic code would be in question. In the case of axons a possible identification for the dark scale would be as the radius of the axonal membrane.

1. Microtubules are hollow cylinders with outer *resp.* inner diameter equal to 24 *resp.* 12 nm (the scales differ by factor 2) so that their thickness is 12 nm is same as the inner radius and would correspond to $L(151) = 10$ nm. They decompose to 13 parallel helical filaments consisting of 13 tubulin proteins having size scale of order $L_e(151)$.

2. Tubulins are dimers of α and β tubulin and the pairs are oriented along the helical filament. One can estimate the size of α and β tubulin by diving the circumference of 24 nm of the microtubule with the number of filaments, which is 13. This gives for the size scale of tubulin the estimate $R_{tub} \sim 12$ nm not far from $L(151)$. This supports the view that p-adic length scale $L(151)$.

   The size scale of the transversal volume associated with lipid is roughly .62 nm that is $L(143) = 2L(141)$ so that they could correspond to $k \in \{141, 143\}$, presumably $k = 141$.

Therefore one could see microtubules as scaled up variants of cell membrane with scaling factor $2^{(151-141)/2} = 2^5 = 32$. Similar scaling would take place for the value of $n = h_{eff}/h$ giving $n = 2^{23}$ so that microtubules would represent a higher level of evolution identified as increase of n. Microtubules have indeed emerged after cell membrane.

3. It has been proposed that the α and β conformations of tubulin give rise to bit or even qubit. If this were the case, single helical filament rotating one full turn would have 2^{13} states and carry 13 bits of information. 13 independent filaments would have $2^{26} \simeq 64 \times 10^6$ states and carry 26 bits of information. One could also think of codon as sequence of 13 filaments with the states of filaments representing 2^{13} letters of the code.

4. Microtubular surface has rather high charge density and is polarized: the almost stationary end has negative local charge density roughly equal to that of DNA whereas the growing end has lower surface charge density. One manner to control the charge of the tubulin dimer is in terms of the charge states of GDP and GTP by ionization of the phosphates. Maximal negative charge for tubulin dimer would be 5 units.

   Microtubules are highly dynamical objects with inherent instability and have varying length: one might say that microtubules are quantum critical objects. Quantum criticality and thus instability might relate to the fact that the metabolic energy quantum is very near to thermal energy at room temperature.

   The dynamics for the length of microtubule could be induced from the dynamics of EZ involving the flow of protons between microtubule and its magnetic body defined by dark DNA. The gradient in charge density would make possible positive net charge density at the growing end of the microtubule.

   In ZEO it looks reasonable to argue that the dynamical patterns are coded by a generalization of genetic code just as computer programs code for deterministic dynamical patterns.

5. What could the dark code behind the dynamics be? The α- and β tubulins of tubulin dimer involve GTP (see `http://tinyurl.com/ybtjluaf`) *resp.* GDP (see `http://tinyurl.com/y8uok7kq`). In the case of DNA one has XMP, $X = A, T, C, G$. The analogs of dark RNA sequences would contain mere G and the information coded by the tubulin would be determined by the conformation of the tubulin dimer giving 1-bit code. This looks somewhat disappointing.

   If the charge states of the phosphates of GDP and GTP can vary and all charge combinations for phosphates are possible, one has 2^3 charge states for GTP and 2^2 charge states for GDP. Together with the bit associated with the tubulin conformation this would give 2^6 states and realize 6 bits of the ordinary genetic code! One would have 2-D realization of the genetic code analogous to that proposed for the lipid layer with the state of tubulin analogous to RNA codon.

   This coding together with thermal criticality would make microtubule a dynamical object since the deviation of the tubulin charge from -1 units would spoil charge local charge neutrality of tubulin-dark RNA pair.

I have proposed that flux tubes connecting tubulins to the lipids of the axonal lipid layer could give rise to topological quantum computation [K4, K4]. The size scale of lipid is about $L_e(141)$ and that of tubulin about $L_e(151) = 32L_e(141)$, and the radius of axonal membrane is by two orders of magnitude larger than microtubular surface. Hence this proposal does not look realistic unless one assumes that sub-structures of cell membrane with size scale of order $L_e(167)/L_e(151) = 2^8$ larger than tubulin size represented as space-time sheets with cell nucleus size $L(167)$ have flux tube connections to tubulins.

This kind of map would give rise to a kind of abstraction about what happens at the level of axonal membrane integrating out un-necessary details. This abstraction is natural since microtubules would indeed correspond to a higher level of cognitive hierarchy. Roughly $N = 2^{16}$ lipids would contribute to the information received by single tubulin. Could nerve pulse patterns can induce braiding of the flux tubes in this scale?

3.5 Freaky DNA

The popular article "*Freaky Eight-Letter DNA Could Be the Stuff Aliens Are Made Of*" (see `http://tinyurl.com/y5wb7cm8`) tells about very interesting discovery related to astrobiology, where the possible existence of variants of DNA and other bio-molecules are of considerable interest. The article "*Hachimojii DNA and RNA: A genetic system with eight building blocks*" (see `http://tinyurl.com/y2mcjb4r`) published in Science tells about a discovery of a variant of DNA with 8 letters instead of 4 made by Hoshika *et al* [I24]. By using an engineered T7 RNA polymerase this expanded DNA alphabet could be transcribed into Hachimoji variant of RNA. The double strand structure of hachimoji DNA is similar to that of ordinary DNA and it is thermodynamically stable.

No amino-acid (AA) counterparts assigned to the hachimoji RNA were engineered: this would require the existence of translation machinery. The possible existence of also additional AAs leads to the speculation is that both alien life forms utilizing this kind of extended code could have evolved. One can also ask whether mere synthetic hachimoji RNA could be enough for synthetic life.

The abstract of the article gives a more technical description about what has been achieved.

> *We report DNA- and RNA-like systems built from eight nucleotide "letters" (hence the name "hachimoji") that form four orthogonal pairs. These synthetic systems meet the structural requirements needed to support Darwinian evolution, including a polyelectrolyte backbone, predictable thermodynamic stability, and stereoregular building blocks that fit a Schrödinger aperiodic crystal. Measured thermodynamic parameters predict the stability of hachimoji duplexes, allowing hachimoji DNA to increase the information density of natural terran DNA. Three crystal structures show that the synthetic building blocks do not perturb the aperiodic crystal seen in the DNA double helix. Hachimoji DNA was then transcribed to give hachimojii RNA in the form of a functioning fluorescent hachimoji aptamer. These results expand the scope of molecular structures that might support life, including life throughout the cosmos.*

If the additional code letters for DNA (8 code letters instead of 4) really carry information, the number of codewords is extended by factor $2^3 = 8$ giving $2^9 = 512$ code words. What the number of AAs would be, can be only guessed: the simplest guess is that also now the number is scaled up by factor 8 but this is only a guess.

In the sequel I consider hachimoji code from TGD perspective. The natural guess is that the hachimoji code corresponds to 8 copies of the ordinary genetic code in some sense. TGD predicts two basic realizations of the genetic code corresponding to dark genetic code and bio-harmony.

1. In the case of the dark code it is possible to imagine an extension of the code based on the notion of dark nucleus and the number codons is multiplied by 8. In the case of bio-harmony fusion of 8 copies of bio-harmony allows to realize hachimoji code.

2. I have considered two basic realizations of bio-harmony [L11, L69] giving also realization of genetic code. The first realization is as a fusion of 3 icosahedral harmonies and tetrahedral harmony. Second realization is as a fusion of 2 icosahedral harmonies and 1 toric harmony. These constructions do not however allow any elegant geometric interpretation since two different geometries are involved in both cases.

   During writing I was forced to reconsider this problem and realized that a fusion of 2 icosahedral harmonies with 20 chords and 2 dodecahedral harmonies with 12 chords produces genetic code with 20+20+12+12=64 codons. Icosahedral and docecadedral harmonies correspond to dual tessellations of sphere so that bio-harmony can be represented as a bundle over sphere with two notes represented as points of the fiber. Hachimoji harmony is obtained by replacing 2-point fiber with 8×2-point fiber. The presence of the dual tessellations conforms with the fact that Eastern music uses micro-intervals, which rather naturally correspond to 20-note dodecahedral scale.

3. The reason why for the hachimoji code could the basic problem of the music scale realized in terms of rational frequency ratios. Already Pythagoras was aware of this problem. The construction of the scale as powers of quint (3/2-fold scalings of the basic frequency) using

octave equivalence produces with 12 iterations 7 octaves but only approximately: the 12th iterate does not quite correspond to the basic note in the octave equivalence. Performing the 12-fold iteration 8 times gives therefore a refined scale with each note replaced with 8 almost copies identifiable as hachimoji scale.

4. A further discovery was that the quint scaling appearing in the earlier model can be replaced with a unique scaling, which is same for icosahedral and dodecahedral codes. One must however generalize the notion of Hamiltonian cycle by introducing the analog of gauge symmetry in a discrete bundle over sphere and allowing to generate new Hamiltonian cycles from given cycle by gauge transformations. In this manner one obtains extremely rich harmony from single basic chord transposable to $CEG\sharp$.

3.5.1 Icosa-tetrahedral and icosa-dodecahedral bioharmonies as candidates for genetic code

Both the icosa-tetrahedral [L11] and icosa-dodecahedral harmony to be discussed below can be considered as candidates for bio-harmony as also the harmony involving fusion of 2 icosahedral harmonies and toric harmony [L60]. The basic reason is that the third harmony corresponds to doublets. One cannot exclude the possibility of several equivalent representations of the code.

Icosa-tetrahedral harmony

Icosahedral harmonies can be characterized by a subgroup of icosahedral isometries A_5 having 60 elements. If reflections are included the isometry group, oneas $A_5 \times Z_2$ with 120 elements. The group of symmetries is Z_6, Z_4, or Z_2. There are two choices for Z_2 and the interpretation has been that Z_2 correspond to either reflection or rotation by π. A_5 however allows also $Z_2 \times Z2$ as subgroup. AAs correspond to orbits of the symmetry group and DNA codons coding for the AA correspond to triangles (3-chords) at the orbit. In purely icosahedral model on obtains 20+20+20 codons. A fusion with tetrahedral harmony gives 64 codons.

1. Z_6 gives rise to 3 AAs coded by 6 codons each (leu,se,arg) and 2 AAs coded by 2 codons: the choice of the doublet would require additional conditions. One option is ile doublet.

2. Depending on whether one includes reflection or not, one can have either $Z_4 \subset A_5$ ($60 = 4 \times 15$) or $Z_4 = Z_{2,rot} \times Z_2 \subset A_5 \times Z_2$. I have assumed that $Z_4 = Z_{2,rot} \times Z_2$ but the recent argument suggests the first option. This does not have any implications for the earlier model. Icosahedral Z_4 gives rise to 5 AAs coded by 4 codons each ($5 \times 4 = 20$). This leaves 11 AAs and 3 "empty" AA formally coded by stop codons.

3. Icosahedral Z_2 gives rise to 10 dublets. These 4-plets would correspond to (phe, tyr, his, gln, asn, lys, asp, glu, cys, stop-doublet) This leaves (stop,trp) double and (ile,met) doublet with broken Z_2 symmetry.

   The fusion with tetrahedral code with 4- codons and 4 AAs should explain these 4 AAs. Tetrahedral isometries form group S_3 and reduce to group Z_3 for tetrahedral cycle.

   (a) One could argue that ile-triplet and met correspond to 3-element orbits with 1-element orbit. (stop,trp) would be formed by Z_2 symmetry breaking from trp doublet and there is no obvious mechanism for this.

   (b) If one tetrahedral face is fixed as a face shared with icosahedron, the symmetry group of tetrahedral cycle reduces to Z_1. This would give 4 singlets identifiable as (ile,met) and (stop,trp) symmetry broken doubles. Since ile appears also in doublet, tetrahedral 1-orbit and icosahedral 2-orbit must have a common doubled triangle identifiable as the common face of icosahedron and tetrahedron. The doubling of the common triangle replaces ile-doublet with ile-triplet. This option looks rather reasonable.

Dodecadedral harmony

Dodecahedral harmony correspond to the unique Hamilton cycle at dodecahedron. Dodecahedral harmony as 20 notes and 12 5-chords. If one assumes that the octave divides to 20 notes, this brings in mind "eastern" view about harmony.

The obvious objection against dodecahedral harmony is that dodecahedral faces are pentagons so that dodecahedral chords would be 5- rather than 3-chords so that the correspondence between chords and DNA codons would be lost. The situation changes if 3 notes - 3-chord - determine the 5-chord completely and one can assign a unique 3-chord to each pentagon. This is indeed the case!

1. 3-edges meet in every dodecahedral vertex (this makes the dodecahedral cycle unique apart from rotations) and each edge pair in the vertex belongs to same pentagon (in the case of icosahedron there are 5 edges per vertex so that this is not true). Therefore each pentagon must contain at least 2 edges of Hamilton's cycle.

   The cycle must visit all vertices of pentagon, and the visit to the vertex means that the cycle shares at least one edge with pentagon. Since all vertices of the pentagon must be visited, there are two options. For option a) given pentagon shares with the cycle disjoint 2-edge with 3 vertices and 1-edge with two vertices. For option b) the pentagon shares with the cycle 4-edge with 5 vertices.

2. The numbers n_a of pentagons with 4-edges and $n_b = 12 - n_a$ 2-edge+ 1-edge (making 3 edges) can be deduced easily. Cycle has 20 edges. Pentagon of type a) shares 3 edges with the cycle and the edge is shared by 2 pentagons. This gives $3n_a/2$ edges. Pentagon of type b) shares 4 edges with the cycle. This gives $2n_b = 2(12 - n_a)$ edges. The total number of edges is $3n_a/2 + 2n_b = 20$, which gives $n_a = 8$ and $n_b = 4$. Dodecahedral Hamilton's cycle can be found from web (see `http://tinyurl.com/y5woajcb`). The structure is as deduced here.

   For case a) the 3-chords correspond naturally to the 3 vertices of the 2-edge shared with the cycle. Therefore it is possible to assign unique 3-chords to the dodecahedral harmony and to obtain connection with codons in this case. One however obtains also 12 2-chords: could they have some genetic counterpart?

   What about 5-chords for pentagons of type b)? Hamiltonian cycle can be oriented and this is induces orientation of the pentagons. One can say that the first vertex in the 4-edge is the vertex at which cycle arrives to the pentagon and identify the 3-chord as the first three vertices. It turns out that for the replacement of quint cycle this is not actually necessary.

Is icosa-dodecahedral harmony consistent with the genetic code?

One must check whether icosa-dodecahedral harmony is consistent with the degeneracies of the genetic code.

1. A fusion of 2 icosahedral harmonies and 2 copies of dodecahedral harmony would be in question. As in the case of icosahedral harmony already discussed, the two icosahedral harmonies would have symmetry groups Z_6 and Z_4 and give the codons coding for 3 6-plets and 1 doublet+ 5 4-plets + two copies of dodecahedral harmony.

2. Can the model predict correctly the numbers of codons coding for AAs? It is known that dodecahedral Hamilton cycle divides dodecahedron to two congruent pieces related by Z_2 symmetry (see `http://tinyurl.com/yy6pcogt`). Also the Hamiltonian cycle defining the common boundary has Z_2 symmetry. A good guess is that these Z_2:s corresponds to reflection symmetry and rotation by π but I am not able to exclude $Z_4 \subset G_0$, where G_0 consists of 60 orientation preserving isometries. In this case some orbits - presumably all 3 of them - could contain 4 pentagons. This is not consistent with the condition that one has doublets and singlets.

   If the second symmetry corresponds to reflection, it can be excluded by simply assuming that reflections change the orientation of the cycle.

3. Rotation by π has two fixed points corresponding to opposite poles so that one has 5 2-orbits and 2 1-orbits giving 12 triangles for each copy. Two copies of dodecahedral harmony would give 5+5=10 doublets and 2+2=4 singlets. A possible interpretation would be as (ile,met) and (stop,trp).

Consider now objections against dodecahedral harmony.

1. Why two copies of dodecahedral code? What distinguishes between them? If imirror symmetry leaves the cycle invariant apart from orientation the copies could be mirror images and consist of same faces. The second option is that they related by a rotation?

2. The number of dodecahedral AAs is 24 rather than 20. Could the additional 4 AAs as orbits have interpretation as AAs in some sense. Could the "empty" AAs coded by stop codons be counted as AAs exceptional in some sense. In TGD framework one can consider the possibility that although AA is "empty", there is analog of AA as physical signature for the end of protein telling what stopping codon it corresponds. The magnetic body of protein is a good candidate.

   Genetic code has several slightly differing variants. Could the 2 additional exotic AAs Pyl and Sec correspond in some situations to the additional AAs?

3. Essential for the bio-harmony as a fusion of harmonies is that one can select from each orbit single face as a representative of the AA it codes - kind of gauge choice is in question - and that the orbits corresponding to different AAs can be chosen to be disjoint. Otherwise codons belonging to the orbits of different Hamilton cycles can code for the same AA if the AA can be chosen to be in intersection. If not, the same codon can code for 2 different AAs - this can indeed occur in reality [L67]!

   The condition that orbits of different cycles do not interesect seems quite stringent but has not been proven. But what if it is actually broken? Indeed, in the case of icosahedral harmony with Z_1 symmetry tetrahedron and icosahedron could have common a doubled face the breaking of this condition would geometrically explain why ile belongs to both icosahedral and tetrahedral orbit.

   Ile is the problem also in the case if icosa-dodecahedral harmony. Dodecahedral singlet codes for ile as also icosahedral doublet. Could one talk about doubling of ile face so that it corresponds to a pair of triangle and pentagon (in 1-1 correspondence with triangle as chord).

4. The two copies of the dodecahedral code should correspond to 5 doublets and 2 singlets each. One expects that together they give rise to 10+2 +10+2 =24 faces. Do they? Mirror symmetry and rotation by π act as symmetries of the cycle so that neither can map the two cycles to each other. Dodecahedral (equivalently icosahedral) rotations give rise to new equivalent cycles. The action on pentagons corresponds to the action on vertices of icosahedron so that it easy to understand what happens.

   Each symmetry corresponds to a rotation around some axis and has opposite icosahedral vertices at this axis as fixed points. Hence any two cycles obtained in this manner have 2 common pentagons. This means reduction $24 \to 22$ unless one interprets the situation in terms doubled faces? Could the disappearing doublet correspond to stop-doublet? What about the remaining stop of the vertebrate code pairing with trp? Why does second singlet correspond to empty AA and not something else such as exotic AA.

5. There is also further problem. Suppose that an intersection of orbits takes place at single triangle. Suppose that one cannot choose this triangle to be "AA" triangle for both orbits. In this case it is not clear to which AA the codon codes. This kind of phenomenon actually takes place in some cases and is known as homonymy [L67]. It is associated with the deviations of the code from the vertebrate code and involves exotic AAs Pyl and Sec. Codons can serve as a stop codon or code for an exotic AA.

Clearly, the notion of bio-harmony involves many unclear aspects but my strong feeling is that there is very beautiful mathematics involved.

3.5.2 Hachimoji code and realizations of genetic code suggested by TGD inspired quantum biology

The discovery of Hachimoji code relates interestingly to two realizations of the genetic code inspired by TGD based quantum biology.

1. The first realization is dark genetic code with codons realized as 64 3-proton states made of dark protons having non-standard value $h_{eff} = n \times h_0$ of Planck constant [L58]. The hierarchy of Planck constants is predicted by adelic physics providing physical correlates for correlation in terms of p-adic physics [L51]. Dark genetic code would be fundamental in TGD and bio-chemical realization would be kind of shadow or mimicry of it and not even complete in some cases. One cannot talk about letter decomposition for dark proton triplets since the 3-proton states are entangled.

2. Second realization relies on the notion bio-harmony [L11, L69]: the realization of the genetic in terms of 3-chords of bio-harmony emerged as a by-product from a model of harmony.

Does dark realization of genetic code allow hachimoji code?

Could one realize hachimoji codons as dark codons?

1. If the proposed dark proton triplets [L58, L57] is the only fundamental realization of genetic codons, the real information storage capacity should not increase but the correspondence between dark codons and chemically realized codons would not be 1-to-1 but 1-to-8. Furthermore, the transcription of dark DNA to ordinary one would not be possible in 1-to-1 manner so that hachimoji code could not have evolved.

2. One can however imagine of having also neutrons rather than only protons in the dark nuclear string. If one can have both dark protons and neutrons, one could obtain effectively 8 letters. Also the number of dark RNA codons and perhaps also of ordinary AAs would increase - presumably by factor 8. Since the dark nucleons would be located along magnetic flux tube, Fermi statistics, which does not allow protons to have the same position, would not affect the situation and one would indeed obtain just the factor 8.

   There is however an objection. Dark proton sequences would be generated by the formation of exclusion zones in Pollack effect [L15] [L15], and would be stable against transformation to those containing neutrons since the energy needed to transform proton to neutron is about MeV and huge in the scale of biochemistry.

   Is it possible to overcome this objection?

1. TGD inspired nuclear physics relies on nuclear string model [L1] for which unexpected correlations between nucleons (EMC effect) provide support. Nucleons would be connected bo nuclear string by color bonds having quark and antiquark at their ends. Bonds could be color neutral and color confinement would make the bonds stable.

   The bonds connecting nucleons to nuclear string would have u/d type quark and antiquark at their ends and could have total charges +, -1, and 0. This would predict new exotic states of nuclei with binding energy differences of order keV (small scale compared to MeV scale of nuclear binding energies). There is evidence for keV energy scale.

   In fact, several scaled variants of dark nuclear physics are predicted [L58], and the nuclear binding energy scale would behave like $1/L$, where L is the size scale of dark nuclei identifiable as p-adic length scale in TGD framework. Even dark nuclear binding energy scale of order metabolic energy quantum of order .5 eV can be considered.

2. Same would apply to dark nuclei formed from dark protons. The bonds connecting dark protons to nuclear string could also have total charge +1,-1, and there could exist two states with charge 0. Only 3 spin states analogous to those of (neural) ρ_0 meson are accepted in the original model whereas neural pion-like state is not allowed. Now the states analogous to both ρ_0 and ρ_{-1} are accepted. One can denote the bond as $B(q)$, $q = 0, +1, -1$.

The pair $p + B(-1)$ would behave like neutron effectively. The pair $p + B(1)$ would have charge +2 and could be be unstable due to repulsion whereas neutron like state could be stable by attraction. This could give rise to an effective doubling of letters.

Remark: A possible objection is that the neutral ρ meson like color bond is expected to have energy higher than neutral pion by spin-spin splitting as in the case of ordinary mesons. A good argument for throwing out the pion-like bond is needed.

Is the realization of hachimoji code in terms of bio-harmony possible?

What about the realization of hachimoji code as a bio-harmony [L11, L69]? Bio-harmony makes it possible to transfer the genetic information at the level of dark variants of basic bio-molecules (also RNA, AAs, and tRNA) in terms of 3-chords of dark photons coupling via frequency resonance. The coupling to ordinary variants of DNA would take place via energy resonance and involve the transformation of dark photon to ordinary photon or vice versa coupling. Music expresses and induces emotions and the music of dark photons would provide fundamental expression of emotions realized at the bio-molecular level [L64].

Can one scale the number chords of bio-harmony by factor 8 by using icosa-dodecahedral bio-harmony?

The number 64 of 3-chords defining the bio-harmony should be scaled up by 8. As far as chords are considered, each note appearing in the chord should be doubled.

1. There are two variants for bio-harmony. 12-note scale is represented as a Hamiltonian cycle defined as a closed path (by octave equivalence) going through all vertices of as tessellation of sphere or torus and not intersecting itself. Both icosahedron and tetrahedron can be regarded as tessellations of sphere by triangles.

   The first realization [L11, L69] involves fusion of 3 Hamiltonian cycles at icosahedron defining 20 chord harmony H_{20} each and 1 cycle at tetrahedron defining 4-chord harmony H_4. This gives 20+20+20+4=64 3-chords defining the codons.

   Second realization [L60] is a fusion of 2 20-chord harmonies H_{20} defined by Hamiltonian cycles at icosahedron and 24-chord harmony H_{24} by cycle associated with torus tessellation. The fusion of two icosahedral cycles gives 20+20 3-chords and torus cycle gives 24 chords: 64 altogether. There are large number of Hamiltonian cycles and their fusions would correspond to different emotional states.

2. Can one imagine any modification of the model giving rise to 8-fold increase of the basic chords? One can consider doubling of the 4 basic frequencies to 8. For instance, splitting of each frequency could correspond to the doubling of the code letters. One can also imagine that each triplet of dark nucleons (dark neutron would be now dark proton+the bond with varying charge) corresponds to its own cyclotron frequency triplet so that 8-fold increase of 3-chords would become possible.

3. Could one have a geometric interpretation for the 8-fold increase of 3-chords realized as faces of Platonic solid or toric triangular tessellation. Could summand in the sum of 3 icosahedral harmonies and one tetrahedral harmony (of 2 icosahedral and toric harmonies) be replaced with an analog of tessellation having 8-fold number of triangles? The splitting of each triangle to 8 smaller equilateral triangles so that the 12-note scale would have now $8 \times 12 = 96$ notes, is not possible since the side of the smaller triangle should be $2^{-3/2}$ times smaller than that of the original triangle: inverse integer scaling would be required.

4. The simplest manner to get 8-fold scaling for the number of chords is some kind of fusion of 8 octaves of bio-harmony. By octave equivalence the 8-letter code would bring new information at the level of bio-harmony perceived in an improved resolution only. New information would require that the fused scales differ slightly. A natural interpretation for the fusion would be as formation of a discrete bundle structure in which 8-fold increase of notes of the scale corresponds to 8-point fiber.

The fusion of fundamental harmonies with 20, 4 or 24 3-chords is used in the proposed models of bio-harmonies. The geometric interpretation of the fusion is not quite clear. For a fusion of 3 icosahedral code one could imagine a discrete bundle structure in which 3 copies of note as points of icosahedron form a 3-point fiber. The addition of tetrahedron could be seen as a union of icosahedron and tetrahedron with gluing along common face. This does not however fit with the bundle interpretation.

Same applies to the union of 2 icosahedral codes with $(V, F) = (12, 20)$ and 1 toric code with $(V, F) = (20, 24)$. One could ask whether the latter option could allow interpretation as singular bundle structure such that in the fiber space two tori collapse to spheres. This would correspond to a disappearance of 4 faces so that one has 20 faces instead of 24. This does not look like an attractive option.

5. Could one find a realization of the code consistent with the bundle interpretation? Could one have 64 codons by using fusion of 2 icosahedral and 2 dodecahedral codes (forget for a moment that the faces of dodecahedron are pentagons!)? Dodecahedron has 20 vertices (maybe 20-note scale might relate to micro-intervals used in Eastern music) and 12 faces. The fusion would give 20+20+12+12= 64 chords. Dodecahedral harmony is unique since there is only single Hamilton's cycle.

   One would have only single topology and the interpretation as fiber space with 2 points in the fiber would make sense if the dodecahedral tessellation is constructed as a dual of icosahedral one with new vertices as centers of icosahedral triangles. Music, even the music of light realized as triplets of dark photons with frequencies equal to those of the chords of bioharmony, expresses emotions and this leads to the suggestion that emotions are expressed even at the level of bio-molecules [**?**] Therefore I cannot avoid the temptation to ask whether the uniqueness of the dodecahedral harmony could relate to the eastern notion of empty mind empty of any emotions and thoughts.

6. For this realization of bio-harmony the fusion of 8 bio-harmonies could be seen as a transition to a higher hierarchy level considering structures made of structures and would produce the required number 96 of notes. These bio-harmonies would have slightly different 12-note scales. Octave equivalence would suggests that 12-note scale is effectively replaced with $8 \times 12 = 96$ note scale. The interpretation in terms of fiber space structure with 2×8 points in the fiber would make sense.

The problem of Pythagoras a motivation for the fusion 8 copies of bio-harmonies

Could one imagine any justification for the fusion of 8 copies bio-harmonies possibly with slightly differing scales? A problem that teased already Pythagoras suggests this kind of justification!

1. The basic problem of Pythagorean scale based on rational frequencies realized as quints of the basic frequency modulo octave equivalence is that octave equivalence is not quite exact. The octave projections by scaling by a power of 2 of the scale in higher octaves to the lowest octave do not quite quite coincide with the 12-note scale assigned with it: the reason is that no power of $x = 3/2$ can exactly coincide with power of 2 so that $x^{12} = 2^7$ is true only with 1 per cent accuracy.

   Pythagoras who firmly believed that Nature relies on the arithmetics of rationals was even ready to believe that Nature is imperfect! In TGD framework one could say that only the cognition based on rationals is imperfect (also cognition using algebraic numbers is predicted to be possible and evolution would mean increase of the complexity for the extension of rationals). Tempered scale would require the powers of algebraic number $x = 2^{1/2}$ to belong to the extension.

   The problem is that Pythagorean scale seems however to have a deeper meaning (people with absolute ear love it) [L25]. Could some number of octaves - say 8 - give a more precise mathematical model of music experience in the case of people having absolute ear? Could it be that people with absolute ear have a better pitch resolution and are able to distinguish between notes of 96-note scale?

Remark : The realization of 12-note scale using irrational frequency ratios coming as $2^{1/12}$-powers of the fundamental frequency does not have problem with octave equivalence.

2. The 8×12-note would be obtained as follows. One performs first 12-fold iteration to get 12-note scale. The 12th iterate is very near to the basic note by octave equivalence. After that one repeats 12-iteration 7 times so that each note in the original 12-note scale is mapped to 8 notes. These notes must be within interval corresponding to half-note (say E-F), which corresponds to the scaling $r = 2^{1/12}$ in good approximation. This gives the condition $(x^{12\times 8}/2^8)^8 < r$ giving the condition $x < 2 \times r^{1/(8\times 12)} = 2 \times 2^{1/96} \simeq 2.0145$ satisfied for $x_8 = 27/17$.

3. The construction of bio-harmony was based on the assumption that the subsequent vertices along Hamiltonian cycle (neighboring points of tessellation) are related by the scaling of frequency by $x_7 = 3/2$ (Hamiltonian cycle would correspond to quint cycle especially familiar for jazz musicians) and projecting to the basic octave. 12 scalings of this kind give slightly more than 7 octaves ($(3/2)^{12} \simeq 129.746..$ rather than $2^7 = 128$): there relative error is about 1 per cent. $x_7 = 3/2$ would suggest 7 rather than 8 copies of the basic bio-harmony.

   Quint rule is consistent with 8-fold repetition of the basic 12-iteration but one can imagine also alternative rules for generating the notes of the scale using powers of some number x reduced to basic octave. Could a simple choice for $x = x_8$ give $x_8^{12} = 2^8$ in a better approximation than $x_7 = 3/2$ gives $x_7^{12} = 2^7$? The replacement $x_7 = 3/2 \to x_8 = (3/2) \times y$, where y is rational approximation for $2^{1/12}$, gives a natural guess for x_8. For $y = 18/17$ giving $x_8 = 27/17$ (to be compared with $x_7 = 27/18$ one obtains $x_8^{12}/2^8 = 1.006...$, so that the error is .6 per cent whereas for $x_7 = 3/2$ the corresponding error is around 1 per cent. Note that $p = 17$ is Fermat prime of form $F_n = 2^{2^n} + 1$ near to power of 2. Primes near power of two are in fundamental role in TGD.

4. It will be found that the recent proposals for bio-harmony have drawbacks, and that a more elegant identification of bio-harmony as a fusion of icosahedral and dodecahedral harmonies leads to a replacement of powers of quints $(C - G)$ with powers of slightly larger interval $(C - G\sharp)$ and a generalization of Hamiltonian cycle by introducing the analogy of gauge symmetry.

Details of the icosa-dodecahedral harmony

Consider now the details of the icosa-dodecahedral harmony.

1. Dodecahedral harmony involves $n_{20} = 20$ notes. The generalization of the quint cycle means that the frequencies in the basic octave are obtained from the base frequency as scalings by octave equivalence: $f/f_0 = x_{20}^k/2^{r(k)}$, $k = 0, 1, .., 19$ with $r(k)$ fixed by the condition that $1 \leq f/f_0 \leq 2$. x_{20} is a rational number determined by the condition that x_{20}^{20} is as near as possible to power $2^{k_{20}}$, where k_{20} can have several values.

   $k_{20} = 12$ gives $x_{20} = 127/40$ as optimal choice. $x_{20}^{20}/2^{12} = 1.0007$, so that the error is very small. What puts bells ringing that Mersenne prime 127 appears in the numerator of x_{20}: it appears also in the model of genetic code based on Combinatorial Hierarchy [K39].

2. One can argue that the values of x should be such that 20-note scale shares the notes of 12-note scale under octave equivalence. This requires that x_{12} and x_{20} differ by a power of 2. For $n_{12} = 12, k_{12} = 8$ $x_{12} = 127/80 = x_{20}/2$ gives $x_{12}^{12}/2^8 = 1.0007$, which is an excellent accuracy. Note that x_{12} is not very far from quint $x = 3/2$. 20-note scale shares under octave equivalence the notes of 12-note scale in the sense that one has $x_{12}^r 2^{-r} = x_{20}^r$.

   8 icosahedral octaves emerges a as a prediction of icosa-dodecahedral codes and this is the number of octaves required by hachimoji DNA. Presumably there is a connection between these two identical numbers.

3. To get some idea about dodecahedral harmony one can use the fact that $x_{12} = 1.5875..$ is near to $2^{8/12} = 1.5874...$, which corresponds to the interval $C - G\sharp$ rather than quint $C - G$. For case b) the notes of 4 pentagons containing 4-edge would can be transposed to $CG\sharp ECG\sharp$

so that the notes begin to repeat themselves approximately and one would indeed obtain only 3-chords modulo octave equivalence! If the notes of 3-chord correspond to same power of x, all 3-chords would be of the same type: the melancholic 3-chord with which so many finnish tangos end! Since the repetition is not exact the notes of dodecahedral scale cover the entire octave. The basic $CEG\sharp$ chord transponated by the powers of x_{20} covers entire octave.

4. For 8 pentagons of type a) one would obtain 3-chord transposable to $CG\sharp E$ and 2-chord transposable to $CG\sharp$.

5. Should one allow also for the icosahedral harmonies only chords for which the notes belong to the cycle and triangle? This would allow 3-chords for triangles containing two edges of the cycle: these chords would be of type CGD involving two quints. Triangles containing single edge would correspond to 2-chords with separation by quint. The triangles containing no edges would correspond to notes. The choice of the note would not be unique. The model of icosahedral harmony indeed predicts this kind of 3-chords. For instance, dissonant chords involving 3 subsequent notes are possible [L11] and more natural interpretation would be as possible notes of melody.

Is gauging of sphere needed to make icosa-dodecahedral harmony non-trivial?

There is also a second objection. If the notes of the chord correspond to same power of $x_{20} = 127/40$, only the notes $C, EC, G\sharp$ would appear in the 3-chords the approximation that $x^{20}/2^{12} = 1$ as is obvious from the fact that one $x_{20} \simeq 2^{4/12}$. Both icosahedral and dodecahedral harmonies based on $x_{20} = 127/40$ would be trivial. As noticed, one obtains the 20 transposes of this chord but having only chords with same structure looks still trivial.

1. One could solve the problem by allowing combinations of notes of 3-chord with different values of k in x_{20}^k (or x_{12}^k). The division of octave to 20 (12) notes guarantees that the chords obtained in this manner allow to realize very rich repertoire of harmonies. Essentially $20^3 = 8000$ chords become possible. What looks like a weakness of Pythagorean view about music based on rationals would become a strength.

   The analogy with the non-uniqueness of gauge choice in gauge theories is obvious. Gauge transformations changing the value of k in local manner give new Hamiltonian cycles from given cycle. Mathematically this solution looks elegant since one can also choose $x_{20} = 127/40 = 2x_{12}$. This also gives 8 octaves for icosahedral harmony as hachimoji code requires.

2. Although the proposed solution is mathematically elegant, it is interesting to look also for the case $x_{12} = 3/2$. The first problem is that x_{12}^{20} deviates 20 per cent from base note, and would correspond to $E\flat$ rather than C. What is however nice is that the notes for a pentagon containing 4-edge would correspond to C, G, D, A, E, H. From these one can select major chords CEG, GHD, and minor chords ACE, EGH. One could obtain the basic harmonies from the dodecahedral part by allowing all possible choices.

   Could one assume a slightly modified quint scale and different scales for icosahedron and dodecahedron? Icosahedral and dodecahedral scales are roughly consistent if k_{20} corresponds to an integer multiple of k_{12}. For $k_{12} = 7$ and $k_{20} = 2k_{12} = 14$ one has $x_{12} = 3/2$ and $x_{20} = 13/8$. One has $x_{20}^2 0/2^{14} = 1.006$. One has $x_{20}/x_{12} = 13/12 = 1.08..$ to be compared with $2^{1/12} = 1.059...$ The difference is more than half-note that x_{20} corresponds roughly to $C - G\sharp$ interval as for $x_{20} = 127/40$ as above. Therefore this option does not look attractive.

Summarizing

Some concluding remarks are in order.

1. Hachimoji DNA turned out to be extremely inspiring discovery also from TGD point of view and led to a more refined vision about bio-harmony with elegant mathematical interpretation.

2. If the above arguments make sense, one cannot avoid the question whether the fact that some people have absolute ear mean that genetic code with 8-fold number of codons is realized at the level of dark codons and bio-harmony? Chemical realization would have been probably discovered.

3. 8×12-note scale would allow discretized glissandos and also discretized blue notes appearing in popular music. Purely electronic production of this kind of music using computer programs is possible using Garage Band or some other similar program, and it would be interesting to test how the discretized glissando is heard.

   One can imagine also instruments producing this kind of music. A hybrid of piano and violin comes first in mind. The keys of piano would be replaced by keys sensitive to touch - the technology used in smartphones would allow to realize this. The 8 1/16 notes associated with a given ordinary half-note would correspond in an increasing order to linearly ordered regions along the key, and one could change the note or chord by shifting the fingers along the key. The strength of touch could code for the volume. The chords of the harmony do not consist of arbitrary notes of the 8×12 note scale but are obtained by transposing the chords of the basic bio-harmony. This would help enormously in playing since one can shift all fingers along the keys defining the chord.

Chapter 4

Geometric Theory of Bio-harmony

4.1 Introduction

The model for bio-harmony predicted vertebrate genetic code correclty has evolved to its recent form during 4 years. The recent progress in the understanding of the model motivated writing of a separate chapter summarizing the earlier results and adding the new results achieved during 2018.

Remark: In the sequel I will use the shorthand AA for amino-acids and shorthands DDNA, DRNA, DtRNA, DAA for the dark analogs of DNA, RNA, tRNA, and AA realizes as dark proton sequences with codon represented as dark proton triplet.

4.1.1 Some background

For some years ago I introduced the notion of Hamiltonian cycle as a mathematical model for musical harmony and also proposed a connection with biology: motivations came from two observations [L16]. The number of icosahedral vertices is 12 and corresponds to the number of notes in 12-note system and the number of triangular faces of icosahedron is 20, the number of amino-acids (AAs) and the number of basic chords for the proposed notion of harmony. This led to a group theoretical model of genetic code and replacement of icosahedron with tetra-icosahedron to explain also the 21st and 22nd AA and solve the problem of simplest model due to the fact that the required Hamilton's cycle does not exist.

The article [L11] was meant to be a continuation to the mentioned article providing a proposal for a theory of harmony and detailed calculations. It however turned out that the proposed notion of bio-harmony was too restricted: all isosahedral Hamilton cycles with symmetries turned out to be possible rather than only the 3 cycles forced by the assumption that the polarity characteristics of the AAs correlate with the properties of the Hamiltonian cycle. This working hypothesis had to be given up. The fuel of the minirevolution was the observation the symmetries of the Hamiltonian cycles (Z_6, Z_4, Z_2) are nothing but the icosahedral symmetries needed to predict the basic numbers of the genetic code and its extension to include also 12st and 22nd AAs. Thus icosahedral Hamiltonian cycles predict genetic code without further assumptions.

One also ends up with a proposal for what harmony is leading to non-trivial predictions both at DNA and AA level.

1. 3-adicity and also 2-adicity are essential concepts allowing to understand the basic facts about harmony. The notion of harmony at the level of chords is suggested to reduce to the notion of closeness in the 3-adic metric using as distance the distance between notes measures as the minimal number of quints allowing to connect them along the Hamilton's cycle. In ideal case, harmonic progressions correspond to paths connecting vertex or edge neighbors of the triangular faces of icosahedron.

2. An extension of icosahedral harmony to tetra-icosahedral harmony was proposed as an extension of harmony allowing to solve some issues of icosahedral harmony relying on quint identified as rational frequency scaling by factor 3/2.

This extension is kept also now. One must however give up the idea about correlation between polarity characteristics of proteins and properties of Hamilton cycles. One must allow *all* 11 icosahedral harmonies with symmetries as bio-harmonies: their symmetry groups Z_6, Z_4, Z_2 can be identified as the symmetry groups defined the decomposition of 60 DNA codons to 20+20+20 codons in the model of the genetic code. The 4 remaining DNAs and AAs can be assigned to both tetra-icosahedron and tetrahedron and icosahedron regarded as defining separate genetic codes. This explains why stopping codons can code for the 21st and 22nd AA under some circumstances.

Tetrahedral code is second member in the hierarchy of genetic codes [K39] inspired by the notion of Combinatorial Hierarchy $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$ giving the numbers $2, 4, 7, 64, 2^{126}, ...$ as numbers of DNA codons. The fourth member would correspond to what I called "memetic code" allowing representation of codons as sequences of 21 DNAs. It is not known whether the Combinatorial Hierarchy of Mersenne primes continues as Hilbert conjectured.

3. The notion of bio-harmony is partially characterized by the triplet $n = (n_0, n_1, n_2)$, characterizing the numbers of 0-, 1-, and 2-quint chords which in turn correspond to DNA codons in consistency with the observation that codons indeed correspond to triplets of nucleotides. n-quint chord corresponds to a triangle (face of icosahedron) containing n edges of the Hamiltonian. Particular bio-harmony requires a selection of a specific Hamiltonian cycle from each class of cycles (1 Z_6 symmetric cycle having $n = (2, 12, 6)$, 2 Z_4 symmetric cycles $n \in \{(0, 16, 4), (4, 8, 8)\}$, 3 $Z_2 = Z_2^{rot}$ with $n \in \{(0, 16, 4), 1(2, 12, 6), (4, 8, 8))\}$ and 5 $Z_2 = Z_2^{refl}$ symmetric cycles with $(n \in \{(2, 12, 6), (4, 8, 8)\}$. Note that the are only three different triplets n.

4. The original idea was that the rules of bio-harmony could be applied to AA sequences interpreted as sequences of basic 3-chords. DNA would have represented the notes of the music. For *given choice of harmony* as Hamiltonian cycle meaning selection of of 4, 5 or 10 AAs coded by the 20 DNAs in question, the hypothesis had to be modified by replacing AA sequences with DNA sequences.

   These DNA sequences however define also AA sequences identifiable as specific triangle at the orbit of Z_n defining the DNA codons assigned to that AA (there is a singular fiber space structure). Together the three 20-plets of DNAs define an AA harmony with (4+5+10 =19 chords with tetrahedral extension defining a harmony with 22 chords/AAs). Hence both DNA sequences and AA sequences define "bio-music".

5. The assumption that harmonic transitions between chords (DNA codons) minimize the distance between chords defined by quint-metric leads to highly non-trivial and testable predictions about both DNA sequences and AA sequences. Negentropy Maximization Principle (NMP) [K50] suggests that evolution favors the generation of harmony which should thus increase in the proposed sense for DNA sequences defining particular genes or other functional units of DNA during evolution. Large quint-distances between subsequent codons/chords would tend to polished out under evolutionary pressures.

6. Could icosahedron, tetrahedron, and tetra-icosahedron have direct physical counterparts in living matter? For instance, water molecules form icosahedral clusters and the chlathrates associated with synaptic contacts have icosahedral symmetries. Tetra-icosahedron has 13 vertices with the added vertex representing one note- say E- in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more that 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.

7. Music is language of emotions and peptides are molecules of emotion as Candace Pert [J5] expressed it. Could bio-harmonies serve as direct correlates for emotions? What is bio-music? A natural TGD inspired guess is that sounds can be replaced with $h_{eff} = n \times h$ dark photons with low frequencies and having energies in the range of bio-photons (visible and

UV range maximally effective biologically) as proposed on basis of some physical facts and theoretical ideas [K67]. The frequency spectrum of dark cyclotron photons along magnetic flux tubes would define bio-music as "music of dark light" and bio-harmonies would correlate with emotions and moods.

If one can find various icosahedral Hamilton's cycles one can immediately deduce corresponding harmonies. This would require computer program and a considerable amount of analysis. My luck was that the all this has been done. One can find material about icosahedral Hamilton's cycles (see `http://tinyurl.com/pmghcwd`) in web, in particular the list of all 1024 Hamilton's cycles with one edge fixed [A7, A16] (this has no relevance since only shape matters). If one identifies cycles with opposite internal orientations, there are only 512 cycles. If the cycle is identified as a representation of quint cycle giving representation of 12 note scale, one cannot make this identification since quint is mapped to fourth when orientation is reversed. The earlier article about icosahedral Hamiltonian cycles as representations of different notions of harmony is helpful [L16].

The tables listing the 20 3-chords of associated with a given Hamilton's cycle make it possible for anyone with needed computer facilities and music generator to test whether the proposed rules produce aesthetically appealing harmonies for the icosahedral Hamiltonian cycles. Biologist with access to DNA sequences could experiment with DNA codons to see whether their are harmonious in the sense that the distance between subsequent chords assignable to DNA codons tend to be small in quint metric. Note that DNA decomposes to pieces corresponding to different Hamiltonian cycles (harmonies) so that the comparison is not quite straightforward.

This summarizes the original article about geometric model of harmony [L11] and contributions in online books [K87, K67]. This chapter contains besides this article also some new results and considerations related to music harmony. Most of them have emerged during 2018.

4.1.2 Questions emerged during 2018

The model of music harmony is separate from the model of genetic code based on dark proton triplets [L27] and one of the challenges has been to demonstrate that they are equivalent. One can raise several questions.

1. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton's cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied.

   (a) There is purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20?

   (b) There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies.

2. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could AAs couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA? Could coding by the sum of frequencies appear in the coupling of tRNA with mRNA by codewords and coding by separate frequencies to the letterwise coupling of DNA and RNA nucleotides to DNA during replication and transcription? Could the emergence of DNA be interpreted as an evolutionary step from a holistic picture using codons as basic units (dark codons cannot be decomposed to letters) to more analytic picture in which letters are treated separately?

3. As I developed the model of bio-harmony [L11] (see `http://tinyurl.com/yad4tqwl`) it did not occur to me that also the tRNA part of the dark code should have counterpart in the icosahedral model. Could tRNA correspond to pairs of harmonies with 20+20+4=44 codons? What about single 20+4=24 codon representation as kind of pre-tRNA? Could tRNA correspond to a union of 2 20-codon codes? Combining only 2 20-codon codes with

40 codons and tetrahedral code with 4 codons would give maximally 44-letter code and the upper bound for tRNAs is according to Wikipedia 45! Dark proton model predicts 40 DtRNAs suggesting that only the 40 isosahedral codons contribute to DtRNA code. The additional tRNAs could result from homonymy. The code sequences could be seen as a hierarchical sequence $3 \to 2 \to 1$ in this framework.

An important implication is that there are many realizations of DtRNA and tRNA harmony: (Z_6, Z_4), (Z_6, Z_2), (Z_4, Z_2) and Z_2 could be either $Z_{2,rot}$ or $Z_{2,refl}$. This could explain the homonymy of mRNA-tRNA pairing via difference in the chords in turn affecting biochemical counterparts. Note however that the chords for tRNA must be a subset of chords for mRNA so that RNA harmony determines tRNA harmony apart from the three choices (Z_6, Z_4), (Z_6, Z_2) or (Z_4, Z_2) giving rise to 3 different contexts. If DAAs code by 3-chords the AAs then this choice does not affect AAs.

4. What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetry arguments fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible.

   Hence it would be possible to listen what DNA sequences sounds in given mood characterized by the bio-harmony: the allowed 3-chords of harmonies with symmetries are given in [L11] and I can provide the basic Python modules allowing to transform DNA sequences for given harmony to audible form using Garage Band program.

5. What disharmony could mean? A possible answer comes from 6 Hamiltonian cycles having no symmetries. These disharmonies could express "negative" emotions.

Remark: I proposed the theory of bio-harmony in the article [L11]. I have discussed the model of bio-harmony also in the chapter "Quantum Model of Hearing" [K67] of book "TGD and EEG" and in the chapter "Three new physics realizations of the genetic code and the role of dark matter in bio-systems" [K87] of book "Genes and Memes". The recent findings motivated writing a chapter including the previous results plus new results emerged during 2018.

4.2 What could be the basic principles of harmony?

It indeed seems that the idea about definition of notion of harmony in terms of Hamiltonian cycles makes sense.

4.2.1 Icosahedral harmonies

1. Chords (major and minor) are labeled by their basic tones and comes either as major or minor. Harmony in classical sense requires that the transitions from key to another take place by a small number of quints and that the piece does not wander too far from the major key, say C.

   If quint corresponds to a step along the edge of the cycle in the direction of its orientation, the notion of tonal closeness corresponds to the closeness in the metric of icosahedron. For instance C, F, and G are commonly used keys in same piece and correspond to 3 subsequent points along Hamiltonian cycle. Note that the number of ♯s of the key increases by one unit in standard direction and the number of ♭s by one unit in opposite direction.

2. It turns out that major and minor 3-chords and are mapped to each other in the orientation reversal for icosahedral path so that basic moods "happy" and "sad" in music have this orientation as a geometric correlate. The effect of orientation reversal does not actually depend on the icosahedral representation but is implied by quint cycle representation alone. C and half-octave $F\sharp$ defining the tritonus interval are the fixed points of the orientation reversal. Orientation reversal induces pairings ($C \leftrightarrow C$, $F\sharp \leftrightarrow F\sharp$, $G \leftrightarrow F$, $D \leftrightarrow B\flat$, $A \leftrightarrow D\sharp$, $E \leftrightarrow G\sharp$, $H \leftrightarrow C\sharp$. Quints of cycle correspond to the fourths of oppositely oriented cycle so that majors and minors are mapped to each other and one can say that the

moods "happy" and "sad" have geometric correlates in the sense that majors and minors are transformed to each other in the reversal of orientation of the cycle.

The notion of harmony can be characterized in terms of numbers of basic 3-chords identified as faces of the icosahedron and their neighborhood relationship telling when corresponding chords are near to each other or vertex or face neighbours. The wall neighbours assignable to given edge are expected to be in very special relationship harmonically since they possess a common quint.

The basic classification is according to the number $n = 0, 1, 2$ of edges of cycle contained by them and the triplet $n = (n_0, n_1, n_2)$ for the numbers of faces of various kinds gives the first rough classification. 2-quint chords have common edge and thus two common notes with two 1-quint chords and are therefore natural intermediates in transitions between them. 0-quint chords are tonal loners having no edge neighbours turns out that they involve dissonances since they consists of three notes spanning length of 1 or 3/2 steps (say EFG, $EF\sharp G$ or $D\sharp EF$). Maximally symmetric harmony is an exception: 0-quint chords correspond to augmented chords of type $CEG\sharp$ with two major thirds.

The numbers of three different kinds of face neighbor pairs for the 12 edges of the path serve as an additional classification criterion in terms of the $p = (p_{1,1}, p_{1,2}, p_{2,2})$ for the numbers $p_{i,j}$ of different kind of edges. Note that the neighbor faces of an edge correspond to 3-chords, which possess two common notes and are in this sense close to each other. These numbers characterize the most natural transitions between the chords of the harmony. A further criterion is the distribution of these neighbor pairs along the cycle.

4.2.2 Why quints are near to each other harmonically?

The naïve expectation would be that frequencies near to each other (using half-note as unit) are close to each other. This is not true. Their simultaneous presence is experienced as dissonance. This probably has a neurophysiological correlate: in ear the hair cell groups detecting notes which are near to each other in frequency space are overlapping. This explanation does not however tell why the conscious experience is dissonance.

The distance measure for notes could be formulated in terms of distance defined as the number of quints connecting them. For quint the distance would be minimal. This measure applies also to chords and allows to understand the basic rule of classical harmony stating that harmonic transitions take place the chords related by quint shift of the basic note (adding either one $\sharp$ or one $\flat$ to the scale). Also the key changes can be understood using the same rule: consider the changes C$\rightarrow$ G and C$\rightarrow$F as examples. Note that in this case the chords have common note.

One could of course question the assumption that it is possible to choose the shortest route. The notes obtained by quint scaling are not quite same in the two directions and means that $\sharp$ is the inverse of $\flat$ in well tempered scale only. Could it be that people with absolute ear are able to distinguish between the two slightly differing scales and experience notes of quint C-G as harmonically close when 1 quint connects them but as harmonically distant 11 quints in opposite direction connects them?

If cognition is p-adic, one can ask whether the notion of harmony can be formulated in terms of p-adic distance concept.

1. By octave equivalence the scaling by power of two means nothing so that the scalings by 3/2 are equivalent with scalings by 3 and the distance defined by 3-adic norm having values 3^k, where k is the number of quints makes sense. The distance defined as quints could be identified the absolute value of k along the quint cycle in the direction in which the distance is shorter. If so, the maximal distance is 6 units.

2. 3-adic measure of distance seems to be rather realistic. Quint corresponds to 1 unit distance. Half step corresponds to a distance of 5 units and 6 units defines the largest distance and corresponds to the tritonus interval which was forbidden by catholic church. Fourth (C-F) corresponds to 1- step in opposite direction and 11 steps in standard direction.

3. There is also a problem. Second (C-D) corresponds to 3 quints but third (C-E) corresponds to 4 quints and small third to 3 quints in opposite direction. Major third would thus correspond to a longer harmonic distance than second. This is a genuine problem, whose solution might

be provided by the extension of icosahedral scale to icosatetrahedral one bringing in one additional note which is very near to one of the icosahedral notes and is major or minor third of icosahedral note.

4. Could one use the number of icosahedral edges as distance between notes but not as a minimal distance along the Hamiltonian cycle but along a minimal edge path along icosahedron? The icosahedral measure of distance would be analogous to a distance between points of object along shortest route in space that it inhabits and depends on harmony characterized by the shape of icosahedral cycle. C and E (and also C and $F\sharp$!) could be close to each other in some harmony and distant from each other in some other harmony. Icosahedral geometry would become an active determinant of the harmony.

To sum up, music seems to have both 2-adic (octave equivalence) and 3-adic (12-note scale by quint scalings) characters. The principle of tonal unity for classical music stating that modulations of key should not lead too many quints away from the basic chord would have 3-adic interpretation.

4.2.3 What could be the rules for building a harmony?

What guarantees good harmony when one has fixed the key/harmony/representation of particular Hamilton cycle?

1. One should pose conditions on the allowed transitions between chords. Are there principles would imply harmonic smoothness in geometric sense? Could the transitions occur only between chords with a common note? Or can one require a common pair of notes? Or can one require even a common quint. If so, 0-quint chords would become tonal hermits and could not be used at all. In practice their dissonant character has eliminated them in popular music and much of classical music too.

   The standard quint and fourth transitions (say C to G and C to F) are basic examples in which there is only one common note between chords, and it seems that one cannot require more than this in the general case. Playing with the chords of bio-harmony however suggests that smooth bossa nova/jazz emotionally ambivalent mood is created if common pair of notes or even quint connects the neighboring chords. The rule is that only transitions between chords with same basic note are allowed. Obviously this is too stringent a condition.

2. Could 2-quint chords act as bridges between two 1-quint chords? For instance, for the maximally symmetric harmony consisting of disjoint groups of chords related by half-octave scaling the augmented chords ($F^{aug} = FAC\sharp$ and G^{aug} mapped to each other both by half-octave scaling and reversal of orientation could serve as mediating bridges.

3. Could harmonic transitions take place only between neighboring faces of icosahedron (see `http://tinyurl.com/ns9aa`) or should it only tend to minimize the quint distance between subsequent chords (this distance vanishes if they have a common note)? For the 0-quint distance harmony, the harmonic movement could be seen as a path in dodecahedron which is dual of icosahedron. In the most general case the transition can take place to both wall and vertex neighbors, whose total number is 3+3=6. In this geometric picture harmony and melody could be seen as duals of each other.

   Dodecahedron is dual of icosahedron and one can ask whether the harmonic motion could correspond to a path at dodecahedron. The vertex of dodecaehdron is pentagon and has 3 neighbours (see `http://tinyurl.com/mp5d8`). The above argument gives $3 + 3 > 3$ neighbors for the triangle of icosahedron. Are the wall neighbors of icosahedral triangle mapped to nearest neighbor vertices? If so then transitions between vertex neighbor triangles should correspond to longer steps at dodecahedron. By the duality triangles of icosahedron correspond to three pentagons associated with the vertex of dodecahedron. The rule that comes in mind is that steps can occur between vertices for which the 3-pentagons have one or 2 common pentagons.

   Note that if the dodecahedral path is Hamiltonian cycle, it is unique apart from isometries of dodecahedron and would define a unique chord progression. One can - and of course must

- allow self-intersecting harmonic paths. The condition that there exists a basic chord from which everything begins and to which everything ends implies that closed but in general self-intersecting path is in question.

4. An interesting test for the idea would a computerized generation of random chord sequences satisfying at least one common vertex rule and finding whether they are aesthetically appealing. Incidence matrix (see Appendix) for the icosahedral (and tetra-icosahedral) triangles wholes element tells how many common vertices two chords have have allows computational construction of the allowed chord sequences as random sequences.

5. For most harmonies 0-quint chords involve dissonances induced by three nearby notes (such as $CC\sharp D$) and spanning large number of quints (maximally symmetric harmony has 2 0-quint chords, which do not have dissonances and second harmony with 2 reflection symmetries has no 0-quint chords). Also maj7_-, $sus4_+$, and 6_- 1-quint chords have half-note dissonances. Dissonances as such are however not un-sesthetical. For instance, Bach used them to create a deeply melacholic feeling.

4.2.4 More general notion of harmony

The notion of harmony discussed in previous section is rather conservative and certainly too stringent.

1. 0-quint rule is too restrictive already in chord based music. For instance, the downwards progression Am, G, F, E appearing in Spanish music and music forms like Passacaglia would have chords with 1-quint distance. Hence one must consider also a weaker notion of harmonic chord progression according to which this distance is minimized and below some maximum value k_{max}. One quint would define the smallest non-vanishing maximal distance. One can define incidence matrices for chords with n-quint distance. The incidence matrices with different values of k_{max} have disjoint sets of non-vanishing elements and the total incidence matrix is their sum.

2. Even this is not enough. The direction of step matters for scales (major-minor difference) and it seems to matter also for chord harmonies. The inverse E, F, G, Am of the above mentioned progression does not sound harmonic in the same Am key. The impression of achieving the goal/ending down to something dictated by fate is lost.

   Instead of $EFGA$ one often has $EF\sharp G\sharp A$ as a melodic progression and with $E, B7, E7, Am$ as a chord progression having only 0-quint steps. The rule seems to be that 1-quint steps are possible only downwards in minor harmony, whereas upwards steps are 0-quint steps. Climbing slowly upwards by 0-quint steps and falling down by 1-quint steps! Could this "gravitational analogy" serve as a metaphor?

   Also the number of n-quint steps between chords matters. The larger this number, the closer the chords are. Two 0-quint steps means that chords have two common notes, 1 0-quint stet that they have single common note. The two 1-quint steps for downwards step $Am - G$ are between 3rd and 1st ($C \to G$) and 5th and 3rd ($E \to H$). For upwards 0-quint steps $E - H7$ 1-quint steps are between 5th and 5th ($H \to F\sharp$) and 1st and 1st ($E \to H$). For $H7 \to E$ the reversals of these steps occur. For $E7 \to Am$ one has 3 1-quint steps: (the reversals 1-quint steps $E \to A$ and $H \to E$ steps and 1 quint step $D \to A$. The laste step seems to be the smallest one in a well-defined sense.

   For G-F step the number of 1-quint steps is one ($C \to C$): same is true for F-E step (A and E).

   Using geometry language, for chords connected by 1-quint step(s) the mutual orientation of corresponding triangles with shape defined by the intervals involved matters since the number of 1-quint steps depends on the orientation.

The notion of chord harmony does not apply as such to polyphonic music with several simultaneous melodies unless on can say that it involves definite chord sequence. One could try to apply the concept of harmony for melody also in this case. The challenge is to guess what harmony for melodies could mean.

1. A conjecture inspired by the genetic code is that the codons defining the allowed melody notes associated with a given chord are in one-one correspondence with the triangles at the orbit of the triangle associated with the chord under the group Z_6, Z_4, or Z_2 characterizing the chord as a counterpart of amino-acid. In table 5.2 the Z_6 orbits are represented as groups of 6 similar chords (2 for 1-quint chords and 1 for 2-quint chords). In table 5.3 for Z_4 chords the groups consist of 4 similar chords and in the tables 5.4 and 5.5 for Z_2 harmony the chord groups consist of 2 similar chords.

2. The first guess is that the union of the notes of these chords could define the chords, whose notes are compatible with chord in the time scale shorter than the duration of the chord. Note that same triangle can appear at orbits of several chords since the orbits of each group span entire icosahedron.

   If the note lasts for a duration of several chords, the notes must be consistent with all the chords involved. The rule would explain why fast chromatic sequences (in the scale of chord duration) sound harmonic but slow chromatic sequences do not.

   For melodies in Am key $EFGA$ is rare and does sound harmonic being often replaced with $E, F\sharp, G\sharp, A$. As far as intervals are considered, this is the inversion $D\sharp, F, G, G\sharp$ of $AGFE$ shifted upwards by 5 quints. Could one regard progressions (say Am, G, F, E) breaking the strongest rule for chord harmony as polyphonic progressions satisfying the rules for polyphonic progressions.

To conclude whether the DNA inspired notion of harmonic is realistic, one should understand how the sub-groups Z_n, $n = 6, 4, 2$ of the isometries of the icosahedron and defining the genetic code act on the Hamiltonian cycles.

1. The simplest guess is that these groups are represented as subgroups of Z_{12} (also a subgroup of icosahedral group) representing quint cycle. Z_n generator would shift the basic note of the chord by $12/n$ - that is $2, 3, 6$ quints.

2. Z_n maps chords of same type to chords of same type only if it is a *rotational* symmetry of the harmony. For instance, the action of Z_6 (see **Fig. ??**) on icosahedron allows doublet orbit consisting of $Xaug$ type chords, since Z_3 maps 2 0-quint triangles in the middle of the figure to themselves and reflection group Z_2 permutes them. 6-element orbits consist of either minor or major chords. More generally, the inspection of the cycles shows that the cyclic orbits of triangle under Z_n correspond to the orbits of corresponding subgroups of icosahedral group.

3. $Z_2 refl$ maps the shape of the chord to its mirror images and so that the character of the chord can vary along Z_4 orbits. The rules are $(M \leftrightarrow m)$, $(6 \leftrightarrow 7)$). For other chords the character is unaffected.

4. Any subgroup of icosahedral isometry group $A_5 \times Z_2^{refl}$ having 120 elements must map chords to chords (faces to faces). In particular any Z_n) even if it is not a symmetry of a particular harmony. The character of the chord is not preserved and the number of quints can change. Whether these maps have interpretation in terms of music remains unclear.

These considerations forced me to finally realize that the 3 groups Z_6, Z_4, and Z_2 that I had assigned to 20+20+20 DNA codons in the model of the genetic code are nothing but Z_6-, Z_4-, and Z_2-symmetric Hamilton cycles! The numbers of amino-acids associated with various types would be 3+1=4, 5, and 10 (with empty amino-acid included). Tetrahedral extension based on gluing of tetrahedron at triangle corresponding to $X6$ type chord possessed by all Z_2^{refl} type harmonies would give 3 additional real amino-acids giving altogether real 22 amino-acids as required. This has implications.

1. All 11 Hamilton cycles are realized separately as DNA level harmonies. Amino-acid level harmonies would correspond to selection of three Hamiltonian cycles, one for each Z_n.

2. To get something one must give something away. Now one must give up the idea that $(4, 8, 8)$ is special via the corresponding of n-quint property with polarity properties. This is a pity, since just taking this correspondence seriously led to the extension of the icosahedral cycles to tetra-icosahedral ones. Fortunately, the extension itself makes sense for all Hamiltonian cycles.

To understand the action of symmetries one must look how the groups Z_n act on C major chord.

1. Z_2 would induce half-octave shift and map $C = (C, E, G)$ to $F\sharp m = F\sharp, B\flat, D\sharp)$. The assignment of $F\sharp$ -tritonus - with C note sounds strange in the ears of harmonic conservatives.

2. Z_4 would map $C = (C, E, G)$ to $A = (A, C\sharp, E)$, $F\sharp = (F\sharp, B\flat, C\sharp)$ and $D\sharp = D\sharp = (D\sharp, G, B\flat)$. These would span 8 notes since $E, G, B\flat, C\sharp$, appear twice. Note that C, E, G, A are the notes assignable to the tetrahedron in the extension of the scale and pentatonic scale corresponds to C, D, E, G, A. Z^4 orbit does not contain the notes $DFG\sharp H$ but the orbit of G chord does so. The orbit of C chord plus $G7$ chord alone define the notes of C major key.

3. Z_6 would map C and E to the same "impressionistic" 6-note scale consisting of 6 whole notes. Together with the Z_6 image of G one obtains all 12 notes of the scale.

4.3 Harmony and biology

4.3.1 Could harmonic principles be realized in biology?

The basic idea behind icosahedral harmony is the connection with biology suggested by the fact that the number of icosahedral basic chords is 20 which is also the number of amino-acids. Actually there are two additional amino-acids and one ends up to an extension of genetic code by attaching to icosahedron a tetrahedron and thus adding one vertex more. The number of DNA codons increases from 60 for icosahedral code to 64 for the real code. The triangle along which icosahedral and tetrahedral amino-acids are attached together corresponds to punct coded by stopping codons.

Could the application of harmonic principles to biology make sense? The triangles of the icosa-tetrahedron correspond to amino-acids or DNA codons for the amino-acids coded by 20 codons in question.

1. The strictest rule stating that there must be common edge of Hamiltonian cycle between the amino-acids/DNAs cannot be satisfied since 0-quint amino-acids/DNA codons would be total loners and effectively eliminated from biology.

2. The weaker "common edge or vertex" rule could however make sense. A given codon in the group of 20 codons/amino-acid could be followed only by 3+3 different nearest neighbor similar codons/amino-acids. If the first amino-acid is fixed there would be only 6^N N-amino-acid sequences instead of 20^N sequences. This kind of symmetry would have been probably observed if exact but one can ask whether harmonic pairs could more probable than completely random pairs.

3. A more plausible formulation is obtained by restricting the rule to the level of DNA sequences and generalizing it so that it applies also to transitions between harmonies with different symmetries so that a transition between corresponding amino-acids is induces.

4. An even weaker formulations states that the transitions occur with highest probabilities between codons/amino-acids having shortest quint distance.

A natural conjecture is that evolution favors the generation of harmony even in the very concrete sense that proteins defined by harmonious chord sequences for bio-harmony are emerge as what Darwinist would call the fittest ones.

Icosahedral water clusters made from tetrahedra

The obvious questions concern the concrete realization of the icosahedron - or more generally icosahedral symmetries. One should also understood what the attachment of tetrahedron to icosahedron means (note that tetra-icosahedron is not the same thing as icosi-tetrahedron, which is Archimedean (not Platonic) solid (`http://tinyurl.com/6onvry`)). What comes in mind is attachment of an information molecule to the receptor of cell membrane.

Water molecules form icosahedral structures and - what is amazing to me - Plato regarded icosahedron as a symbol of water (`http://tinyurl.com/y7bo9omm4a3378c13bcad793a52213a325db7db0-30.html`)! The page "Water structure and science" of Martin Chaplin gives illustrations about the rather complex icosahedral structures. Icosahedral structures of size 3 nm can be formed from 20 14-molecule tetrahedral water molecule clusters containing 280 water molecules altogether. They can also consists of cyclic pentamers and tricyclo-decamers and also from bi-cyclo-octomers. The 20 tetrahedrons correspond to the faces of the icosahedron and tetra-icosahedron would be formed as tetrahedron is glued to the icosahedron along one of the faces.

The bioharmonies could manifest themselves already in the structure of water molecules. Second - more plausible - option is that they differ only at the level of the magnetic body of the biomolecule. Bio-harmony suggests that 3 radial magnetic flux tubes or flux tube pairs emerge from each water tetrahedron. Hamilton's cycle could be realized as a flux tube connecting the vertices of the icosahedron and assigning the quint cycle to the cyclotron frequencies (magnetic field strengths).

This scenario raises several questions related to the pairings between ordinary DNA/amino-acids, their icosahedral representations, and their representations as dark proton sequences.

Suppose that one takes seriously the idea that genetic code is represented as dark proton sequences with the states of dark protons formed from 3 quarks representing DNA and RNA codons, amino-acids, and even tRNA.

1. How dark proton sequences are realized? Could one regard them as icosahedral bound states of 20 dark protons? Or with a Hamiltonian cycle consisting of penta-quarks and representing dark nuclear string? Could the icosahedral representation as dark nucleus consisting of 20 dark protons and dodecahedral representation as dark nucleus consisting of 12 dark 5-proton states be dual ways to interpret the state or are they different states related duality. Equivalence of the two pictures would require that dark protons are color excited and in an entangled state.

2. Could dark proton sequences correspond to sequences of icosahedrons connected by flux tubes connecting the dark protons assignable to the dark proton states assignable to the faces of the icosahedrons? These dark nuclei would be definitely different from those possibly associated with the Hamiltonian cycle.

3. What about the tetrahedral part of the genetic code in relation to dark protons sequences? What dark proton states could tetrahedral codons and amino-acids correspond? Are they associated with water tetrahedrons representing the faces of the water icosahedron? Note the amusing numerological coincidence that the vertices of tetrahedron have 3 quarks associated with them and those of icosahedron 5 and that the quint for icosahedral edge is replaced with third for tetrahedral edge.

4. Could the chords correspond to triplets of cyclotron frequencies for quarks associated with the three flux tubes emanating from the each face of the icosahedron? Could the breaking of the rotational symmetry from SO(3) to SO(2) - now actually $Z_3 \subset SO(2)$ - assumed to occur for dark proton states correspond to the reduction forced by the triangular geometry?

5. How DNA -amino-acid correspondence is represented at the level of dark DNA? The correspondence should be realized in terms of magnetic flux tube triplets connecting dark DNA and dark amino-acid and resonance condition would be essential. When the chords at the orbits of Z_n are of same type, different DNAs correspond to the same chord but with different key. When Z_2^{refl} is involved, the two chords at the orbit are not of same type (note the analogy with left and right-handed biomolecules). The only manner to circumvent the problem is to assume that the chord associated with amino-acids magnetic body is that of

DNA. Information is not actually lost in translation, it is only transformed to different kind of information perhaps representing correlates of emotions.

6. Could the non-representability of one of the Z_6 codons as amino-acid have an analog?

The fiber space having icosahedron as a base and 3 copies of icosahedron assigned with 3 regions of icosahedron corresponding to Z_n, $n = 6, 4, 2$, defines a formal geometric representation of genetic code. Could this space represented in terms of water icosahedra?

1. Perhaps one should first try to identify the function of water icosahedrons. The first guess is that they serve as local bridges between dark DNA/amino-acid sequences and ordinary DNA/amino-acid sequences. This would suggest that dark proton of dark DNA forms a flux tube connection with the face of water icosahedron dictated by the state of the dark proton: this would take place by flux tube reconnection and cyclotron resonance. Water icosahedron in turn couples with the DNA/amino-acid like DNA conjugate codon with codon so that kind of double helix is formed.

2. What about the pairing of ordinary DNA/amino-acids and water icosahedrons? Water icosahedron has size of about 3 nm. The size of single DNA codon is about 1 nm. Single codon corresponds to a twist of $3\pi/5$=36 degrees, an angle closely related to Golden Mean. If the radius of the helix consisting of water icosahedrons is above some minimal radius which is easy to estimate from an equation for the helix. There are 10 DNAs per $L(151) = 10$ nm and they correspond to a total twist of $3 \times 2\pi$. Therefore the twist angle is $\Delta\Phi = \pi/5 = 36$ degrees for single codon and corresponds to a distance of $L(151)/10 = 1$ nm). From this one has equation for DNA and icosahedron helices as $z = k\Phi$, $k = h/(6\pi)$, $h = L(151) = 10$ nm (radii are constant). Single codon corresponds to a distance $s = \sqrt{dz^2 + R^2 d\phi^2}\Delta\Phi$ along the water icosahedron helix of radius R accompanying DNA helix. One must have $s \geq L = 3$ nm defining the size of water icosahedron in order to avoid overlap. $\Delta s \geq L = 3$ nm gives the condition $R \geq 10 \times \sqrt{2}/(3\pi)$ nm $\simeq 1.5$ nm.

3. If the representation of genetic code is possible, do the fiber icosahedrons correspond to subsets of faces of the icosahedron itself? Or do they correspond to faces the of icosahedrons in some manner associated with the amino-acid icosahedron. Direct attachment is not possible but association could be achieved by connecting the icosahedrons by flux tubes with the tetrahedron at the ends of flux tubes identified as representation of the same amino-acid. This kind of structure with three icosahedra emanating from a given icosahedron could be iterated and one would obtain a fractal structure representing a binary tree. Could the water icosahedrons organize in this manner to form larger clusters?

What could be the physical correlates of Hamilton cycles representing harmonies?

1. Could Z_6, Z_4 and Z_2 orbits associated with the Hamiltonian cycles be realized even in the structure of water icosahedrons? Could they be realized as structures formed by the water tetrahedra and correspond to three separate regions of these icosahedral structures? Could one assign to each of the three regions of icosahedron icosahedron such that the attached icosahedron decomposes to the orbits associated with that particular region? Could the hierarchy of the icosahedral symmetry breakings have a direct counterpart at the level of the icosahedral structures formed by water molecules? My intuitive feeling is that the answer to these questions is negative.

2. Could Hamiltonian cycles be realized only at the level of dark photons as quint cycles defined by closed flux tube giving rise to dark nucleus, that is in terms of 3-chords formed by dark photons propagating along flux tubes emanating from the icosahedron? If cyclotron frequencies of dark quarks are in question then the magnetic fields associated with the flux tubes would define the notes.

3. The breaking of Z_2^{refl} symmetry is of special interest since it could serve as a prebiotic analog of chiral selection and could relate to dark variant of weak physics with effectively massless weak bosons in nano-scales. This would require dark magnetic body. Half-octave scaling

is second broken symmetry and would have also an analog in Z_2^{refl} variant of icosahedron. Note that 256 variants of the bio-harmony are predicted and could be realized for magnetic body naturally. The presence of electric fields at flux tubes is possible and if the electric and magnetic fields are non-orthogonal, U(1) instanton density is non-vanishing and induces parity breaking. Is this breaking associated with Z_2^{refl} only?

Clathrin molecules as icosahedral structures

Clathrin (`http://tinyurl.com/y8ho23zf` is a structure appearing at the ends of microtubules and necessary for the transmission of signals between the presynaptic and post-synaptic neurons. Clathrin consists of triskelions - kind of triangular structures with three spiral like legs and having as symmetries the rotational symmetry group Z_3 of equilateral triangle. Clathrins can form hexagonal planar lattices and pentagonal icosahedral lattices consisting of 12 pentagonal faces - the number of vertices of icosahedron. One can associate 3 triskelions with each pentagonal face: this makes $12 \times 3 = 36$ triskelions altogether. One can regard the centers of the 12 faces as vertices of icosahedron and assign to this structure 20 faces, which are triangles formed by 3 pentagons.

If proteins and other molecules attach to the faces of clathrin, one can ask whether each icosahedral triangle of this kind has an address formed by the three notes associated with it and serving as a password: only those molecules, which "know" this password can attach to the face. The realization would be in terms of three U-shaped magnetic flux tubes emerging from the 3 pentagonal faces representing the three notes as frequencies of dark $h_{eff} = n \times h$ cyclotron photons with ELF frequencies but energies of bio-photons (in visible and UV range). The binding of the molecule to the face triangle would be preceded by reconnection of U-shaped flux tubes of the clathrin and molecule, by a resonant interaction by dark cyclotron photons, and by an h_{eff} reducing phase transition bringing the molecule to the face.

Microtubules as music instruments?

It has become clear that microtubules have a central role in biology, neuroscience and perhaps also in consciousness theory and the evidence that they are quantum coherent systems is accumulating. Could music metaphor could help to understand microtubules?

1. Tetra-icosahedron has 13 vertices with the added vertex representing one note- say E- in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more that 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.

2. The recent TGD inspired model of microtubules [L14], [K64] was inspired by the findings of the group of Bandyopadhyay (see `http://tinyurl.com/ze366ny`) [J1], [J18] relies on the general vision about bio-communications and control as being based on dark cyclotron photon radiation travelling along magnetic flux tubes.

   These dark photons have a universal energy spectrum in the range of bio-photons (visible and UV) to which they transform as the value of $h_{eff} = n \times h$ reduces to its standard value. Frequencies would span a wide energy range but EEG frequencies would be of special importance since they would also couple to acoustic vibrations. The precise value of the energy scale of cyclotron photons would be determined by the strength of the magnetic field at flux tube.

3. Frequency modulation would be the general manner to code information in living matter: "whale's song" would be a good metaphor for it. This is assumed in the model for cell membrane as generalized Josephson junction: the modulation would be now induced by the variations of generalized Josephson frequency by variations of the membrane potential. Also microtubules have been proposed to base their communications on frequency modulation.

4. The first possibility coming in mind is that the continually varying microtubule length codes for the frequency [L14]. The change of the frequency by say octave would however require

quite fast and large variations of microtubule length. Neither does this realization conform with the idea that the state of single tubulin corresponds to frequency. Microtubule length could also code for the length of the music piece represented by the microtubule serving as a music instrument or musician at the bio-molecular level. It would also the number of microtubular units and thus the size of the orchestra consisting of 13-units.

5. Another possibility inspired by the proposal is that magnetic flux tubes form an analog of 3-D grid ideal for communication purposes using 12-note (or actually 13-note) system as a code equivalent with genetic code. Also microtubules would involve three kinds of flux tubes [L14] defining coordinate grid of cylindrical coordinates: longitudinal, radial and those which rotate along the microtubule. Radial flux tubes would be ideal for communication using 13-note system as a realization of genetic code.

6. 13-note system as cyclotron frequency spectrum for given value of h_{eff} would be determined by the spectrum of the magnetic field strengths going transversally through the microtubule and each tubulin would correspond to one particular note represented as magnetic field strength. The system would be highly analogous to the system formed by hair cells in cochlear. Note would indeed characterize single tubulin molecule rather than entire microtubule as required if one wants to code chords using the two tubulin conformations as a bit. Tubulin conformation would determine whether the tubulin serves as a sending/receiving antenna or not.

7. Melody in 12-note system can be interpreted as a discretized version of frequency modulation with frequency being piece-wise constant in time. Obviously the 13 bit sequences defined by tubulin conformations code for the chords of rational 12-note scale involving a representation of one particular note (the third note of the Pythagorean scale) with two slightly different frequencies in order to avoid problems caused by the rational number ratios of frequencies. 13th bit could also serve as a kind of period. Also chords could be coded up to a chord with 13 notes so that microtubules would have quite a high representative power.

The is an objection against the model.

1. One could argue that a unit consisting of 13 tubulins allows only one octave to be represented. One can of course assume that the magnetic field strengths for subsequent units differ by octave. What makes this interesting is that microtubules allow two variants, called A and B. B type microtubules appear as 13-units since microtubular surface has a gap so that the helical symmetry is broken. For variant A, which is not found in vivo or in vitro, 13-units integrate to form longer helical units. This is assumed in Penrose-Hameroff model and the experimental absence of A type microtubules is one of the basic objections against Penrose-Hameroff hypothesis.

2. The TGD inspired proposal is that A type microtubules corresponds to a critical state having therefore an enhanced symmetry and long range correlations: criticality would explain their experimental absence. The experiments of the group of Bandyopadhyay support that the critical state is induced by a resonant excitation at specific AC frequencies [L14]. Long range correlations would mean enchance helical symmetry - that is fusion of several 13-units to form a longer helical structure. This structure would allow an interpretation as a structure with frequency spectrum of several octaves represented coherently in terms of magnetic field strength: the 10 octave span for hearing would mean the integration of 10 microtubule units meaning length scale of order micrometer assuming that tubulin size is of order 10 nm.

3. If the field strength for subsequent units differ by octave, one can argue that for variant B various octaves play their own music without knowing of each other and thus without coherence. In state A they would play together forming something analogous to orchestra or choir.

   If the octave is same for all 13-units, the phase transition would involve octave scaling of the magnetic field strength at the flux tubes. The flux tube radius should suffer p-adic scaling by an integer number of half-octaves, which makes sense if one accepts p-adic length scale hypothesis. This kind of phase transition have been proposed as candidate for a basic step of energy metabolism since they can store or liberate cyclotron energy as metabolic energy.

4. Microtubules could directly couple with both DNA and clathrin molecules if they represent 12 note system as a resonant system able to receive the radiation with corresponding frequencies. 12-note system and the 3-chord system associated with it could define universal communication code allowing communications between DNA, proteins, and microtubules.

To sum up, 13-note extension of 12-note system could be seen as a realization of the genetic code in terms of frequencies. The existence of kind of realization was obvious from the beginning and I proposed it in the model of microtubules as quantum antennas during the first years of TGD inspired theory of consciousness [K59]. Discovering the precise realization of the proposal has however required time.

4.3.2 Could biology help in the understanding of musical harmony?

One can also ask whether biology could provide ideas about the notion of harmony. Could icosatetrahedral harmony possessing additional 13th note very near to the fourth of basic major chord provide a better view about harmony?

1. The extension of the ideas about harmony to the case of isosatetrahedron is a non-trivial task. If one assumes that the extended Hamiltonian cycle is obtained by deforming tetrahedral Hamiltonian cycle according to the proposal made earlier, one ends up with a problem since the cycle makes a wedge while making a side track of two steps via the new vertex. The two steps must give one quint so that the new vertex must correspond to either minor or major third of note where it started from (and ended to). This would add to the scale a chord of type CGD a chord of type CEG or $CE\flat G$ (plus two other chords containing major or minor third. Depending on the orientation of the cycle one would obtain major or minor key. The remarkable feature of icosahedral harmonies is that they often lack a unique basic chord. Could it be that the addition of tetrahedron breaks the symmetry and fixes the key?

2. The added third could be slightly different from the icosahedral third and this could allow to resolve the problems due to the fact that quint cycle does not quite close ($(3/2)^1 2 = 2^7$ does not hold true exactly. The problems can be of course solved by introducing well-tempered scale defined in terms of powers of $2^{1/12}$: for this choices the topologically induced by these scalings is same as that induced by real topology in frequency space. Algebraically this means introduction of an algebraic extension of rationals. The problem is that persons with absolute ear prefer rational number based scale and experience tempered scale as unaesthetic.

The problem with 3-adic distance of notes was already described: the distance is 4 quints for major third (C-E) and 3 quints for minor third ($C - E\flat$). A smaller distance is suggestive for major third.

1. The proposed extension of the scale would break symmetry by bringing a third which is indeed nearest neighbor of the basic note plus two other notes, which are in corners of a *1-quint* triangle in the biological realization. Thus chord CEGandchord containing EG and third note would be introduced.

2. Using the general results one can readily find the possible extensions of harmony if one assumes that both major and parallel minor with same number of $\sharp$s or $\flat$s are obtained. The chord chosen for extension must be CGA, which an be seen as part of $C6$ or $Am7$. If the added vertex corresponds to E one obtains $C = CEG$, $Am = CEA$, and the GEA which is part of $C6/Am7$ as also the lost chord. In amino-acid analog CGA would become "empty" amino-acid, punct, and would be replaced with GEA contained also in C6. One can perform this kind of realization for all 11 harmonies and/or their mirror images. The modification induces symmetry breaking and defines a key which is otherwise not obvious for the icosahedral harmonies. Also half-octave symmetry is broken.

3. One can perform the modification also for the inverted harmony. The transformation to reverted harmony $X \to Y$ corresponds to $X7 \leftrightarrow Y6$ and vice versa so that the presence of $X7$ type chords in harmony guarantees the existence of the required type extension in the reverted harmony. One can of course define extension also using X^7 type chords. This would generate besides CEG two dissonant chords of type $GEE\flat$ and $CEE\flat$.

4. In maximally symmetric harmony (2, 12, 6) with 6-fold rotation symmetry, there are as many as 6 ways to perform this modification so that any note of the 6-note scale spanning "impressionistic" octave can define the key. The key is either F, G, A or $Dm, E, F\sharp m$. The harmony contains however no $X7$ type chords and since the transition to the reverted harmony acts as $X6 \leftrightarrow Y7$, it does not allow a modification generating both major and parallel minor. There are also other harmonies possessing no $X6$ type chords such as $(2, 12, 6)$ and bio-harmony $(4, 8, 8)$ with 2-fold rotational symmetry so that the extension in the simplest form can be performed only for their reversals.

5. For the two harmonies with 4-fold reflection symmetry there are 2 ways to perform the modification and modified chords are related by half-octave shift. With the conventions of Table **??** the modification introduces key which is either A ($F\sharp m$) or $D\sharp$ (Cm) for both harmonies (second one is bio-harmony $(4, 8, 8)$).

4.3.3 About the interpretation of bioharmonies

1. How ideas about harmony evolved?

A brief summary about the evolution of the notion of bio-harmony is in order.

1. The first guess [L16] was that amino-acids could be understood as chords of icosahedral bio-harmony characterized by 3-tuples (3, 10, 7), where the integers tell the numbers of icosahedral triangles with 0, 1, or 2 edges of the Hamiltonian cycle and identifiable as 3-chords with 0, 1, or 2 quints. The interpretation was that 3 0-quint chords correspond to 3 basic polar amino-acids, 10 1-quint chords to the 10 non-polar amino-acids, and 7 2-quint triangles to the 7 polar and acidic polar amino-acids. It turned out however that (3, 10, 7) does not appear as Hamiltonian cycle although it satisfies the necessary conditions.

2. I introduced also a model of genetic code motivated by the properties of the code table suggesting that 60 DNA codons are grouped into 3 groups of 20 codons. The idea that DNA codons coding for a given amino-acid form an orbit of a subgroup of icosahedral group with order which is not smaller than the number of these DNAs and has the aminocid at it. Three subgroups Z_6, Z_4, and Z_2 would predict 3 amino-acids coded by 6 codons and two amino-acids coded by 1 codon, 5 amino-acids coded by 4 codons, and 10 amino-acids coded by 2 codons. The total number of codons would be $3 \times 6 + 2 + 4 \times 5 + 10 \times 2 = 20 + 20 + 20 = 60$ rather than 64. The number of doublets is 10 instead of 9. Could one Z_2 orbit corresponds to punct coded by two stopping codons? But what about the codon triplet associated with Ile? Something is clearly missing.

   There is also second problem: a really realistic model of genetic code should include also 21st and 22nd amino-acids (Pyl and Sec). Pyl or pyrrolysine is modification of Lys and is basic polar amino-acid so that the number 3 of basic polar amino-acids increases to 4. Contrary to the original naïve extrapolation Sec (selenocystein) is acidic polar rather than non-polar so that the number 2-quint triangles increases from 7 to 8. For the properties of amino-acids see `http://tinyurl.com/y8b7fumq`. The notion of hydrophobicity is discussed at `http://tinyurl.com/9qr8e7q`).

3. The solution of the problems came from the extension of icosahedral code with tetrahedral code bringing 4 additional codons and 3 amino-acids assigned with the external faces of the tetrahedron (Ile, Pyl, and some standard non-polar amino-acid), and increasing the number of stopping codons from 2 to 3. This gives 60+3+1=64 codons but one should code also Pyl and Sec. The solution of the problem would be that stopping codons code also these under some conditions. Are DNA codons or their mRNA counterparts pairing with tRNAs - perhaps their magnetic body - modified somehow?

   For instance, Pyl and Sec could correspond to icosahedral codons before fusion. After fusion they cease to be coded - most naturally because the group orbits containing punct are replaced with those associated with tetrahedron. The 3 ordinary amino-acids represented by tetrahedron are Ile, 1-quint amino-acid and 2-quint amino-acid. As fusion is broken temporarily Pyl and Sec are coded.

4. The geometric correlate for the fusion of the codes is gluing of tetrahedron to icosahedron along one face which corresponds to "empty" face identifiable as punct coded by stopping codons. The icosahedral Hamiltonian cycle (4, 8, 8), which exists as two variants, is extended to (4, 10, 8) with two new amino-acids.

5. The music analogy for the fusion of tetrahedron is symmetry breaking bringing in a definite key by introducing the major and minor chords as 1-quint chord (but with 2-edges since tetrahedral edges correspond to major and minor thirds).

2. Understanding the misunderstanding

This was the picture as I started to work again with the notion of bio-harmony. Just when I thought that I understand the notion, I realized that something very essential is missing and even wrong.

1. One could argue that the assumption about the correlation of forms of amino-acid polarity with character of Hamiltonian cycle leading to (4, 4, 8) identification is ad-hoc: why not allow all harmonies? One can also wonder whether the group structure behind the genetic code leading to the identification of sets of DNA codons coding for a given amino-acid as orbit of the corresponding triangle can be totally dependent on the group structure emerging from the construction of the Hamiltonian cycles.

2. The question whether the group structures associated with genetic code and with the Hamiltonian cycles might have something to do with each other leads to the realization of the obvious: the groups involved are the same: Z_6, Z_4, and Z_2! The symmetries of DNA are the symmetries of cycles. DNA code would be inherent to the Hamiltonian cycles, and the triangles of the icosahedron representing the harmony would correspond to DNA codons! 20+20+20 icosahedral triangles to 60 genetic codons and 4 icosahedral triangles the remaining 4! The three 20-plets corresponds to 3+1 amino-acids coded by 6 (resp 2) codons, to 5 amino-acids coded by 4 codons, and to 10 amino-acids coded by two codons.

   By direct inspection of the illustrations of the appendix one can indeed convince oneself that the groups in question map chords to chords of same type and one obtains appropriate number of orbits. This of course follows from group theory alone.

3. One must give up the assumption that the integers $n = (n_0, n_1, n_2)$ correspond to the numbers of the basic polar, non-polar, and polar and acidic polar implying that only $n = (4, 4, 8)$ would define bio-harmony. All Hamiltonian cycles with symmetries define bio-harmonies and both Z_2^{rot} and Z_2^{refl} define Z_2 type bio-harmonies assignable to 10 amino-acids coded by 2 codons. This is somewhat frustrating outcome, since just this correspondence served as guideline leading to the extension of the icosahedral code. The extension as such is however independent of this identification and needed in order to get the 4 missing DNA codons and to understand the coding of 21st and 22nd amino-acids Pyl and Sec.

   What do the Hamiltonian triplets n then correspond? Harmonies correlate with moods in music: maybe the serve as mathematical correlates for emotions and moods.

4. Harmonies are not for amino-acids but for DNAs coding them. One can however identify amino-acids as specific triangles the orbits and the chords associated with the amino-acids define much more restricted notion of harmony involving one representative of each basic type of chord. Perhaps the additional chords correspond to modulations of the harmony.

5. The rules of harmony generalize as such to transitions between DNA codons regarded as chords. If chords are near to each other with respect to the distance measured as quints, the transition between the chords respects harmony. One must think that DNA codons form a singular fiber space such that the union of fibers for type n gives the space of 20 amino-acids. The "gauge group" Z_n acting in the fiber is different in the 3 regions of the amino-acid space and the number of elements in the fiber is factor of n actually equal to n for $n \neq 6$ and having values 6 and 2 for $n = 6$. Each choice for the 3 Hamilton cycles of type Z_n, $n = 6, 4, 2$ defines a variant of this fiber space. The distance along the fiber isomorphic to the space of amino-acids is measured as minimal quint distance.

Note that the DNA codons for two different variants of the fiber space need not define same kind of chord so that also given amino-acid can correspond to several different chords. It is enough that the notes of the chords are specified - as they indeed are. The Z_n, $n = 6, 4, 2$ in turn can correspond to any Hamilton cycle with symmetry Z_n so that for $n = 1, 4, 2$ one can have $1, 2, 3 + 5 = 8$ different fiber spaces. The hierarchy of Fibonacci numbers is involved. A hierarchy of symmetry breakings is highly suggestive and leads to increasingly richer harmonies.

Z_6 has maximal symmetry but Z_4 is not a subgroup of Z_6 so that only the symmetry breakings $Z_4 \to Z_2^{rot}$ and $Z_4 \to Z_2^{refl}$ can be said to occur. Note that transition between different realizations of the covering space has interpretation as a phase transition and that it could occur at RNA rather than DNA level. These phase transitions need not relate to the biochemistry but to serve as correlates for emotions and moods. Also the degeneracy due to the existence of several DNAs coding given amino-acid could have similar interpretation.

One can of course play with more stringent scenarios for the transitions between DNAs or RNAs). For instance, the assumption that transitions can occur between chords of same type, leads to contradiction since the $Xaug$ chords of Z_6 harmony do not appear in any other harmony.

In any case, the quint-rule in its various forms is readily testable for DNA sequences.

6. An open question concerns the change of the key. The convention of the illustrations is that 1-2 edge corresponds to C-G quint. Should one allow the DNAs at various sheets of covering space to be in different keys? Change of the key could be identified as a rotation by some number of quints. It would change the graph representing icosahedron and change the chords. Z_{12} would allow to realize all keys. Z_{12} is not however a subgroup of the icosahedral isometries (whereas $Z_6 = Z_3 \times Z_2^{rot}$ is) so that the transformation should be interpreted as a translation in quint space acting as coordinate transformation.

   The active transformations induced by isometries of icosahedron do not change the graph and would map chords to new ones. The action of Z_6 is well-defined also for other harmonies than Z_6 symmetric ones. Could the modulations of the basic key correspond to Z_6 transformations. If so, one would have 6 keys. Unfortunately, the most common modulation by quint ($G \to G$) would be missing.

   The change of key could correspond also the change of the chords defined by the extension to tetra-icosahedral harmony. One can choose the chord for extension in several ways for Z_2^{rot} and Z_2^{refl} and these choices could define the allowed modulations of the key.

7. What would be the correlates of different keys the level of DNA? An attractive assumption is that notes are realized in terms of dark photons, which could also transform to ordinary sound since living matter is piezo-electric system. The general hypothesis is that dark photons have universal energy spectrum, which is that of bio-photons. Change of key corresponds to a change of frequency scale and would correspond the change of either Planck constant or of magnetic field strength the flux tubes of the magnetic body associated with DNA codon (or amino-acid perhaps). This would mean that 12-note scale would correspond to 12-note scale for the magnetic fields strength to which cyclotron frequency is proportional or equivalently for the thickness of the flux tube since magnetic flux is quantized if monopole fluxes are in question. 12-note scale could mean in biology a standardization of frequencies used.

One must modify the extension of the icosahedral Hamiltonian cycles to tetra-icosahedral ones appropriately.

1. The Z_6 symmetric 20-plet contains 3 6-plets and 1 doublet and the Z_2 symmetric code contains 10 doublets so that here is one 11 DNA doublets in the icosahedral code. "Ordinary" amino-acids have only 9 doublets. The interpretation is that the Z_6 doublet corresponds to ile and the additional ile is coded by tetrahedral codon. The second surplus doublet can be identified as 2 codons coding for punct, "punct". This gives 4+5+ 10 =19 amino-acid if "punct" is counted.

2. What is lacking is one ile, met, trp, plus Pyl and Sec. Also 4 DNA codons are needed. One of them must code ile, one met, one for punct, and one for trp. The tetrahedral codons would thus correspond to orbits of Z_1. This is actually the only possible subgroup since for the choices $Z_n = 2, 3, 4$ the numbers of codons and amino-acids are not correct. This exhausts all DNA codons.

3. The only manner to proceed is to assume that icosahedral and tetrahedral codes can appear also as unfused versions. This would naturally occur for Z_2^{ref} for which all cycles contain $X6$ type chord but can occur also for Z_2^{rot} if the completion is done for the inverse harmony and then mapped to the harmony back. The icosahedral code would be as already described. The "free" tetrahedral codes would correspond to Z_1 and the faces coding punct in the two codes would code for Pyl and Sec. The fusion of the tetrahedral and icosahedral codes codes gives just the ordinary genetic code so that the proposal is consistent with the proposal that dark proton sequences realize genetic code [K41].

4. Note that geometrically this extension means only that the amino-acid sheet of the fiber space is extended by tetrahedral sheet.

The challenge is to construct the covering space of the icosahedron representing amino-acids.

1. The has as a local fiber the orbit under Z_n associated with the amino-acid defining base point. The space of amino-acids decomposes to disjoint regions corresponding to the 20+20-20 DNA codons. Z_n is the analog of gauge group and by symmetry breaking is different from three different regions of amino-acid space. There are $1 \times 2 \times 8 = 16$ variants of this space due to existence of several harmonies for given symmetries. There are actually only three different options for n given by $n = (0, 16, 4)$, $(2, 12, 6$, and $(4, 8, 8)$.

2. The Z_n orbits of the three disjoint amino-acid regions (containing 3+1=4, 5, resp. 10 amino-acids) intersect each other. The challenge is to choose the representative amino-acids from the orbits of Z_n in such a way that the chosen amino-acids belong to the three disjoint regions. It remains to be proven that this is possible. One must also understand how uniquely this can be done.

3. One could think of choosing a set P_2 of 10 representatives from the 10 orbits of Z_2 related by 6-quint scaling along Hamiltonian cycle. The 3+1+5=9 amino-acids associated with Z_6 and Z_4 would belong to the mirror images $P(S)$ of this 10-element set. $P(S)$ decomposes into set P_6 of 3+1 triangles and set P_4 of 5 triangles and there are 2-element, 4-element and 6-element orbits connecting the elements of the sets P_2, P_4, and P_6.

The following observations lead to a rather detailed and surprisingly simple picture.

1. The key observation is that the construction of the covering space - that is identifications of amino-acids at the orbits of the groups involved - depends only on whether the choice of Z_2 as Z_2^{rot} or Z_2^{refl}! Thus the two codes (ordinary one and code with Pyl and Sec coded by stop codons) are distinguished by different DNA-amino-acid covering spaces. The details of the Hamiltonian cycle do not matter. Only the structures and mutual relationships of the groups $Z_6 = Z_3 \times Z_2^{refl}$, $Z_4 = Z_2^{rot} \times Z_z^{refl}$ and Z_2^{rot} and Z_2^{refl} matter. Furthermore, the actions of the groups Z_2^{rot}, Z_3 and Z_2^{refl} determine also the actions of Z_6 and Z_4. Only Z_2^{rot} and Z_3 are non-commuting actions.

2. One can decompose amino-acids to 10 pairs of Z_2^{ref} orbits and visualize the 20 codons involved as two layers on top of each other such that two on top of each other correspond to the same 2-orbit - 2 boxes on top of each other. The choice of the two layers is not unique since one can permute the members of any vertical box pair.

3. By a suitable choice of the members of vertical box pairs one can arrange that Z_3 and Z_2^{rot} act along the two layers horizontally. Z_2^{rot} orbits divide each layer to 5 pairs of horizontal boxes. One can also permute the vertical pairs horizontally in such a way that the 5+5 Z_2^{rot} orbits correspond to neighboring horizontal boxes along upper and lower layer giving

4	6	4	6	4		4	6	4	6(2)
2	2	2	2	2	2	2	2	2	2
2	6	2	6	2		2	6	2	6(2)
4	2	4	2	4	2	4	2	4	2

Table 4.1: The representations of the associations of amino-acids to the orbits of of Z_n, $n = 6, 4, 2$ for $Z_2 = Z_2^{refl}$ (upper two rows) and $Z_2 = Z_2^{rot}$ (lower two rows). The integer n in box tells that the amino-acid associated with that box corresponds to Z_n type amino-acid. "(2)" tells that the Z_6 orbit in question consists of 2 codons.

2+2+2+2+2 decomposition. This still leaves the possibility to permute these 5+5 horizontal pairs defining 4-orbits of Z_4 horizontally with each other.

Simply by drawing one find that Z_3 orbits divide each layer to 3 triplets and 1 singlet and by a suitable choice Z_3 singlets correspond to the 10th box on the right for both layer. The Z_3 orbits and Z_2^{rot} orbits overlap in such a way that the middle Z_3 orbit contains entire Z_2^{rot} orbit.

4. It is clear how to choose amino-acids from the orbits.

   (a) Consider first the $Z_2 = Z_2^{refl}$ case. The lower layer corresponds to the 10 Z_2^{refl} amino-acids (punct included) coded by 2 codons. One must choose from each Z_4 orbit consisting of a square of 4 boxes one upper box to represent Z_4 amino-acid (ala, val, gly, pro, thr). Each 4-unit contains one free upper box to which one can assign 1 Z_6 amino-acid. One cannot however put two amino-acids on 3-orbit. There are 3+1 Z_6 amino-acids and 5 boxes so that one box remains unused. This must be the case. The used box must belong to either second or third horizontal Z_2^{rot} 2-box: if it were filled, the middle Z_3 3-orbit would contain 2 Z_6 amino-acids and the fiber space-structure would fail.

   Contrary to the original intuition, the unfilled box is *not* at the 2-orbit of Z_6 containing as Ile but at the middle upper 3-orbit, which would contain 2 amino-acids if filled. It is associated with one of the 10 amino-acids coded by two codons and is same for both Z_2^{rot} and Z_2^{refl}. One expects that this amino-acid is somehow special: maybe it is punct. Also the corresponding 6-amino-acid (Ser, Arg, or Leu) might be somehow special.

   (b) $Z_2 = Z_2^{rot}$ can be treated similarly. The upper row of boxes is filled in the same manner as in the previous case. The horizontal box pairs in the lower row contain one Z_2rot box and one Z_4 box. The difference to the previous case is that Z_2 boxes are now shared by the both rows: in the previous case they belonged to the lower row.

5. The assignment of amino-acids to the orbits is not unique: for n similar orbits there are n! different assignments. Inside orbit there is also some non-uniqueness.

Table 4.1 represent the two situations graphically.

3. Music and physical correlates of emotions

Peptides are regarded as molecules of emotion and also information and positive/negative coloring of emotions would naturally correlate with the increase/reduction of negentropic resources of the system as negentropy is transferred to or from it away or increases as a whole. Music induces and expresses emotions. Therefore the idea that music in generalized form - say represented by dark photons with ELF frequencies and having energy spectrum in visible and UV energy range of bio-photons- could be the fundamental correlate of emotions and whether tetra-icosahedral music could be in special role (note that one can associated Hamilton's cycles and "music" with any graph).

There are 11 candidates for the icosahedral harmony and its extensions. The candidates have either Z_6 (**Fig. ??**, Z_4 reflection symmetry (**Figs. ??**, **??**), or Z_2 rotation symmetry (**Figs. ??**, **??**, **??**), and Z_2 reflection symmetry (**Figs. ??**, **??**, **??**, **??**, **??**). For the first case Z^2 reflection symmetry and for the second case Z_2 rotation symmetry are represented as as half-octave shift. Second reflection symmetry corresponds geometrically to reflection in horizontal direction. The extension assigns to them definite key and adds to 1-quint chords minor and major chords absent for the icosahedral bio-harmonies. The question is whether one of these harmonies is selected in biology or whether all three can appear and are perhaps realized at the level of magnetic bodies of amino-acids.

The reversal of the harmony differs from the original one and major-minor transformation takes place. Could it be that both "moods" are realized at the level of magnetic body and even serve as the physical correlates of moods and emotions? Could emotions be realized at the level of amino-acid magnetic bodies as phase transitions affecting parts of organism or even entire organisms and in this manner changing the mood. Peptides are regarded as molecules of emotion: could these phase transitions occur only for peptides and other information molecules involving proteins? Could peptides also serve as seeds of these phase transitions? Could even the Hamiltonian cycle be changed for the magnetic body of the entire organism and correspond to some importance two-valued characteristic of emotional profile?

Could orientation reversal relate to time reversal, which in Zero Energy Ontology (ZEO) corresponds to state function at opposite boundary of causal diamond (CD)? This reversal would occur in volitional acts: the subsequent reduction would not affect the quantum state in positive energy but in TGD framework they affect the state at opposite boundary CD and in this manner give rise to the experience flow of time.

The simplest extension of the harmony in the proposed form requires that harmony possesses X_6 chord. It does not exist for for the candidate with Z_2^{rot} symmetry but for its reversal 4 of them are present as images of $D7, E7$ and $G\sharp 7, B\flat 7$ which are chords of type X^6. One can however map the harmony to its reversal, perform the completion for it, and perform the reversal back to the original harmony. The reversal depends on what note remains invariant in the reversal. One can require that it is the basic note of the chord to itself: with this condition one would obtain $Dm, Em, G\sharp m, B\flat m$ and major keys $C\sharp, F, A, H$. 4 different harmonies would result. Without the restriction the number of harmonies is different and each has different emotional characteristics.

4. Religious myths, music, and biology

These symmetries define a hierarchy of symmetry breakings. This hierarchy has amazing connections with the myths, which I believe to reflect deep facts about consciousness and biology at fundamental level expected if also consciousness is fractal. The story of genesis is a good representative in this respect.

1. The hierarchy of symmetry breakings proceeding from Z_6 down to Z_2^{refl} brings strongly in mind evolution as loss of innocence. For Z_6 one as 4 orbits. One orbit contains 2 triangles (chords, DNA codons assignable to ile). The other orbits correspond to six codons assignable to amino-acids ser, arg, and leu. The chords at the orbits are major chords and 7-chords, and minor chords and 6-chords for the inverse of the harmony.

   There are no dissonant chords in 0-quint sector: dissonances appear only for the remaining groups as 0-quint chords. This is musical representation of paradize. This harmony is based on 6-note scale for the basic notes of the chords and used by impressionistic composers. Amino-acids correspond to selections of preferred chord from each orbit and there are only four different chords: this sub-harmony is very simple. Life in paradize is simple!

2. Next comes an intriguing observation. The number of amino-acids obtained as projections of the icosahedral DNA orbits is 19, not 20. Could it be impossible to have 20 amino-acids as projections of the orbits and that 19 is the maximum number? The reason for 19 is that the number of amino-acid of type Z_6 is $3 + 1 = 4$ rather than 5. Therefore there is one "non-playable" chord - located at some "paradize orbit" -, which does not correspond to any amino-acid.

   The first guess for the non-playable chord is as one of the *aug* type chords (say $CEG\sharp$, which is the last breath in many finnish tangos telling about unhappy love end - it is something

between happy CM and sad Am, "raueta" is finnish word for this manner to come to an end: "expire" might be the nearest english counterpart). This chord is located at the 2-chord orbit related to the other chord of the orbit by half-octave shift (chords could be $CEG\sharp$ and $F\sharp B\flat D$), the tritonus denied by church.

Unfortunately, this identification is not consistent with the argument identifying the amino-acid chords at Z_n orbits (see table 4.1) the non-playable chord must belong to an intersection of 6-orbit and 4-orbit and is not completely unique without further assumptions. It belongs to a 2-orbit of Z_2^{refl}: if it is somehow special, it could belong to the 2-orbit assignable to punct. If the chords at the 2-orbit have basic notes differing by tritonus, the inspection of the Table 5.5 shows that it is possible to find a unique chord pair having this property for all 5 Z_2^{refl} cycles.

One cannot avoid the associations between non-playable chord and the denied fruit hanging in the tree of good and bad knowledge in the story of Adam and Eve, and its analog in many fairy tales. The non-playable chord also brings in mind the hilarious story of Gödel-Escher-Bach about non-playable record (a truth unprovable in given axiom system).

3. The hierarchy of symmetry breakings leading from Z_6 to Z_2^{refl} encourages one to continue with the biblical analogies. Z^6, Z_4 and Z_2^{rot} cycles have half-octave shift as a symmetry: good and evil do not exist in paradise, but dissonances are already there for Z_4 and Z_2 harmonies - the evil snake! These states correspond to the consciousness of animals, children, and saints. Note that bio-harmony corresponds to the presence of one sub-harmony of type Z_n, $n = 6, 4, 2$.

4. The banishing from the paradize takes place as Z_2^{refl} symmetric harmony replaces Z_2^{rot} harmony: half-octave shift is not a symmetry anymore, and one can tell between good and evil, and eventually church decides to deny tritonus as a symbol of evil! Paradise is left as icosahedral and tetrahedral code are fused to form the tetra-icosahedral code - the ordinary genetic code leading to the breaking of Z_2^{refl} symmetry.

5. In banishment punct ("empty" amino-acid) as a counterpart of chord shared by tetrahedron and icosahedron emerges and means stopping of the music piece altogether. Death of the sinner! For unfused codes this chord is playable as Sec/Pyl and the music piece is never-ending: life is eternal in paradise! No notion of time, no sin, no death! Amusingly, impressionist music with 6-note scale is music of "now", attempt to catch this moment.

6. Also the holy trinity finds an analog as $Z_6 - Z_4 - Z_2$ trinity of the bio-harmony. Holy Spirit, Father, Son: perhaps in this order. Even more, Z_2^{rot} can be associated with Son in Heaven and $Z_2 refl$ with Son at Earth as ordinary mortal!

5. What do DNAs/amino-acids sound like?

If DNA/amino-acid sequences correspond to chord sequences of tetra-icosahedral harmony, one can ask what they sound like. The best manner to study this question is to build concrete simulations of the DNA/amino-acid sequences.

1. This requires specification of harmony by selecting one Hamiltonian cycle from the cycles belonging to the groups of cycles with Z_n, $n = 6, 4, 2$ symmetry and decomposing amino-acids to 3 groups correspondingly (those coded by 6, 4, and 2 codons). One must include tetrahedral codons and amino-acids.

2. The basic rule of harmony would be the minimization of quint distance between initial and final chords of the transition. One can consider probabilistic versions of this rule or pose strict form of the rules stating in the most stringent form that only transitions with vanishing quint distance (between neighboring triangles) are possible.

3. The transitions between different amino-acid regions would be governed by this rule. Aso the transitions between different variants of the DNA-amino-acid space defined by different choices of the Hamilton cycles would be governed by the same rule

4. The most plausible looking model considers only transitions between DNA codons since DNA sequences induce amino-acid sequences.

Appendix represents an example about randomly generated chord sequence assignable to bio-harmony defined as a composite of 3 harmonies - one from each symmetry type and $Z_2 = Z_2^{refl}$ involving tetra-icosahedral extension. Anyone having garage band skills in guitar playing can check what these chord sequences sound like and maybe try to build a melody on the background. One could also test the proposal that codons at the orbit of amino-acid define the melody by finding a concrete representation for the orbits and building random melodies defined by DNA sequences coding for the chord sequence.

Magnetic body, bio-harmonies, morphogenesis, and epigenetics

What TGD can possibly give to biology is the vision about magnetic body as an intentional agent using biological body as a sensory receptor and motor instrument and about various mechanism used by magnetic body for control and communication purposes. A new element is brought in by Zero Energy Ontology: magnetic body is 4-dimensional and thus correlate for a behavioral pattern rather than 3-D state for part of organism. Also the notion of bio-harmony suggests itself as a correlate for quantum coherence at the level of basic bio-molecules. The discussion below raises and tries to answer general questions.

The finding that behavioral patterns of planaria can be remembered also by the piece of split planaria without the brain is consistent with the idea that replication of magnetic body coding for behaviors is behind biochemical replication. That alleles of the same gene have different expression could be understood if the bio-harmony assignable to gene carries additional information besides the biochemical information. An alternative explanation is that emotional memories associated with conditioning are realized at the level of the body of planaria.

These notions might also provide a fresh approach to epigenetics. Histone modification and DNA methylation are believed to induce kind of geometric locking preventing transcription. They could also affect the frequency assignable to DNA codon or some key unit so that the resonance condition making possible reconnection of U-shaped flux tubes allowing biomolecules to get in contact fails and transcription cannot proceed. Epigenetic inheritance could reduce to the inheritance of bio-harmony: the magnetic bodies of cells of offspring get in tune with those of parent. To how high degree magnetic body and bio-harmony are inherited? This becomes the key question.

1. Basic ideas related to magnetic body

Recall first some key ideas of TGD inspired quantum biology.

1. In TGD framework magnetic body extends the pair formed by organism and environment to a kind of holy trinity. Magnetic flux tubes and the realization of genetic code in terms of dark proton sequences has been the key hypothesis. The model for cold fusion [L22] suggests that also more general dark nuclei must be allowed. Dark neutron sequences could correspond to genes separated by dark protons. Dark weak interactions with large value of h_{eff} effectively massless below neuron size scale would play central role and induce large parity breaking effects (chiral selection).

   The chemistry would not be all that matters. DNA-nuclear/cell membrane as topological quantum computer with braided magnetic flux tubes would explain why organisms with virtually identical genomes are so different (we and our ancestors for instance). The hierarchy of magnetic bodies would be responsible for the development of intelligence and for cultural evolution. Flux tubes connecting DNA and mRNA as well as mRNA and tRNA molecules are present but it is difficult to say anything concrete.

2. Ontogeny could be seen as a kind of editing process for the text defined by the DNA. Control of control of... is involved so that situation is very complex. Who performs the editing? Does DNA edit itself and is the editing process defining evolution of genome coded by genome? Or is the editing performed by Darwinian selection at cell level (see `http://tinyurl.com/nd9a9ks`)? Or is the magnetic body the editor using genome also as its tool as TGD would suggest? What is important that in TGD framework self-organization

in 4-D sense implied by Zero Energy Ontology replaces ordinary self organization leading to asymptotic spatial patterns and select spatiotemporal patterns as asymptotic behavioral patterns defining various biological functions. The role of magnetic body is central in this process.

3. Magnetic body contains cyclotron Bose-Einstein condensates and cyclotron frequencies determined by the strength of magnetic field would give for DNA and other biomolecules additional characteristics. In TGD based model for musical harmony DNA codons would correspond quite concretely to 3-chords but played using dark photons (also ordinary music represented as sounds could be transformed to dark photon music). If one accepts the icosahedral model of bio-harmonies predicting genetic code correctly, there would be 256 fundamental harmonies characterised by the allowed collection of 3-chords and they would add to the information carried by DNA molecules. I have constructed a program building random sequences of the allowed chords using the additional harmonic rule that two subsequent chords contain at least one common note and this music sounds rather harmonic (albeit boring in absence of any other elements!)

4. Could one distinguish between different states/phases of DNAs, mRNAs, tRNAs, and amino acids in terms of harmony? Could their functioning depend on the harmony? With the inspiration coming from the connection of emotions and musical harmonies I have proposed that the harmony associated with a gene or organ could correlate with something analogous to an emotional state or mood - maybe micro-mood or microemotion could be the proper notion. Could amino-acids be happy, hilarious, melancholic, sad, depressed? Could one distinguish between different phases of DNA, RNA, tRNA, aminoacid collections characterized by the harmony in turn characterizing the of a cell, organelle, organ, or even organism? tRNA defines the map of the harmony associated with DNA codons to amino-acid harmony. Is the information about DNA codon and about corresponding 3-chord represented at the level of magnetic body of amino-acid- that is as the 3-chord, which it represents, and realized as the rules telling with which tRNAs amino-acid can reconnect?

   In contrast to DNA codons, which represent local information, harmony could represent holistic information and characterize entire genes or their intronic portions.

2. Problem

There is however a problem. DNA codons coding for the same amino-acid correspond to different 3-chords of harmony. One of these chords corresponds to amino-acid itself and the codons coding for amino-acid correspond to the orbit of this chord under subgroup of isometries of icosahedron moving the triangles of icosahedron along the orbit. This would apply also to mRNA and maybe also to tRNA. The chords at the orbit of amino-acid are isomorphic (intervals are same) and obtained as transposes of each other.

The chords are isomorphic but not identical and this leads to the problem with resonance paradigm unless one gives up the idea that amino-acid corresponds to a unique DNA codon and assumes that there is analog of gauge invariance allowing to choose the preferred codon freely.

1. The assumption about preferred DNA codon could be given up if one can choose the preferred DNA codon freely so that also the magnetic bodies of amino-acids are characterized by 3-chords and thus carry information about what DNA codon coded them. This is possible if one has the analog of fiber space structure with DNA codons coding for amino-acid defining the fiber and amino-acids defining the base. This fiber structure with discrete gauge invariance is strongly suggestive and I have proposed it for two decades ago but it seems that it poses strong conditions on the orbits of the subgroups of isometries of icosahedron.

   This condition is very restrictive. Simplifying somewhat: one considers 60 codons decomposing into 20+20+20 codings and each group of 20 codons codes for amino-acids belonging to different groups. There are twenty of them. The 20 triangles of icosahedron correspond to 3 DNA codons each and each of them corresponds to one and only one amino-acid. One has 3 subgroups of isometries corresponding to 20+20+20 decomposition.

Can one perform a global gauge transformations realized as isometries and moving triangles along the orbits of one of the 3 subgroups involved - say isometry g_1 of G_1? These transformations would move the entire orbits of 2 subgroups involved - call them G_2 and G_3. What happens to the chords of G_2 and G_3: is their character changed completely so that these harmonies would be destroyed? It seems that this cannot work. Should one replace G_2 and G_3 with their automorphs $g_1 G_2 g_1^{-1}$ and $g_1 G_3 g_1^{-1}$. Does this make sense? 3-chords defining give orbit should be invariant under automorphisms of G_i? This does not seem to be a realistic condition.

2. Could different automorphs correspond to different collections of chords physically just as global gauge transformations generate different physical situations? Isometries of groups G_i would therefore define physically different realizations of bio-harmonies such that for each of them only one of the DNA codons coding for given amino-acid could actually perform the coding. Ordinary genetic code with many-to-one correspondence would make sense in statistical sense only. If this is true, the cyclotron frequency 3-chord assignable to amino-acid depends on the DNA coding it and implies physical distinctions.

3. One can consider also a third alternative. DNA codon with same 3-chord as coding for amino-acid is in special role in that only it can resonate with the amino-acid! Could DNA codons codons correspond to same cyclotron frequency triplet (magnetic fields) but different value of h_{eff} so that one would have chord with respect to energy rather than frequency. Different values of h_{eff} for DNA codons coding for the same amino-acid would scale their cyclotron frequencies to the same amino-acid frequency while keeping cyclotron energies invariant? Cyclotron energy ratios for codons correspond to rational valued ratios $E_i/E_j = h_{eff}(i)/h_{eff}(j) = n(i)/n(j)$. Amino-acid would correspond to fixed h_{eff} and this creates a problem: can DNA codon code for amino-acid with different value of h_{eff}. This option does not look attractive.

Second option looks most plausible. Of course, it is early to talk about a prediction: it might well be that I have mis-understood something.

3. Questions about bio-harmony

One can pose a lot of questions about bio-harmony.

1. It is not necessary to assign any interpretation on the harmony. Just the harmony could be enough if it is forced to be same for DNA, corresponding mRNA, tRNA, and aminoacids. One can however make questions. Is the harmony inherited invariant and could it distinguish between different personality types about which we learned in old books of psychology? Or could the harmonies correlate with our own moods?

2. Could differentiation selecting particular genes as expressed genes apply also to harmonies so that given gene would correspond only to a particular harmony and different copies of gene could correspond to different harmonies. Could this selection rely on the same mechanisms as ordinary differentiation realized in terms of epigenetic mechanisms and DNA editing? From the magnetic bodies of genes the harmony would be automatically transferred to the magnetic bodies of mRNA, tRNA and aminoacids since otherwise the transcription and translation do not work since magnetic bodies do not have common resonance frequencies and reconnection and resonant interaction is not possible.

3. Does given harmony characterize given gene or the entire cell? All basic biomolecules associated with a gene would naturally correspond to the same harmony. If the rRNAs associated with ribosomes are in harmony mutually cellular harmony seems to be the only option. If ribosomes have their own harmonies, only certain ribosomes can translate given gene. This would bring in additional control tool. The most plausible picture is that the situation depends on what happens in the self-organization process. Some organs/organisms are more harmonious, others not so harmonious. Harmony need not be given fixed to remain the same: magnetic body can have motor actions changing the cyclotron frequencies. Moods could reflect the character of harmony at gene level.

4. Does magnetic body control the differentiation by posing restrictions on gene expression or vice versa? The idea about magnetic body as intentional agent suggests that the first option is correct. There would be hierarchy of magnetic bodies with magnetic bodies at the higher level controlling bodies at the lower level. The value of Planck constant would label the hierarchy levels and also DNA codons would be characterized by "intelligence quotient" defined by h_{eff}/h. This would be nothing but the analog for the hierarchy of program modules and I have earlier considered the realization of this hierarchy [L23].

5. The selection of harmony could take place and be analogous to cell differentiation. This would be a self-organization process in which magnetic bodies of genes, cells, etc.. tune themselves to resonance with each other by modifying their magnetic fields by controlling their thickness (for monopoles flux the flux is invariant). Something analogous to the development of social skills. This could pose resonance as a constraint on processes like replication, transcription, reverse transcription, silencing, enhancing, editing, etc.... It might induce the differentiation at gene level.

   Editing processes for genome could be seen as being induced by the motor actions of the magnetic body involving reconnection and change of the value of h_{eff} changing the length of the flux tube and bringing biomolecules near to each other or separating them. This selection would also apply to the intronic part of DNA proposed to be responsible for topological quantum computation like processes. The copies of same fragment appearing in intronic portion and copies of genes could correspond to different harmonies.

4. Can the notions of magnetic body and bio-harmony explain something that ordinary genetic cannot?

It would be nice to identify some biological phenomenon difficult to understand in standard framework but having an elegant explanation in terms of magnetic body.

1. The notion of harmony could manifest itself at the level of genes as different expressions for the copies of same gene if they correspond to different notions of harmony. The copies of gene are known as alleles (see `http://tinyurl.com/bpee49t`). The alleles can indeed give rise to different phenotypic traits such as different pigmentation.

2. Morphogenesis provides examples of this kind of phenomena [I67, I68, I83]. The first key idea is that DNA and cell replication is induced by the replication of magnetic bodies serving as information carriers [K64]. The second key idea is that in zero energy ontology (ZEO) magnetic body is 4-dimensional and represents behavioral patterns rather than only 3-dimensional patterns. For instance, memory as behavioral patterns can be inherited by the piece of planaria worm not containing the brain. The explanation could be that the magnetic body carries behavioral patterns replicated in the splitting of the worm.

3. Epigenetics (see `http://tinyurl.com/4xpwcm`) studies changes of gene expression not caused by the change of DNA itself. Epigenome (see `http://tinyurl.com/y9xkfb2u`) is the highly dynamic part of DNA controlling expression of the rather stable part of genome. One might regard stable part of genome as hardware and epigenome as topological quantum computer programs assignable to magnetic body and modifying gene expression epigenetically. Comment sign in computer code serves as a computer scientific metaphor for epigenetic control by repression.

The modelling of epigenesis in terms of magnetic body and bio-harmonies deserves a separate discussion.

1. The modification of transcription rate is the basic tool of epigenetic regulation. There are two basic mechanisms involved. Histone modification (see `http://tinyurl.com/y8ywse5v` affects the histones of chromatin so that the transcription is repressed or activated. Histone modification takes place by several mechanisms. DNA methylation occurs for CpG pair and if it occurs for a promoter region it represses the transcription and serves as a kind of gene lock. The degree of methylation serves as a measure for the effectiveness of repression. I do not know whether the locking is absolute at the level of single gene or whether only the

transcription rate is reduced. Two mechanisms are mentioned in the Wikipedia article (see http://tinyurl.com/y9kwrvwx). Methylation can impede geometrically some step in the transcription. Methylated site can be also accompanied by proteins affecting histones in chromatin and in this manner impede transcription.

2. The notions of magnetic body and bio-harmony suggest an alternative - one might even hope fundamental - mechanism of repression. Methylation (histone modification) could affect some cyclotron frequency associated with DNA codon (histone). In the optimal situation for transcription the DNA and protein catalyzing the transcription or mRNA are in resonance. When cyclotron resonance condition is not exactly satisfied, the reconnection rate for the U-shaped flux tubes associated with the molecules involved in the process is reduced and also transcription is repressed.

   I have considered also the radical possibility that the dynamics at the level of magnetic body is fundamental for biology and that magnetic body defines templates for the bio-molecular self-organization making dark matter dynamics visible. This is probably too extremist view and it would seem that biochemistry affects the cyclotron frequencies assignable to the magnetic body by affecting the strengths of magnetic fields also at dark magnetic flux tubes.

3. The notions of epigenetic code (see http://tinyurl.com/y8ztzzza) and histone code (see http://tinyurl.com/y854w58p) have been proposed. Epigenetic code would consist of histone modifications and additional modifications such as DNA methylation. The codeword of the epigenetic code could code for some larger unit than protein: say gene or entire cell. The hypothesis is that the chromatin-DNA interactions are induced by histone tail modifications (such as methylation, acetylation, ADP-ribosylation, ubiquitination, citrullination, and phosphorylation). There are 4 histones and the position of modification varies as well as the modifier (the above modifications are not the only ones) so so that the number of modifications is very large.

   The addition of bioharmonies to the genetic information could simplify the situation dramatically since the modifications could be seen as defining of of the 256 bio-harmonies with 64 chords each (this for fixed scale which varies if the value of magnetic field strength is varied: biophoton spectrum in visible is proposed to represent the range of values of magnetic field). The most plausible starting hypothesis is that given harmony characterizes the gene. Much simpler option would be that the harmony characterizes entire cell or even group of cells.

   If the modification by kicking cyclotron frequency out of harmony is enough to repress transcription, almost endless number of bio-chemical ways to achieve would exist but the epigenetic code could be very simple at the basic level as TGD would predict. Each bio-harmony [L11] [K67] would provide a representation of genetic code in terms of 3-chords predicting correctly the DNA-amino-acid correspondence (there are actually two slightly differing codes explaining the presence of 21st and 22nd amino-acid and deviations from the standard code). The states of dark protons (or neutrons) are also proposed to realize genetic code [L1, K41]: it is an open question whether these codes imply each other as they should.

4. The understanding of transgenerational epigenetic inheritance (see http://tinyurl.com/h6qg64c) raises difficult challenges. One should understand how histone modification and DNA methylation are transferred to daughter cells in cellular division or inherited by the offspring. Transgenerational interaction of the genomes seems necessary. In TGD framework the interaction of magnetic bodies of via resonance mechanism could transfer the epigenetic programs to the offspring. Offspring could "learn" the epigenetic programs of the mother by tuning.

5. Gregory Carey (see http://tinyurl.com/ydyznsaq) gives nice real life examples about the complexities of epigenesis identified quite generally as gene regulation (see http://tinyurl.com/zb97cgs). He compares the gene regulation involved with the handling of a stressful situation to "nightmarish Rube Goldberg mousetrap" and sees the process as extremely ineffective from engineering point of view. For instance, the hormones secreted to blood circulation are distributed to the entire body. The whole thing could be carried out in brain! He also wonders why evolution is so inefficient. All cells have same genome although most of

the genes are silenced. Second strand of DNA is totally un-used and most of DNA consists of introns. His explanation is that evolution does not make long term plans but finds just a solution to a particular without thinking it from a wider perspective: "If it ain't broke, don't fix it".

I tend to see this differently. If entire body is coherent quantum entity, engineering based thinking does not make sense. Entire body and also magnetic body must be informed from the stress situation since the reaction is holistic. The genes which are not used for gene expression might be used for other purposes. Topological quantum computation could be this purpose in TGD framework and repressed genes could be thus used for quantum information processing. Information processing could be actually the dominating function of the DNA of higher vertebrates.

To sum up, magnetic body could be seen as the "boss" controlling the gene expression and also the evolution of genome in longer scales. Magnetic body would use bio-molecular mechanisms for its purposes. This would bring in a new kind of inheritance: bio-harmony would be inherited. The most spectacular almost-prediction would be that genetic code is many-to-one only in statistical sense.

5. RNA is transferred between soma cells and germ cells

The basic question of epigenesis is how the information between soma cells and germ cells is transferred. In standard genetic the transfoer RNA or DNA molecules is necessary to achieve this. In TGD dark DNA, RNA, tRNA, and aminocids consisting of dark nucleons realized as nuclear strings and accompanied by the corresponding biomolecules is one possibility. The extremist view would be that the dynamics of the dark variants of basic bio-molecules induces the dynamics of their molecular shadows making them only visible. Also the transfer of information as cyclotron radiation can be considered in TGD framework and cyclotron resonance could serve as a fundamental mechanism of epigenetic control. The above model suggest that epigenetic control mechanisms rely on resonance mechanism for 3-chords associated with DNA codons and other biomolecules giving them "names" is also at work besides purely geometrical silencing.

The popular article "No Sex Required: Body Cells Transfer Genetic Info Directly Into Sperm Cells, Amazing Study Finds" (see `http://tinyurl.com/hhdth5j`) summarizing the findings discussed in the article [I36] (see "Soma-to-Germline Transmission of RNA in Mice Xenografted with Human Tumour Cells: Possible Transport by Exosomes" (see `http://tinyurl.com/yde7wb55`) as very interesting concerning this basic question.

The abstract of the article gives for a professional a readable summary.

Mendelian laws provide the universal founding paradigm for the mechanism of genetic inheritance through which characters are segregated and assorted. In recent years, however, parallel with the rapid growth of epigenetic studies, cases of inheritance deviating from Mendelian patterns have emerged. Growing studies underscore phenotypic variations and increased risk of pathologies that are transgenerationally inherited in a non-Mendelian fashion in the absence of any classically identifiable mutation or predisposing genetic lesion in the genome of individuals who develop the disease. Non-Mendelian inheritance is most often transmitted through the germline in consequence of primary events occurring in somatic cells, implying soma-to-germ line transmission of information. While studies of sperm cells suggest that epigenetic variations can potentially underlie phenotypic alterations across generations, no instance of transmission of DNA- or RNA-mediated information from somatic to germ cells has been reported as yet.

To address these issues, we have now generated a mouse model xenografted with human melanoma cells stably expressing EGFP-encoding plasmid. We find that EGFP RNA is released from the xenografted human cells into the bloodstream and eventually in spermatozoa of the mice. Tumor-released EGFP RNA is associated with an extracellular fraction processed for exosome purification and expressing exosomal markers, in all steps of the process, from the xenografted cancer cells to the spermatozoa of the recipient animals, strongly suggesting that exosomes are the carriers of a flow of information from somatic cells to gametes. Together, these results indicate that somatic RNA is transferred to sperm cells, which can therefore act as the final recipients of somatic cell-derived information.

Some background is needed to understand this rather technical summary.

1. Darwinism has dominated biology since Darwin. The rules of classical Mendelian inheritance conform with the Darwinian view and can be reduced to genetic level. Various traits are inherited genetically by sexual reproduction and genome would change during lifetime only through mutations. Genome changes exremely slowly by random changes for offspring from which selection pressures choose the survivors.

   Lamarckian view in turn assumed that the external circumstances experienced by organism leave a trace, which can be inherited but it could not be formulated in terms of modern molecular biology whereas the Darwinian dogma could be formulated in terms of Weissman's genetic barrier. Information flows from germ cells to soma but never in opposite direction. If it would do so, the soma interacting with environment could transfer information to germ cells and the experiences during lifetime could leave inheritable trace to germ cells.

   An analogous dogma is that information is always transcribed from DNA to RNA to proteins but never in opposite direction. It is now known that this takes place in case of viruses and retroviruses: there are so called jumping genes which can also make copies of themselves. 5 per cent of human genome conists of endogenous retroviruses capable of doing the same. The huge genome of maize is due to this kind of proces.

2. The development epigenetics has started to shatter the belief on Wessimann's genetic barrier. Gene expression is not fixed by genome alone and can be change even when genes are unaffected. Silencing of genes by DNA methylation and histone modification allow to modify gene expression. Silencing is essentially a locking of gene preventing its expression by transcription followed by translation.

   It is now known that epigenetic changes in the gene expression can be inherited. The mechanisms are still poorly understood. What seems however clear the genome is more like a slowly changing hardware and gene expression or whatever is behind it is the software and programs can change very rapidly by just adding or deleting comment signs in the code. A deeper understanding of this software is needed.

3. Epigenetic inheritance requires that genetic information is transferred from soma cells to germ cells. If only DNA or RNA are capable of representing genetic information, then DNA or RNA must be transferred from soma cells to germ cells. No instance of direct DNA or RNA mediated information from soma to germ cells had been observed before the above mentioned experiments. One can of course challenge the assumption about DNA and RNA as the only representations of genetic information.

The basic idea of the experiment was simple. Use a marker for RNA by using plasmids (DNA strands not belonging to chromosomes) genetically engineered to code for a marker protein making itself visible by fluorescence. Then one just follows the fate of these proteins generated in soma cells and looks whether they end up inside germ cells and how this happens.

More technically: mouse model was xenografted with human melanoma cells stably expessing EGFP-coding plasmid (expressed in a way possibly evoking emotions: human melanoma cancer tissue was implanted in mouse). EGFP-RNA is released from xenografted human cells to blood. One just looks whether it eventually ends up to the sperm cells of mice and tries to identify the transfer mechanism. Only transfer to sperm cells was studied. One might expect that the transfer of RNA can happen also to ovum. I guess that the sperm cells are easier to study.

What was observed?

1. The transfer of RNA from soma cells to sperm cells was indeed found to occur. The transferred RNA can in turn induce epigenetic effects in germ cells known to be inherited by a mechanisms, which however remain poorly understood. Epigenetic mechanisms seem to be involved in the cases considered so that DNA is not changed, only its expression.

2. The transfer mechanism was identified. The transferred RNA is contained by exosomes analogous to synaptic vesicles transferring neurotransmitters from presynaptic to postsynaptic cell. Transfer of RNA takes place via fusion of the membranes just like transfer of neurotransmitters. Maybe genetic engineering using exosomes or analogous structures to transfer the needed material to cells has been tried.

The implications of the findings are dramatic but already implied by the earlier work in epigenetics. What is important that Lamarckian view can be now defended by a concrete genetic mechanism. Lamarckism implies that the time scale of inheritance becomes the time scale for the appearence of a new generation. Nutrition, environment, lifestyle and even meditation and similar practices, are already now known to affect gene expression on daily basis: we are not victims of genetic determinism and are epigenetically responsible for our own well-being. Epigenetic information can be transferred also to germ cells so that we responsible also for the well-being of our children. Our children suffer our sins and share our sufferings.

The precise mechanism of inheritance of epigenetic modifications remains still poorly understood although it seems that the transfer or RNA to germ cells occurs. There are also other hints: it is known that alleles (variants of game gene) can express themselves differently. One allele can also induce other allele to express in the same manner. Somekind of "social pressure" like interaction seems to be involved.

As explained, TGD suggests the notion of magnetic body and cyclotron resonance as this interaction. The DNA of offspring get tuned to the DNA of mother during pregnancy and this gives to epigenetic inheritance. Various epigenetic mechanisms such as methylation and histone modification could affect cyclotron frequencies besides purely geometric modifications of DNA and locking at the level of gene could be accompanied kicking out of tune at the level of magnetic body. In this framework the transfer of RNA to germ cells would be necessary to affect the cyclotron frequencies.

Epigenesis, inherited memories and moods lasting over several generations

Nikolina Benedikovic had an interesting comment concerning multiverse interpretation. This motivated to write a summary about the connection between epigenesis, inherited memories interpreted as behaviors and moods lastring for seveal generations. Nikolina's comment was following.

"*One can imagine an intelligent amoeba with a good memory. As time progresses, the amoeba is constantly splitting, each time the resulting amoebas having the same memories as the parent. Our amoeba hence does not have a life line, but a life tree.*" - Huge Everett

Nikolina: Dear Mr. Everett! Before we find out what the true interpretation of quantum mechanics is, we will have to answer this question; why the amoeba possesses this "super power" of splitting and the electron and human being don't.

I agree with Nikolina. The following is my comment about what is involved. I proceed by questions.

1. What behaviors are?

The behavior of amoeba has nothing to do with parallel universes of Everett. The behavior as such is however highly interesting and challenges standard theories of biology and perhaps also of physics. Memories seem to replicate.

1. What do we mean with memories now: do we mean behaviors, skills, conditionings? Or episodal, sensory memories. I think it is memories in the first sense of the word. Suppose that essentially conditionings are in question.

   In this respect a lot of progress happened as it was discovered that RNA somehow represents the memories: taking RNA of conditioned sea snail and scattering it over the neurons fo second snail in lab induces the conditons of the snail to these neurons.

2. Epigenetic approach would suggest that the behaviours essentially the same but now one does not have any convincing model for the model of the epigenesis.

2. What TGD inspired quantum biology and neuro-science can tell?

There are two key questions that one must answer.

1. What replication is?

   In TGD Universe we are 4-D entities - quantum states are superpositions of space-time surfaces obeying deterministic dynamics. This solves the problem of free will and basic problem of quantum measurement theory. The superposition of space-time surface would

be analogous to superposition of deterministic computer programs, behaviours, or biological functions in classical sense. Free will would select the program [L53, K54, L66, L13] .

2. What memories as learned behaviours are? One can imagine several models, which need not exclude each other.

   (a) For instance, could it be that the replicas of ameba have geometric past that is partially shared: the part of the past as amoeba before the replication?

   (b) Second TGD explanation would be based on what conditionings are? They involve emotions in an essential manner. Emotions are induced and induce behaviors and conditionings involve long term moods. The mysterious epigenetic inheritance could be inheritance of moods affecting gene expression: moods could be inhereted and have time-span of several generations: this conforms with the first option.

3. What moods are?

Suppose that conditions are due to long term moods in turn correlating with behavior and at basic level with genetic expression. Consider a TGD based model for moods, second option.

1. Music - its harmony defined by allowed chords - represents emotions and generates them. The allowed 3-chords of bio-harmony, the set of which can vary, would define the mood.

2. Genes are associated with information. Codon contains 6 bits of information. Magnetic body with large $h_{eff} = nh_0$ is the boss, the "wise guy", controlling biological body and biochemistry so that genetic code must have primary representation at the level of flux tubes. Dark proton sequences at flux tubes interpreted as dark nuclei indeed represent codons as 3-proton units. The states of 3- proton units turn out to correspond to DNA, RNA, tRNA, amino-acids and vertebrate genetic code is predicted.

   Chemical representation would be only a secondary representation only, mimicry, and often incomplete.

   Dark proton sequences also realizing vertebrate genetic code would also have positive charge neutralizing the negative charge of nucleotides and make DNA stable. Pollack effect would generate the dark flux tube and this would require metabolic energy and in absence of it DNA would not be stable.

3. Dark proton sequences must also communicate by dark photons with large h_{eff}. The communications must rely on resonance, actually there must be resonance between similar 3-proton units, dark codons. Therefore 3-chords consisting 3 dark photons must represent the codons represented by 3 protons [L58]. Only identical codons have resonant coupling. This makes possible remote replication of DNA reported by HIV nobelist Montagnier [L3] (see `http://tinyurl.com/yygqen5g`).

4. Allowed 3-chords define the harmony and emotional state mood. In TGD representations of emotions in terms of bio-harmony would provide the representation of genetic codons defined by RNA as 3-chords of light, triplets of 3 dark photons. The icosatetrahedral model for harmony realizing bioharmony [L11, L78]. gives also rise to vertebrate genetic code: the 6-bit units defined by codons correspond to ordinary temporarily local intellect, and the harmony to the holistic emotional intellect.

5. RNA and DNA, tRNA, amino-acids would naturally be represented by light 3-chords in communications. Given codon would only tell its name by the chord and resonate with codon having same name. The codons would couple by chords via triple resonance. Same DNA sequences could be in different mood defined by bioharmony and its expression would depend on this: this would give rise to epigenetics. Epigenetic inheritance would be emotions lasting for several generations.

   The bioharmony associated with RNA could represent the mood infecting also DNA and generating DNA expression giving rise to the behavior related to conditioning.

6. If this were the case then the inheritance of memories (in this sense could be inheritatance of conditionings as long term moods. The replications of RNAs and DNAs and possible other biomolecules carrying the conditioning would give rise to replication of memories as behaviors induced by moods.

7. These moods can be very long term moods and extend over generations. This would fit with the model in which replicated amoebas have the 4-D magnetic body amoeba of the geometric past as part of their 4-D magnetic body.

To sum up, behaviors as conditionings could be caused by moods, which can last for several generations. This would bring in magnetic body as active agent. The representation genetic code in terms dark proton sequences and by 3-chords of dark photons would give a realization of both the "bitty" and emotional aspects of intelligence. Also the notions of 4-D brain and organism having temporal span of several generations as space-time surfaces would be essential for the understanding the inheritance of emotions. We should be very careful for what we do since also our children can feel themselves proud of or guilty for what we did.

E_8 symmetry, harmony, and genetic code

Bee gave in Facebook a link to an article about a connection between icosahedron and E_8 root system [B18] (see `http://tinyurl.com/zotpm4b`). The article (I have seen an article about the same idea earlier but forgotten it!) is very interesting.

The article talks about a connection between icosahedron and E_8 root system (see `http://tinyurl.com/y7csb6uh`). Icosahedral group has 120 elements and its double covering $2\times120 = 240$ elements. Remarkably, E_8 root system has 240 roots. E_8 Lie algebra is 248 complex-dimensional contains also the 8 commuting generators of Cartan algebra besides roots: it is essential that the fundamental representation of E_8 coincides with its adjoint representation. The double covering group of icosahedral group acts as the Weyl group E_8. A further crucial point is that the Clifford algebra in dimension $D = 3$ is 8-D.

One starts from the symmetries of 3-D icosahedron and ends up with 4-D root system F_4 assignable to Lie group and also to E_8 root system. E_8 defines a lattice in 8-D Euclidian space: what is intriguing that dimensions 3,4, 8 fundamental in TGD emerge. To me this looks fascinating - the reasons will be explained below.

1. What I might have understood

I try to explain what I have possibly understood.

1. The notion of root system is introduced. The negatives of roots are also roots but not other multiples. Root system is crystallographic if it allows a subset of roots (so called simple roots) such that all roots are expressible as combinations of these simple roots with coefficients having the same sign. Crystallographic root systems are special: they correspond to the fundamental weights of some Lie algebra. In this case the roots can be identified essentially as the quantum numbers of fundamental representations from which all other representations are obtained as tensor products. Root systems allow reflections as symmetries taking root system to itself. This symmetry group is known as Coxeter group and generalizes Weyl group. Both H_3 and H_4 are Coxeter groups but not Weyl groups.

2. 3-D root systems known as Platonic roots systems (A_3, B_3, H_3) assignable to the symmetries of tetrahedron, octahedron (or cube), and icosahedron (or dodecahedron) are constructed. The root systems consist of 3 suitably chosen unit vectors with square equal to 1 (square of reflection equals to one) and the Clifford algebra elements generated by them by standard Clifford algebra product. The resulting set has a structure of discrete group and is generated by reflections in hyper-planes defined by the roots just as Weyl group does. This group acts also on spinors and one obtains a double covering SU(2) of rotation group SO(3) and its discrete subgroups doubling the number of elements. Platonic symmetries correspond to the Coxeter groups for a "Platonic root system" generated by 3 unit vectors defining the basis of 3-D Clifford algebra. H_3 is not associated with any Lie algebra but A_3 and B_3 are.

Pinors (spinors) correspond to products of arbitrary/even number of Clifford algebra elements. Spinors induced orientation preserving transformations and pinos also orientation reversing ones. They mean something else than usually a bein identified as elements of the Clifford algebra acting and being acted on from left or right by multiplication so that they always behave like spin 1/2 objects since only the left(right)-most spin is counted. The automorphisms involve both right and left multiplication reducing to SO(3) action and see the entire spin of the Clifford algebra element.

3. The 3-D root systems (A_3, B_3, H_3) are shown to allow an extension to 4-D root systems known as (D_4, F_4, H_4) in terms of 3-D spinors. D_4 and F_4 are root systems of Lie algebras (see `http://tinyurl.com/y97dzqc2`). F_4 corresponds to non-simply-laced Lie group related to octonions. H_4 is not a root system of any Lie algebra.

4. The observation that the dimension of Clifford algebra of 3-D space is $2^3 = 8$ and thus allows embedding of at most 8-D root system must have inspired the idea that it might be possible to construct the root system of E_8 in 8-D Clifford algebra from 240 pinors of the double covering the 120 icosahedral reflections. Platonic solids would be behind all exceptional symmetry groups since E_6 and E_7 are subgroups of E_8 and the construction should give their root systems also as low-dimensional root systems.

2. McKay correspondence

The article explains also McKay correspondence stating that the finite subgroups of rotation group SU(2) correspond to simply laced affine algebras assignable with ADE Lie groups.

1. One considers the irreducible representations of a finite subgroup of the rotation group. Let the number of non-trivial representations be m so that by counting also the trivial representation one has $m + 1$ irreps altogether. In the Dynkin diagram of affine algebra of group with m-D Cartan algebra the trivial representation corresponds to the added node. One decomposes the tensor product of given irrep with the spin 2 representation into direct sum of irreps and constructs a diagram in which the node associated with the irrep is connected to those nodes for which corresponding representation appears in the direct sum. One can say that going between the connected nodes corresponds to forming a tensor product with the fundamental representation. It would be interesting to know what happens if one constructs analogous diagrams by considering finite subgroups of arbitrary Lie group and forming tensor products with the fundamental representation.

2. The surprising outcome is that the resulting diagram corresponds to a Dynkin diagram of affine (Kac-Moody) algebra of ADE group with Cartan algebra, whose dimension is m. Cartan algebra elements correspond to tensor powers of fundamental representation: can one build any physical picture from this? For $m = 6, 7, 8$ one obtains E_6 , E_7 , E_8. The result of the article implies that these 3 Lie-groups correspond to basis of 3 3-D unit identified as units of Clifford algebra: could this identification have some concrete meaning as preferred non-orthogonal 3-basis?

3. McKay correspondence emerges also for inclusions of hyper-finite factors of type II_1 [K90] The integer m characterizing the index of inclusion corresponds to the dimensions of Cartan algebra for ADE type Lie group. The inclusions of hyperfinite factors (HFFs) are characterized by integer $m \geq 3$ giving the dimension of Cartan algebra of ADE Lie groups (there are also C, F and G type Lie groups). $m = 6, 7, 8$ corresponds to exceptional groups E_6 , E_7 , E_8 on one hand and to the discrete symmetry groups of tetrahedron, octahedron, icosahedron on the other hand acting as symmetries of corresponding 3-D non-crystallographic systems and not allowing interpretation as Weyl group of Lie group.

3. Connection with the TGD based model of harmony

These findings become really exciting from TGD point of view when one recalls that the model for bioharmony [K67] [L11] (see `http://tinyurl.com/yad4tqwl`) for 12-note harmonies central in classical music in general relies on icosahedral geometry. Bioharmonies would add

something to the information content of the genetic code: DNA codons consisting of 3 letters A,T,C,G would correspond to 3-chords defining given harmony realized as dark photon 3-chords and maybe also in terms of ordinary audible 3-chords. This kind of harmonies would be roughly triplets of 3 basic harmonies and there would be 256 of them (the number depends on counting criteria). The harmonies could serve as correlates for moods and emotional states in very general sense: even biomolecules could have "moods". This new information should be seen in biology. For instance, different alleles of same gene are known to have different phenotypes: could they correspond to different harmonies? In epigenetics the harmonies could serve as a central notion and allow to realize the conjectured epigenetic code and histone code. Magnetic body and dark matter at them would be of course the essential additional element.

The inspiring observations are that icosahedron has 12 vertices - the number of notes in 12-note harmony and 20 faces- the number of amino-acids and that DNA codons consist of three letters - the notes of 3-chord.

1. Given harmony would be defined by a particular representation of Pythagorean 12-note scale represented as self-non-intersecting path (Hamiltonian cycle) connecting the neighboring vertices of icosahedron and going through all 12 vertices. One assumes that neighboring vertices differ by one quint (frequency scaling by factor 3/2): quint scale indeed gives full octave when one projects to the basic octave. One obtains several realizations (in the sense of not being related by isometry of icosahedron) of 12-note scale. These realizations are characterized by symmetry groups mapping the chords of harmony to chords of the same harmony. These symmetry groups are subgroups of the icosahedral group: Z_6, Z_4, and two variants of Z_2 (generated by rotation of π and by reflection) appear. Each Hamiltonian cycle defines a particular notion of harmony with allowed 3-chords identified by the 20 triangles of icosahedron.

2. Pythagoras is trying to whisper me an unpleasant message: the quint cycle does not quite close! This is true. Musicologists have been suffering for two millenia of this problem. One must introduce 13th note differing only slightly from some note in the quint cycle. At geometrical level one must introduce tetrahedron besides icosahedron - only four notes and four chords and gluing along one side to icosahedron gives only one note more. One can keep tetrahedron also as disjoint from icosahedron as it turns out: this would give 4-note harmony with 4 chords something much simpler that 12- note harmony.

3. The really astonishing discovery was that one can understand genetic code in this framework. First one takes three different types of 20-chord harmonies with group Z_6, Z_4, and Z_2 defined by Hamiltonian cycles: this can be done in many different maners (there are 256 of them). One has 20+20+20 chords and one finds that they correspond nicely to 20+20+20=60 DNA codons: DNA codons coding for a given amino-acid correspond to the orbit of the triangle assigned with the amino-acid under the symmetry group of harmony in question.

   The problem is that there are 64 codons, not 60. The introduction of tetrahedron brings however 4 additional codons and gives 64 codons altogether. One can map the resulting 64 chord harmony to icosahedron with 20 triangles (aminoacids) and the degeneracies (number of DNA codons coding for given amino-acid in vertebrate code) come out correctly! Even the two additional troublesome amino-acids Pyl and Sec appearing in Nature and the presence of two variants of genetic code (relating to two kinds of Z_2 subgroups) can be understood.

4. What could the interpretation of the icosahedral symmetry?

An open problem is the proper interpretation of the icosahedral symmetry.

1. A reasonable looking guess would be that it quite concretely corresponds to a symmetry of some biomolecule: both icosahedral or dodecahedral geometry give rise to icosahedral symmetry. There are a lot of biomolecules with icosahedral symmetry, such as clathrate molecules at the axonal ends and viruses. Note that dodecahedral scale has 20 notes - this might make sense for Eastern harmonies - and 12 chords and there is only single dodecahedral Hamiltonian path found already by Hamilton and thus only single harmony. Duality between

East and West might exist if there is mapping of icosahedral notes and to dodecahedral 5-chords and dodecahedral notes to icosahedral 3-chords and different notions of harmony are mapped to different notions of melody - whatever the latter might mean!).

2. A more abstract approach tries to combine the above described pieces of wisdom together. The dynamical gauge group E_8 (or Kac-Moody group) emerging for m=8 inclusion of HFFs is closely related to the inclusions for the fractal hierarchy of isomorphic sub-algebras of super-symplectic subalgebra. $h_{eff}/h = n$ could label the sub-algebras: the conformal weights of sub-algebra are be n-multiples of those of the entire algebra.

   The integers n_i resp. n_f for included resp. including super conformal sub-algebra would be naturally related by $n_f = m \times n_i$. $m = 8$ would correspond to icosahedral inclusion and E_8 would be the dynamical gauge group characterizing dark gauge degrees of freedom. The inclusion hierarchy would allow to realize all ADE groups as dynamical gauge groups or more plausibly, as Kac-Moody type symmetry groups associated with dark matter and characterizing the degrees of freedom allowed by finite measurement resolution.

3. E_8 as dynamical gauge group or Kac-Moody group would result from the super-symplectic group by dividing it with its subgroup representing degrees of freedom below measurement resolution. E_8 could be the symmetry group of dark living matter. Bioharmonies as products of three fundamental harmonies could relate directly to the hierarchies of Planck constants and various generalized super-conformal symmetries of TGD! This convergence of totally different theory threads would be really nice!

5. Experimental indications for dynamical E_8 symmetry

Lubos (see `http://tinyurl.com/htjp55h`) (thanks to Ulla for the link to the posting of Lubos) has written posting about experimental finding of E_8 symmetry emerging near the quantum critical point of Ising chain at quantum criticality at zero temperature. Here is the abstract (see `http://tinyurl.com/zulzk9y`):

Quantum phase transitions take place between distinct phases of matter at zero temperature. Near the transition point, exotic quantum symmetries can emerge that govern the excitation spectrum of the system. A symmetry described by the E_8 Lie group with a spectrum of eight particles was long predicted to appear near the critical point of an Ising chain. We realize this system experimentally by using strong transverse magnetic fields to tune the quasi–one-dimensional Ising ferromagnet CoNb2O6 (cobalt niobate) through its critical point. Spin excitations are observed to change character from pairs of kinks in the ordered phase to spin-flips in the paramagnetic phase. Just below the critical field, the spin dynamics shows a fine structure with two sharp modes at low energies, in a ratio that approaches the golden mean predicted for the first two meson particles of the E8 spectrum. Our results demonstrate the power of symmetry to describe complex quantum behaviors.

Phase transition leads from ferromagnetic to paramagnetic phase and spin excitations as pairs of kinks are replaced with spin flips (shortest possible pair of kinks and loss of the ferromagnetic order). In attempts to interpret the situation in TGD context, one must however remember that dynamical E_8 is also predicted by standard physics so that one must be cautious in order to not draw too optimistic conclusions.

In TGD framework $h_{eff}/h \geq 1$ phases or phase transitions between them are associated with quantum criticality and it is encouraging that the system discussed is quantum critical and 1-dimensional.

1. The large value of h_{eff} would be associated with dark magnetic body assignable to the magnetic fields accompanying the E_8 "mesons". Zero temperature is not a prerequisite of quantum criticality in TGD framework.

2. One should clarify what quantum criticality exactly means in TGD framework. In positive energy ontology the notion of state becomes fuzzy at criticality. For instance, it is difficult to assign the above described "mesons" with either ferromagnetic or paramagnetic phase since they are most naturally associated with the phase change. Hence Zero Energy Ontology (ZEO) might show its power in the description of (quantum) critical phase transitions.

Quantum criticality could correspond to zero energy states for which the value of h_{eff} differs at the opposite boundaries of causal diamond (CD). Space-time surface between boundaries of CD would describe the transition classically. If so, then E_8 "mesons" would be genuinely 4-D objects - "transitons" - allowing proper description only in ZEO. This could apply quite generally to the excitations associated with quantum criticality. Living matter is key example of quantum criticality and here "transitons" could be seen as building bricks of behavioral patterns. Maybe it makes sense to speak even about Bose-Einstein condensates of "transitons".

The finding suggests that quantum criticality is associated with the transition increasing $n_{eff} = h_{eff}/h$ by factor $m = 8$ or its reversal - maybe the standard value $n_{eff}(i) = 1$. $n_{eff}(f) = 8$ could correspond to the ferromagnetic phase having long range correlations. Could one say that at the side of criticality (say the "lower" end of CD) the $n_{eff}(f) = 8$ excitations are pure gauge excitations and thus "below measurement resolution" but become real at the other side of criticality (the "upper" end of CD)?

3. The 8 "mesons" associated with spin excitations naturally correspond to the generators of the Cartan algebra of E_8. If the "mesons" belong to the fundamental (= adjoint) representation of E_8, one would expect 120+120 additional particles with non-vanishing E_8 charges. Why only Cartan algebra? Is the reasons that Cartan algebra is in preferred role in the representations of Kac-Moody algebras in that charged Kac-Moody generators can be constructed from Cartan algebra generators by standard construction used also in string models. Could this explain why one expects only 8 "mesons". Are charged "mesons" labelled by the elements of double covering of icosahedral group more difficult to excite?

4.4 Icosahedral harmonies

In the following the icosahedral harmonies are discussed in detail. This includes overall summary and tables giving the 20 3-chords of the harmonies and illustrations of the Hamiltonian cycles.

4.4.1 About symmetries of the icosahedral harmonies

Some words about the symmetries associated with the icosahedral harmonies and genetic code are in order.

There are 3 different kind of bio-harmonies characterized partially by the symmetry group which can be Z_6, Z_4 or Z_2 which acts either as rotations or reflections.

1. The first variant as $Z_3^{rot} \times Z_2^{refl}$ subgroup of icosahedral group as symmetries and its orbits correspond to 3 6-plets and 1 2-plets for which Z_3 leaves the triangle invariant. The counterparts for the orbits are 3 DNA 6-plets and one 2-plet.

2. The second variant has Z_4 symmetry generated by two commuting reflection as symmetries as is obvious from figures **??**, **??**: the reflections act on vertical and horizontal coordinates. The orbits are five 4-plets of chords. Vertical reflection induces half-octave shift and horizontal one permutes the note sequences $B\flat CDG\sharp F\sharp E$ and $D\sharp C\sharp HFGA$.

3. Z_2^{rot} or Z_2^{refl} acts as symmetries of the remaining 3+5 cycles. The covering space of 10 amino-acids involved defined by 20 DNA codons decomposes to 10 2-plets.

   The 2-fold rotation symmetry of the Hamiltonian cycles is obvious from the illustration **??**: it corresponds to 6-quint rotation and the chord sets must be invariant under this rotation. This rotation corresponds to the 1/2 octave shift realized as rotation. These symmetries are realized as "coordinate transformations" for the cycle - a curve in the "embedding space" defined by icosahedron but induced from the "embedding space symmetries" acting as isometries of icosahedron.

DNA codons have also almost exact Z_2 symmetry discussed in [K87, K4, **?**].

1. For the last codon the reflection A-T, C-G is an almost symmetry broken only for special cases. This approximate symmetry could be understood as following from the fact that the number of DNAs coding given amino-adic is even in most cases. The exceptions are ile, met, trp coded by odd number of DNA codons. By mapping DNAs to binary sequences one can order the situation so that the 6: th binary digit is the almost-symmetry digit.

2. What is trivial is that RNA has chosen the third bi-digit to be the almost symmetry digit with the ordering UCAG of the nucleotides so that a genuine physical symmetry is in question. An interesting question is how this symmetry relates to the model of genetic code based on tetra-icosahedral orbits.

   The restriction of DNAs to 60 icosahedral DNAs demonstrates that this symmetry originates from the icosahedral Z_2. The tetrahedral extension of the code breaks this symmetry by extending ile and punct multiples by one codon and introducing also 4 singlets met, trp, Pyl, and Sec.

The detailed correspondence between chords of the harmony and DNA codons is also a problem to be solved.

1. The correspondence matters in the proposed scenario since the chords at at the orbits are different and the gluing of tetrahedron breaks the symmetry in Z_2 sectors so that quint rule determining harmonic DNA sequences is different.

2. The common face of tetrahedron and icosahedron corresponds to punct so that the quint rule for different representations says something about the pairs of form codon-stop codon that is about the codon preceding the last codon of gene! This codon could allow to recognize what Hamiltonian cycle is in question. If C-major is one of the added chords, stop codons correspond to what was $C6 = CGA$ chord and its Z_2 image, which is $X7$ type chord. By the strongest form of the quint rule only the chords having common notes with these chords would correspond to DNA codons of Z_6 and Z_4 cycles which can precede stopping codon.

3. There are some restrictions on the correspondence. Z_2^{refl} symmetry would correspond to the flipping of the 6th bit for the bit representation defined by nucleotides representing 2-bits in the case of $Z^3 = Z_3 \times Z_2^{refl}$. $Z_4 = Z_2^{rot} \times Z_2^{refl}$. For $Z_2 = Z_2^{rot}$ the role of Z_2^{refl} must be taken by Z_2^{rot}. One can of course ask whether Z_2^{rot} cycles are realized at all. For Z_4 cycles Z_2^{rot} would correspond to symmetry permuting the AT, CG doublets for the first nucleotide. For Z_6 subgroup Z_3 would cyclically permute the 3 doublets with respect to third nucleotide. These constraints do not fix the correspondence completely.

To sum up, there is a connection between genetic code and the groups acting along the Hamiltonian cycle. The simplest option fixes the orbits of the triangles and therefore also the representation of genetic code.

4.4.2 Summary of the basic results

One can find the list of Hamiltonian cycles at `http://tinyurl.com/yacgzm9x`. The edge $\{1, 2\}$ is fixed and cycles are oriented so that there are 1024 of them. All of them are relevant from the point of music interpretation and the change of orientation corresponds to major-minor duality, albeit not in the simplest sense. Note that this duality does not affect the characteristics listed above.

The general following general results hold true as one can learn at `http://tinyurl.com/pmghcwd`. One can classify the cycles using their symmetries which can correspond to isometries of icosahedron leaving them fixed or to a reflection taking the vertex n at the cycle to vertex $12 - n$. This symmetry is not same as change of orientation which is purely internal operation and cannot change the cycle.

One can even find images of the cycles possessing symmetries at `http://tinyurl.com/y8ek7ak8` and deduce the triplets n and p characterizing them by visual inspection. Also one can write explicitly the 3-chords defined by the three kinds of faces. I have deduced the triplets n and the 3-chords defining the harmony by the inspection of the images. "Bio-harmony" (4, 8, 8)

$$\begin{array}{llll} CEG \equiv C\ , & CD\sharp G \equiv Cm\ , & CD\sharp F\sharp \equiv C^o\ , & CEG\sharp \equiv Caug\ , \\ CFG \equiv C4\ , & CF\sharp G \equiv C4_+\ , & CGG\sharp \equiv C6_-\ , & CGA \equiv C6\ , \\ CGB\flat \equiv C7\ , & CGB \equiv Cmaj7\ , & CGC\sharp \equiv C9_-\ , & CGD \equiv C9\ . \end{array} \tag{4.4.1}$$

Table 4.2: Notation of chords inspired by popular music notations.

forced by the model of extended genetic code involving also the 21st and 22nd amino-acids is of special interest.The classes of cycles with symmetries 6-fold rotational symmetry and two distinct reflection symmetries realize it.

Before continuing some terminology and notation is in order. Take C as the major key. Submediant or relative minor corresponds to Am, subdominant (sharp or flat) to F major (F) or Fminor (Fm), dominant to G. The notation for chords is such that quints correspond to subsequent notes in the chord. For 1-quint chords this means that first two notes define the quint. **Table 4.2** the notation inspired by the popular music notation. The basic different is that the third is in most cases excluded so that the emotional character of the chord is not fixed.
Besides these notions it is convenient to introduce additional notations for various dissonant chords appearing as 0-quint chords.

$$\begin{array}{llll} CC\sharp D \equiv Cex1\ , & CC\sharp D\sharp \equiv Cex2\ , & CDD\sharp \equiv Cex3\ , & CDE \equiv Cex4\ , \\ CD\sharp E \equiv Cex5\ , & CC\sharp E \equiv Cex6\ , & CDF\sharp \equiv Cex7\ , & CDG\sharp \equiv Cex8\ . \end{array} \tag{4.4.2}$$

Clearly, the sets {ex1}, {ex2, ex3}, {ex4, ex5, ex6}, {ex7}, {ex8}, corresponds to the span of 2, 3, 4, 6, 8 half notes for the chord. The following summarizes the results. Note that $Cex7$ can be seen as part of $D7$ chord.

1. There are 6 collections of cycles without any symmetries containing 48 cycles each: these 48 cycle are mutually isometric so that one can say that there 6 different harmonies.

2. There is a collection with 6-fold rotational symmetry, 48/6=8 examples. $n = (2, 12, 6)$. The chords of this scale define 6-note scale involving only total steps. CDF and its 6 translates by integer number of steps define 6 1-quint chords. $CE\flat G$ (Cm) and its 6 translates (they obviously correspond to the 6-fold rotational symmetry) define also 6 1-quint chords. The reflection transforms these series to those defined by $GB\flat G$ and its translate and byFAC (F major) and its translates. Impressionists like Debussy used 6-note scale of this kind. Half-octave shift is an exact symmetry. 1-chords lack the third so that one cannot assign to 3-chords any emotional quality. The extension to 4-chord can however bring either "happy" or "sad" quality. Clearly, these harmonies have "jazzy" character.

   0-quint chords are $Faug \equiv FAC\sharp$ and $Gaug \equiv GHD\sharp$ are transformed to each other by both half-octave shift and inversion.

3. There are 2 collections with 2 distinct reflectional symmetries with 12=48/4 representatives in each. Half-octave scaling is a symmetry of both these scales as one might guess.

   The first cycle (see **Fig. ??**) has $n = (0, 16, 4)$ so that there are no 0-quint chords which in general are dissonant. Second cycle (see **Fig. ??**) realizes $n = (4, 8, 8)$ bio-harmony and deserves some comments. It will be discussed in detail later.

   (a) The 8 2-quint chords consist of $B\flat FG \equiv B\flat 9$, C9, F9, G9 and their half-octave scalings. Clearly, the simple four-note scale appears here.

   (b) Using the popular notion introduced earlier 1-quint chords consist of two 4-plets $Dmaj7$, $E9_-$, $A7$, $A6$ and $G\sharp maj7$, $B\flat 9_-$, $D\sharp 7$, $D\sharp 6$ related by half-octave shift. The harmony contains no "simple" major or minor chord and only the extension to tetrahedral harmony can provide them. The same is true for the second bio-harmony.

(c) The 4 0-quint chords are $Cex3 \equiv CDD\sharp$ and $Eex2 \equiv EFG$ and their half-octave scalings $F\sharp ex3 \equiv F\sharp G\sharp A$ and $B\flat ex2 \equiv B\flat BC\sharp G$.

4. There are 3 collections with Z_2 rotational symmetry with $48/2 = 24$ representatives in each. The triplets n are $(0, 16, 4)$ (see **Fig. ??**), $(2, 12, 6)$ (see **Fig. ??**), and $(4, 8, 8)$ (see **Fig. ??**). All these harmonies are symmetric with respect to half-octave shift (tritonus), which obviously corresponds to the Z_2 rotation. Tritonus would not have been tolerated by catholic church! This symmetry characterizes all 3 harmonies. Basic 3-chords do not contain pure minor and major chords. The reflection of the scale does not leave the collection of chords invariant but it is not clear whether this corresponds only to a change of scale, probably not.

   Consider the (4, 8, 8) case (see **Fig. ??**).

   (a) The 8 2-quint chords appear as four-plet $H9, C\sharp 9, D\sharp 9, F9$ and its half octave shift (tritonus interval) acting as a symmetry of the harmony. 2-quint chords are always of type X^9 (note that the third is missing) but also 1-quint chord can be of form X^9 as explicit construction of chords demonstrates: I have denoted these 1-quint chords by symbol $X4$ (CDG is obviously equivalent with CDG).

   (b) Using the popular music notation introduced earlier, the 8 1-quint chords are $D7, Amaj7, A4_+, E7$ and their half-octave shifts $G\sharp 7$, $D\sharp 7, D\sharp 4_+, B\flat 7$.

   No major and minor chords are included and only the extension to tetra-icosahedral harmony can provide them and also break the symmetry giving rise to well-defined key.

5. The four 0-quint chords appear in two types. $D\sharp ex2 \equiv D\sharp EF\sharp$ and its half-octave shift $Aex2 \equiv AB\flat C$ plus $Hex3 \equiv HC\sharp G$ and its half-octave shift $Fex3 \equiv FGC\sharp$. According to usual thinking these chords involve dissonances. This dissonance character is a rather general phenomenon for the harmonic loners and classical views about harmony would exclude them as asocial cases! In the case of maximally symmetric harmony the loners are diminished chords and thus not so dissonant. In some cases there are no 0-quint chords.

There are 5 collections with Z_2 reflection symmetry having 24 representatives in each (see **Figs. ??, ??, ??, ??, ??**). The integer triplets n are $(2, 12, 6), (2, 12, 6), (4, 10, 6), (2, 12, 6), (2, 12, 6)$. Bio-harmony has representative also in this class (see **Fig. ??**). The half-octave scaling symmetry is broken for these harmonies. I have not found simple characterization for the symmetry which corresponds to reflection in the direction of x-axis since it changes the interval structure of the chords.

Some comments $(4, 8, 8)$ case are in order (see **Fig. ??**).

1. 2-quint chords appear as reflection related multiplets $C9, D9, H\sharp 9, D\sharp 9$ and $C\sharp 9, H9, F9, B\flat 9$.

2. 1-quint chords appear as symmetry related mutiplets $G, D7, Amaj7, E7$ and $C\sharp m, F\sharp 6, H6_-, E6$. Key G major and $C\sharp$ minor would be natural looking keys even without tetrahedral extension. For the mirror image $B\flat$ minor and E major would be the natural looking keys. For extension E major would be the key.

To sum up, half octave shift is a symmetry of all harmonies expected those having only Z_2 reflection symmetry, and fails thus also for the corresponding bio-harmonies.

4.4.3 Tables of basic 3-chords for the icosahedral harmonies with symmetries

The tables below give list for the three types of 3-chords for the 11 harmonies possessing symmetries. One must remember that the reversal of the orientation for the cycle induces the transformation $C \leftrightarrow C$, $F\sharp \leftrightarrow F\sharp$, $H \leftrightarrow C\sharp$, $F \leftrightarrow G$, $D \leftrightarrow B\flat$, $E \leftrightarrow G\sharp$, $A \leftrightarrow D\sharp$ and produces a new scale with minor type chords mapped to major type chords and vice versa. Also one must remember that all 3-chords except those which are simple majors or minors lack the third so that their emotional tone remains uncharacterized. For instance, $C6$ does could be replaced with $Cm6$ and $G7$ with $Gm7$. The reader can check the chords by direct inspection of the figures. The convention used is that vertex number one corresponds to C note.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(Faug, Gaug)$	$(Cm, Dm, Em, F\sharp m, G\sharp m, B\flat m)$,	$(C9, D9, E9, F\sharp 9, G\sharp 9, B\flat 9)$.
		$(F6, G6, A6, B6, C\sharp 6, D\sharp 6)$.	

Table 4.3: Table gives various types of 3-chords for harmonies with Z_6 rotational symmetry. Note that half-octave shift is an exat symmetry. Note that $G^{aug} = CEG\sharp, F^{aug}$ act as bridges between the groups related by half octave shift. The chords have been arranged so that they form orbits of Z_6. "Amino-acid chords" correspond to preferred chords at the orbits.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(D7, D6, G\sharp 7, G\sharp 6)$,	$(B\flat 9, B9, E9, F9)$.
		$(G4+, A9-, C\sharp 4+, D\sharp 9-)$,	
		$(Emaj7, Gmaj7, B\flat maj7, C\sharp maj7)$,	
		$(C9-, A9-, F\sharp 9-, D\sharp 9-)$.	
(4, 8, 8)	$(Cex3, Eex2, F\sharp ex3, B\flat ex2)$.	$(Dmaj7, E9-, A7, A6)$,	$(B\flat 9, F9, C9, G9)$.
		$(G\sharp maj7, B\flat 9-, D\sharp 7, D\sharp 6)$.	$(E9, B9, F\sharp 9, C\sharp 9)$.

Table 4.4: Table gives various types of 3-chords for the two harmonies with $Z_4 = Z_2^{rot} \times Z_2^{refl}$ symmetry. 4-plets represent the orbits. First cycle has no harmonic loners. Second cycle gives rise to bio-harmony (4, 8, 8) for which 0-quint chords are dissonant. Both cycles have Z_2 rotation symmetry acting as a vertical reflection symmetry in figures and realized also as half-octave shift so that 4-plets contains chords and their half-octave shifts. The genuine reflection symmetry acts as a horizontal reflection symmetry in figures. The cycles correspond to figures **??**, **??**

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(Em, B\flat m), (Cm, F\sharp m)$,	$(D9, G\sharp 9)$,
		$(G6, C\sharp 6), (A6, D\sharp 6)$,	$(E9, B\flat 9)$.
		$(D4+, G\sharp 4+), (B4+, F4+)$,	
		$(Cmaj7, F\sharp maj7), (G6-, C\sharp 6-)$.	
(2, 12, 6)	$(Aex4, D\sharp ex2)$.	$(Am, D\sharp m), (G9-, C\sharp 9-)$,	$(C9, F\sharp 9)$,
		$(C4, F\sharp 4), (E4+, B\flat 4+)$,	$(A9, D\sharp 9)$,
		$(Dmaj7, G\sharp maj7)$,	$(D9, G\sharp 9)$.
		$(Bmaj7, Fmaj7)$.	
(4, 8, 8)	$(Aex2, Hex8, D\sharp ex2, Fex8)$.	$(D7, G\sharp 7), (Amaj7, D\sharp maj7)$,	$(G9, C\sharp 9), (A9, D\sharp 9)$,
		$(A4+, D\sharp 4+), (E7, B\flat 7)$.	$(B9, F9), (E9, B\flat 9)$.

Table 4.5: Table gives various types of 3-chords for harmonies with Z_2 rotation symmetry acting as half-octave shift. The doublets represent 2-chord orbits. The cycles correspond to figures **??**, **??**, and **??**.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(F\sharp ex3, Hex4)$,	$(Am, D\sharp), (A6, D\sharp 7)$,	$(C9, F9), (B9, F\sharp 9)$,
		$(D7, B\flat 6), (G6-, Fmaj7)$,	$(E9, C\sharp 9)$.
		$(D4+, B\flat 9-), (E9-, G\sharp 4+)$,	
(2, 12, 6)	$(Dex4, Hex4)$.	$(F, Fm), (C6-, B\flat maj7)$,	$(C9, D\sharp 9)$,
		$(D7, G\sharp 6), (Gmaj7, D\sharp 6-)$.	$(D\sharp 9, C\sharp 9)$,
		$(C\sharp 4-, A4+), (E4+, F\sharp 6)$.	$(E9, B9)$.
(4, 8, 8)	$(Fex1, D\sharp ex3, G\sharp ex1, Aex2)$.	$(E7, E6), (Amaj7, B9-)$,	$(D9, B9), (C9, C\sharp 9)$,
		$(G, C\sharp m), (D7, F\sharp 6)$.	$(F9, G\sharp 9), (D\sharp 9, B\flat 9)$.
(2, 12, 6)	$(Hex3, Eex7)$.	$(D7, G\sharp 6), (G, D\sharp m)$,	$(C9, D\sharp 9)$,
		$(F, Fm), (C6-, B\flat maj7)$,	$(D9, C\sharp 9)$,
		$(A9-, C\sharp 4+), (E7, F\sharp 6)$.	$(E9, B9)$.
(2, 12, 6)	$(F\sharp ex2, Fex3)$.	$(F, B\flat m), (C7, G\sharp 6)$,	$(B\flat 9, D\sharp 9)$,
		$(Amaj7, B9-), (E6, E7)$,	$(C9, C\sharp 9)$,
		$(G, C\sharp m), (D7, B6)$.	$(D9, H9)$.

Table 4.6: Table gives various types of 3-chords for harmonies with single reflection symmetry. The cycles correspond to figures **??**, **??**, **??**, **??**, **??**.

4.5 New results related to the notion of bio-harmony

This section contains some new results related to music harmony. During 2018 some new results related to the model of bio-harmony emerged. In the sequel they are collected together.

Remark :In the sequel I will use the shorthand AA for amino-acids and shorthands DDNA, DRNA, DtRNA, DAA for the dark analogs of DNA, RNA, tRNA, and AA realizes as dark proton sequences with codon represented as dark proton triplet.

4.5.1 Summary of the background

For some years ago I developed a model of music harmony [L11] (see `http://tinyurl.com/yad4tqwl`), which should define map of dark codons to 3-chords represented as dark photon triplets and defining allowed 3-chords of music harmony (music of light and perhaps also of sound). The Appendix provides the tables describing the details of the harmonies.

1. The model relies on the geometries of icosahedron and tetrahedron and representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron [A19, A7, A16, A5, A12]. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 AAs.

   Single step of Hamiltonian cycle connecting vertices of a face of icosahedron (triangle) is assume to correspond to a scaling of the frequency by factor 3/2. This leads to a problem since 12 scalings of this kind does not quite given 7 octaves which reduced octave equivalence to the basic octave would give 12-note scale. The solution is to add single note slightly differing from 7 octaves and represented as vertex P of a tetrahedron glued to icosahedron along face. The Hamilton cycles are deformed so that they begin and end from this vertex. This also gives the missing 4 DNA codons realized as 3-chords and also defines unique ground note for the scales.

2. One obtains 3 basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6, Z_4 or Z_2. For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle.

   Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA.

4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint. The model predicts a highly unique and realistic model for numbers of DNA codons coding for a given AA. The model in its original form predicts two codes and also explains the fact that there are two additional AAs Pyl and Sec that appear as end-products.

3. AAs correspond to single 20-codon code, DNA and RNA to a union of 3 20-codon codes with symmetries Z_6, Z_4 or Z_2: here Z_2 would correspond to $Z_{2,rot}$ or $Z_{2,refl}$ and this would give to two two different codes.

4. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA.

   Music expresses and creates emotions and the natural proposal is that these bio-harmonies correlate with moods that would appear already at molecular level. They could be realized in terms of dark photon triplets realized in terms of light and perhaps even music (living matter is full of piezo-electrets). In fact, also the emotions generated by other art forms could be realized using music of dark light. [L64]. Dark photons in various wavelength ranges and correspond to various values of h_{eff} would correspond to various sensory qualia and are represented at pineal gland ("third eye") as imagined sensory percepts [L42]. They can be transformed to real sensory percepts at sensory organs by using DMT molecules as bridges allowing the propagation of dark photons (or the bio-photons resulting in their energy conserving transformation to ordinary photons) to sensory organs, where they generate genuine sensory experience identified as dream, psychedelic experience, hallucination, etc...

The model of music harmony is separate from the model of genetic code based on dark proton triplets [L27] and one of the challenges has been to demonstrate that they are equivalent. One can raise several questions.

1. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton's cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied.

   (a) There is purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20.

   (b) There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies.

2. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could AAs couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA?

3. As I developed the model of bio-harmony [L11] (see `http://tinyurl.com/yad4tqwl`) it did not occur to me that also the tRNA part of the dark code should have counterpart in the icosahedral model. Could tRNA correspond to pairs of harmonies with 20+20+4=44 codons? What about single 20+4=24 codon representation as kind of pre-tRNA? Could tRNA correspond to a union of 2 20-codon codes? Combining only 2 20-codon codes with 40 codons and tetrahedral code with 4 codons would give maximally 44-letter code and the upper bound for tRNAs is according to Wikipedia 45! Dark proton model predicts 40 DtRNAs suggesting that only the 40 isosahedral codons contribute to DtRNA code. The additional tRNAs could result from homonymy. The code sequences could be seen as a hierarchical sequence $3 \to 2 \to 1$ in this framework.

   An important implication is that there are many realizations of DtRNA and tRNA harmony: (Z_6, Z_4), (Z_6, Z_2), (Z_4, Z_2) and Z_2 could be either $Z_{2,rot}$ or $Z_{2,refl}$. This could explain the

homonymy of mRNA-tRNA pairing via difference in the chords in turn affecting biochemical counterparts. Note however that the chords for tRNA must be a subset of chords for mRNA so that RNA harmony determines tRNA harmony apart from the three choices (Z_6, Z_4), (Z_6, Z_2) or (Z_4, Z_2) giving rise to 3 different contexts. If DAAs code by 3-chords the AAs then this choice does not affect AAs.

4. What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetry arguments fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible so that it would be possible to listen what DNA sequences sounds in given mood characterized by the harmony.

5. What disharmony could mean? A possible answer comes from 6 Hamiltonian cycles having no symmetries. These disharmonies could express "negative" emotions.

4.5.2 Some questions about the realization of the bio-harmony

In the sequel by I will proceed by posing questions related to the relationship between the 3 representations of genetic code [K87] in terms of bio-molecules, their dark analogs represented as sequences dark proton triplets, and as 3-3-chords of bio-harmony.

What conditions pairings pose on the frequency triplets?

The realization of DDNA-DtRNA and DDNA-DAA pairings in terms of frequencies must involve a loss of information since the correspondence is many-to-one.

1. For DNA-mRNA pairing information is not lost and the pairing must be of form $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$. Note that the frequencies cannot be associated with the letters. It is however possible to consider the assignment of (f_1, f_2) to the first letter pair XY as a whole and f_3 to the third letter Z.

2. For DDNA-DAA and DmRNA-DAA pairing the natural hypothesis is $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$. AA couples to the sum of the frequencies of the triplet. The simplest possibility is that the $f_1 + f_2 + f_3$ is same for all codons codin for given AA. One might say that AA sequence defines melody and mRNA sequence the accompaniment.If the sums for codons coding given AA are different they must couple resonantly to it. If there are several harmonies the sum must same for all realizable 3-harmonies or all chords of 3-chord harmonies coding for same AA couple to it resonantly. Since one has linear 1-D structures one might ask whether frequency differences coming as multiples of lattice frequencies are allowed. Second natural possibility is octave equivalence. mRNA-AA pairing would take place directly rather than with the mediation of of tRNA.

3. In the case of DmRNA-DtRNA pairing one one does not lose so much information since the number of dark DNAs is 40 (as also the 3-chords if tetrahedron does not contribute). One must remember that tRNAs are pairs of RNA like codons - call them RNA_t, and AAs. Therefore there pairing involves also the pairing mRNA-AA give by $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$ and guaranteeing that the code is realized by this pairing alone irrespective of mRNA-RNA_t pairing. At chemical level the first to mRNA codons pair with tRNA anticodons according to the standard rules. Could RNA_t have completely passive role in carrying the AA? This cannot be the case since the last two letters of RNA_t couple in standard manner to the first two letters of mRNA.

   Remark: tRNA is analogous to melody + accompaniment using one of the 3 possible 2-harmonies for a given 3-harmony.

   Suppose that mRNA-RNA_t pairing corresponds to 3 possible choices of 2-harmonies as sub-harmonies of 3-harmony. This would suggest these different sub-harmonies define maps $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$ such that RNA_t pairs only with two sub-harmonies. For each choice RNA_t would correspond effectively to 40 sub-codons of the entire code (forgetting the

tetrahedral part giving 4 additional codons). The three different realizations of the projection would give rise to the homonymy. Also the AA-trNA coupling would come out correctly.

DAAs would be different in the sense that they couple only to the sum of the frequencies. This is in accordance with bio-harmony in which AAs correspond to orbits of 3-chords for DNA under isometries rather than single 20-chord harmony. The coupling to the sum of frequencies is in accordance with the quantal interpretation as 3-dark-photon state whose energy is $E = h_{eff}(f_1 + f_2 + f_3)$ and couples to AA chemically via the transition to ordinary photons with the same energy.

This leaves some questions.

1. Could one consider the possibility that the chords of one of the 20-chord harmonies corresponds to AAs? There would be 3 basic types of AAs. This does not look plausible and the association of AAs with the orbits of 20-note chords is more natural and fits nicely with $f = f_{XYZ}$ picture.

2. It would be nice to assign notes to the individual letters of codons. This is not possible since codons with 2 or 3 identical letters would reduce to 2-chords or 1-chords. It is also impossible to assign frequencies with letters at dark level since letter decomposition does not exist. Thus the 3-chord has resonant interaction with the entire codon.

3. The symmetries of the genetic code however suggest that it might make sense to treat the first two letters XY of the codon as a single unit and the third letter as separate single unit. Could one assign to XY a 2-chord not reducible to frequencies for the letters X and Y, and to letter Z its own frequency. The frequencies of A, G, T, C as third letter must be different. Four 32 codons of standard code the AA would not be sensitive to the frequency of Z: this is possible if these frequencies are resonance frequencies of the same AA. For the remaining 32 codons the AA would not distinguish between frequencies of T and C *resp.* A and G so that the two frequencies would be both resonance frequencies of the corresponding AA.

Probabilistic estimates for single 20-chord harmony

One can make first some naïve probabilistic estimates about single 20-chord harmony.

1. Given 20-chord harmony makes $20/220 = 1/11 \simeq 9$ per cent about al possible 3-chords. Three 20 chord harmonies would make $3 \times 9 = 27$ per cent about all possible 3-chords if there are no common chords so that the optimistic expectation might make sense. Of course, one cannot exclude the possibility that there are also triplets of 20-codon codes which gives smaller number of codons.

2. The total number of chords with different notes is $12 \times 11 \times /3! = 220$. Bio-harmony has 64 chords corresponding to faces of icosahedron: this is about $64/220$ making 29 per cent of all possible 3-chords with different notes. Given bio-harmony thus throws out roughly $2/3$ of all possible codons. This should be easy to test. For instance, does given gene correspond to a fixed bioharmony? Or does even entire genome do so. If bio-harmony is realized for non-nuclear genomes, it must satisfy rather strong constraints.

3. Given 20-chord harmony corresponds to 12 edges. Each edge is shared by two adjacent triangles. If all 20 triangles would contain just single face, there would be 24 triangles altogether. Therefore there must be triangles containing two subsequent edges of the cycle. Each triangle of this kind reduces the number of 24 neighbours by 2 units. Hence it seems that one must have at least 2 triangles with 2 edges at the cycle (two quints in the 3-chord).

   If there are more than 2 triangles of this kind, there must be triangles having no edges along the path. Each vertex of icosahedron is shared by 5 triangles and there are 5 edges starting from it.

4. The notion of Hamilton cycle generalizes to any graph and magnetic flux tube networks define such graphs as tensor networks. Why only icosahedron? Could one consider the possibility that any tensor network is characterized by harmonies characterize by Hamiltonian cycles

and that one could assign some kind of codes with the combinations of these cycles? In the general case symmetries would be absent so that the notion of code in the proposed sense would fail: one could not identified codons as points at orbits of symmetry group. Rather, one can imagine that the notion of code could be defined quite generally in terms of orbits as AAs and points at them as DNAs coding them. For regular polygons in any dimension the symmetries are present and one could define the notion of code and also fuse the codes.

For arbitrary tensor network the faces need not be symmetry related and one can also have faces that can be interpreted as higher-dimensional polytopes.

One can also ask whether the icosahedron is realized physically. Icosahedral geometry is indeed very common in biology. Could the fusion of icosahedral and tetrahedral geometries have some concrete realization at molecular level?

Is the maximal number of codons for the fusion of 3 20-codon codes possible?

It has not earlier occurred to me to wonder whether the chords associated with the 3-different icosahedral harmonies giving 20 codons each correspond to 20+20+20=60 different chords as assumed. Could there be common 3-chords? This question could be answered by studying the Hamiltonian cycles at icosahedron.

Remark: Perhaps more important constraint than absence of common chords is the chemical realizability of the codes. If same mRNAs and DNAs realized different bio-harmonies then they must be able to respond resonantly to several 3-chords.

One can make naïve probability estimates for a pair of codes to allow the maximal number of 60 codons. It seems natural to assume that the isometries of icosahedron (or their subgroup) can be applied separately and only the isometries acting on both in similar manner are symmetries. The situation would be the same as in the case of many-particle system: only the translations acting on all particles simultaneously remain symmetries and relative translations cease to be symmetries.

With this assumption the icosahedral group gives a large number of code pairs. For the fusion of 3 20-codon codes giving DNA/RNA the number is even higher. By choosing suitably the relative isometries it might be possible to obtain the maximal number of 60 different codons for the icosahedral genetic code. On the other hand, by a suitably choice of relative isometries one might have undesired common 3-chords. In any case, the earlier estimate 256 for the number of bio-harmonies [L11] suggested to correlate with "emotional" states of the basic biomolecules is expected to change.

Before going to estimates one must consider some delicacies related to the notion of 12-note scale as Hamiltonian cycle.

1. One can regard the cycles as purely geometric objects without orientation or assign to them orientation. For two different orientations the scales would run in opposite directions as scalings by 3/2 along single edge of the cycle. If two codes have common edge, the scaling must be same along it. If the orientation of the second cycle is changed, the common edge ceases to be common.

2. The basic note of the 12-note scale at cycle can be chosen arbitrarily: this corresponds to the choice of the key in music (one could of course argue that the key does not make sense in 12-note scale if one has tempered scale with notes comes as powers of $2^{1/2}$ scaling of ground note rather than Pythagorean scale with rational ratios of notes).

   The fusion of tetrahedron to icosahedron selects one particular triangular face and brings in one additional vertex outside the icosahedron, call it P. It would be natural to assign the ground note as P. The isometries not affecting P would correspond to those of icosahedron leaving the common face invariant and isometries of tetrahedron leaving P un-affected and continuable to icosahedral isometries. One would have subgroup of icosahedral group as allowed isometries acting on the cycles to be fused.

3. If one assigns note sequences to the cycle by quint rule, cycles C_1 and C_2 can have common triangle in geometric sense but if the distances of the vertices A, B, C of the triangles from P measured as the number of edges of cycle portion connecting them are not same along C_1 and C_2, the triangles correspond to different chords and are thus orthogonal in the proposed description as many-fermion states.

4. To sum up, the states associated with triangles would be characterize by the position of triangle (20 values), by the notes of the triangle characterized by the distances from P, and the number 0, 1, 2 of the edges belonging to the cycle and should make easier to find ortogonal basis.

Again one can make probabilistic estimates: cycles are treated as purely geometric entities without orientation and without assignment of notes to the triangles.

1. Given cycles C_1 and C_2 what is the probability that they have at least one common edge as purely geometric entities without the sequence of notes? There are 30 edges so that given edge is shared with probability 1/30. If the edges of cycles were chosen randomly (certainly not true), the probability of having a common edge for two cycles would be $P(1) = 12/30$. The assumption of note sequence reduces this probability dramatically.

2. By the above estimate each cycle contains at least two triangles with 2 edges at the cycle with minimal angle between them. One can call these these edge pairs V-corners. Assume that for cycle C_1 one has V-corner ABC at vertex A, call it $V_{1,A}$. What is the probability that one one of the V-corners of C_2 is located at A coincides with ABC. The probability of V-corner of C_2 to locate at A is 1/12 and the probability that the edge of C_2 from B is BC is is 1/4 so that the probability of having common V-corner is 1/48. If C_2 contains n V-edges the probability is naïvely $n/48$.

   This estimate takes into account only geometry. The situation changes if one assumes that the cycles are oriented. In this case one can have common V-corner if the local orientations of C_1 and C_2 are opposite at the V-corner. If one assumes that the external vertex P of the tetrahedron defines the ground note then the number of edges connecting P to A defining distance $d(P, A)$ must be same for C_1 and C_2.

3. Given C_1 and C_2 (and vertices A with same distance $d(P, A)$) it might be possible to perform suitable isometry for C_2 that there is common V-corner. Therefore not all possible combinations of three code types allowing relative isometries need not maximal number of 3-chords.

   Remark: An interesting question is whether these can be allowed meaning that some codons are missing in the chemical realization of the dark codons in terms of ordinary DNA codons. Also the 1-1 pairing between dark DNA and and dark RNA would not be 1-1 if mediated by 3-chord resonance and one would have homonymy. This suggests that only codes without common chords can be allowed.

4. What about chords having 1 edge at cycle for two cycles C_1 and C_2? Let the edge be AB. As found, the naïve probability for this is $P(1) = 12/30$. Both cycles must go through the third vertex C of the triangular face. The subsequent notes along cycle differ by a quint that is scaling of the frequency by factor 3/2. Notes are same if the numbers of the needed quints are same for C_1 and C_2 For C_1 the number $n_B > 1$ of quints is known. In the approximation that possible portions of C_1 represent n-step non-self-intersecting random walks from B to C, one must estimate the number of all non-self-intersecting n-step-paths from B to C and find what is the number of the paths leading to C. One can go from A to C with n_A steps and similar estimate applies.

5. The third possibility is that the one has 3 common vertices A, B, C forming a triangular face such that neither cycle contains any of its edges.

The cautious conclusion is that it is plausible that one can find 3 cycles having no common chords if one allows relative rotations of the cycles and that this condition is necessary for realizing the absence of homonymies at dark level. The automatic orthogonality of the Hamiltonian cycles cannot be excluded but would allow also codes with codons containing more than 3 letters so that one could have kind of super-DNA. Whether they can be realized chemically depends on whether there are biomolecules resonating with the the n frequency triplets involved. Octave equivalence for frequencies might give hopes about chemical realization of several harmonies. Therefore the evolution might be seen as gradual emergence of molecules able to pair with DDNA and one can even imagine artificial evolution by tailoring the frequencies involved (maybe cyclotron frequencies).

How the symmetries of the model of harmony could relate to those of the genetic code?

Genetic code has surprisingly strong symmetries. I have discussed a possible interpretation of these symmetries using analogies with particle physics and considered also a mechanism explaining their emergence earlier [K4, ?]. The proposal was that 3-letter code emerged as a fusion of 2-letter code with 16 codons and 1-letter coded with 4 codons. In the recent framework, a more natural option is that the third codon of 3-letter code was originally passive and became active via symmetry breaking distinguishing first between UC and AG pairs and later between U and C *resp.* A and G. Note that for the standard code the breaking is minimal and caused by odd number of Start and Stop codons.

1. For vertebrate code one half of codons has very high symmetry in the sense that the two first letters dictate the AA for 32 cases. Exception is UUU, which codes for Phe or Leu for some modifications of the standard code. UUU $\rightarrow$ Leu means breaking of maximal symmetry.

2. There is also a second symmetry, which I have referred to as isospin symmetry. It is only slightly broken. For general codons XYU and XYC code for same AA as also XYA and ad XYG. For the standard code this symmetry is broken only in columns containing initiation codon or stop. The Start codon AUG codes also for met. UGA and UGG code for Stop and Trp. For the remaining codons one has slightly broken "isospin symmetry". The breaking of isospin symmetry is minimal for vertebrate code. The modifications of the code tend to break the isospin symmetry and even the maximal symmetry of 32 codons. This must be important.

If the model of genetic code based on music harmony [L11] is correct, the symmetries for the model of music harmony must relate to those of genetic code.

1. How the symmetries of the genetic code relate to the symmetries of icosahedron (60-element group) and tetrahedron (permutation group S_4 with 24 elements) in the model of bio-harmony? Icosahedral symmetry group has 60 elements and has sub-groups $Z_2, Z_4, Z_5, Z_6 = Z_2Z_3$. Note that there are two Z_2:s having rotation by π and reflection as generators.

   The gluing of tetrahedron to icosahedral along single face reduces its group of symmetries to S_3 leaving the point P not belonging to icosahedron invariant. S_3 has as subgroups reflection group $Z_{2,refl}$ and Z_4 consisting of rotations.

2. What is the counterpart for maximal symmetry in icosahedral and tetrahedral groups? Do the 3-chords for codon XYZ decompose to two-chord characterizing XY and a note characteriing Z= A,U,C,G, which can depend on XY. The symmetry relating UC pair and AC pair could correspond to $Z_{2,refl}$ reflection symmetry, which is shared by icosahedral and tetrahedral groups. For 32 icosahedral codons the action of $Z_{2,refl} \times Z_{2,rot}$ would be trivial so that AA would not depend on the third letter at all. For most of the remaining codons the action of the symmetry group on icosahedral codons would reduce to $Z_{2,rot}$ permuting the third letters U and C *resp.* A and G. At the level of frequencies the sums of frequencies for codons coding for the same AA sould be same modulo octave equivalence.

   The addition of tetrahedron brings in 4 tetrahedral codons with one of them shared with icosahedron. Icosahedral $Z_{2,rot}$ does not make sense for these codons. Intriguingly, there are 4 codons in vertebrate code which break isospin symmetry AUA and AUG coding for I and Met/start and UGA and UGG coding for Stop and Trp. If these codons correspond to the tetrahedral codons which cannot have $Z_{2,rot}$ as isospin symmetry, the breaking of $Z_{2,rot}$ would follow from the breaking of symmetry induced by the attachment of tetrahedron to icosahedron.

What is the origin of 12-note scale?

One fundamental question is why dark photon realization of genetic code should involve 12-note scale as icosahedral model requires.

Remark: The gluing of tetrahedral codons gives 4 additional codons but if tetrahedron is glued to icosahedron along one of its faces, the additional vertex gives only one additional note,

which should be very near to the 12:th one. This could relate to the basic problem observed already by Pythagoras that 12-note Pythagorean scale with rational valued frequency ratios does not quite close.

A popular article in Spacedaily with title "*Scientists crack how primordial life on Earth might have replicated itself*" (see `http://tinyurl.com/y92ng5vd`) led to a possible answer to the above question. The research paper [I46] is titled "*Ribozyme-catalysed RNA synthesis using triplet building blocks*" and published in eLife (see `http://tinyurl.com/ya5qyjfn`).

It is possible to replicate unfolded RNA strands in Lab by using enzymes known as ribozymes, which are RNA counterparts of enzymes, which are amino-adic sequences. In the presence of folding the replication is however impossible. Since ribozymes are in general folded, they cannot thus catalyze their own replication in this manner. The researchers however discovered that the replication using RNA triplets - genetic codons - as basic unit can be carried out in laboratory even for the folded RNA strands and with rather low error rate. Also the ribozyme involved can thus replicate in codon-wise manner. For units longer than 3 nucleotides the replication becomes prone to errors.

These findings are highly interesting in TGD framework. In TGD the chemical realization of genetic code is not fundamental. Rather, dark matter level would provide the fundamental realizations of analogs of DNA, RNA, tRNA, and amino-acids as dark proton sequences giving rise to dark nuclei at magnetic flux tubes [L58] (see `http://tinyurl.com/yalny39x`). Also ordinary nuclei correspond in TGD Universe to sequences of protons and neutrons forming string like entities assignable to magnetic flux tubes.

The basic unit representing DNA, RNA and tRNA codon and amino-acid would consist of 3 entangled dark protons. The essential aspect is that by entanglement the dark codons do not decompose to products of letters. This is like words of some languages, which do not allow decomposition to letters. This representation is holistic. As we learn to read and write, we learn the more analytic western view about words as letter sequences. Could the same hold true in evolution so that RNA triplets would have come first as entities pairing with dark RNA codons from from dark proton triplets as a whole? Later DNA codons would have emerged and paired with dark DNA codons. Now the coupling would have have been letter by letter in DNA replication and transcription to mRNA.

It is intriguing that tRNA consists of RNA triplets combined from amino-acids and analogs of mRNA triplets! The translation of mRNA to amino-acids having no 3-letter decomposition alone forces the holistic view but one can ask whether something deeper is involved. This might be the case. I have been wondering whether during RNA era RNA replicated using a prebiotic form of translational machinery, which replicated mRNA rather than translated RNA to protein formed from amino-acids (AAs) with AA serving as a catalyst.

1. During RNA era amino-acids associated with pre-tRNA molecules would served as catalysts for replication of RNA codons. The linguistic mode would have been "holistic" during RNA era in accordance with the findings of the above experiments. RNA codon would have been the basic unit.

2. This would have led to a smaller number of RNAs since RNA and RNA like molecules in tRNA are not in 1-1 correspondence. A more realistic option could have been replication of subset of RNA molecules appearing in tRNA in this manner.

3. Then a great evolutionary leap leading from RNA era to DNA era would have occurred. AA catalyzed replication of RNA would have transformed to a translation of RNA to proteins and the roles of RNA and AA in tRNA would have changed. [Perhaps the increase of h_{eff} in some relevant structure as quantum criticality was reached led to the revolution]

4. At this step also (subset of) DNA and its transcription to (a subset of) mRNA corresponding to tRNA had to emerge to produce mRNA in transcription. In the recent biology DNA replicates and is transcribed nucleotide by nucleotide rather than using codon as a unit so that helicases and DNA and RNA polymerases catalyzing replication and transcription should have emerged at this step. The ability of DNA to unwind with the help of helicase enzyme helping DNA to unwind is essential for the transcription and translation of DNA. Therefore helicase must have emerged together with the "analytic linguistic mode" as an analog of

written language (DNA) decomposing codons to triplets of letters. This would been a crucial step in evolution comparable to the emergence of written language based on letters. Also the counterpart of RNA polymerase and separate RNA nucleotides for transcription should have emerged if not already present.

An alternative option would involve "tDNA" as the analog of tRNA and the emergence of helicase and polymerases later as the transition from holistic to analytic mode took place.

The minimal picture would be emergence of a subset of DNA codons corresponding to RNAs associated with pre-tRNA and the emergence of the analogs of helicase and DNA and RNA polymerases as the roles of amino-acid and RNA codon in tRNA were changed.

5. How DNA could have emerged from RNA? The chemical change would have been essentially the replacement of ribose with de-oxiribose to get DNA from RNA and U→ T. Single O-H in ribose was replaced with H. O forms hydrogen bonds with water and this had to change the hydrogen bonding characteristics of RNA.

   If the change of $h_{eff} = n \times h_0$ was involved, could it have led to stabilization of DNA? Did cell membrane emerge and allow to achieve this? I have proposed [L58] (see `http://tinyurl.com/yalny39x`) that the emergence of cell membrane meant the emergence of new representation of dark genetic code based on dark nuclei with larger value of h_{eff}.

   Remark: One has $h = 6 \times h_0$ in the most plausible scenario [L31, L63] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`).

One can of course ask whether something simpler could be imagined by utilizing the potential provided by dark variants of bio-molecules present already from beginning and providing both genes and metabolism simultaneously.

1. Viruses are probable precedessors of cellular life. So called positive sense single stranded RNA (ssRNA) associated with viruses can form temporarily double strands and in this state replicate just like DNA (see `http://tinyurl.com/yc5f8b3t`). The resulting single stranded RNA can in turn be translated to proteins by using ribosomal machinery. RNA replication takes place in so called viral replication complexes associated with internal cell membranes, and is catalyzed by proteins produced by both virus and host cell.

   Could ribozyme molecules have catalyzed RNA replication during RNA era? For this option AA translation would have emerged later and the storage of genetic information to DNA only after that. There is however the question about the emergence of AAs and of course, DNA and RNA. Which selected just them from enormous variety of options.

2. Lipid membranes are formed by self-organization process from lipids and emerge spontaneously without the help of genetic machinery. It would be surprising if prebiotic life would not have utilized this possibility. This idea leads to the notion of lipid life as a precedessor of RNA life. In this scenario metabolism would have preceded genes (see `http://tinyurl.com/y7ehv8cq` and `http://tinyurl.com/y8nltb9e`). The basic objection against both genes-first and metabolism-first options is that they need each other!

3. In TGD framework the dark variants of DNA, RNA, AA, and tRNA would provide the analogs of genes and all basic biomolecules. They would also provide a mechanism of metabolism in which energy feed by (say) solar radiation creates so called exclusion zones (EZs) of Pollack [L15] in water bounded by a hydrophilic substance. EZs are negatively charged regions of water giving rise to a potential gradient (analog of battery) storing chemically the energy provided by sunlight and the formation of these regions gives rise to dark nuclei at magnetic flux tubes with scaled down binding energy.

   When the p-adic length scale of these dark nuclei is liberated binding energy is liberated as metabolic energy so that metabolic energy feed giving basically rise to states with non-standard value $h_{eff}/h = n$ of Planck constant is possible. For instance, processes like protein folding and muscle contraction could correspond to this kind of reduction of h_{eff} liberating energy and also a transformation of dark protons to ordinary protons and disappearance of EZs.

The cell interiors are negatively charged and this is presumably true for the interiors of lipid membranes in general and they would therefore correspond to EZs with part of protons at magnetic flux tubes as dark nuclei representing dark variants of basic biomolecules. Already this could have made possible metabolism, the chemical storage of metabolic energy to a potential gradient over the lipid membrane, and also the storing of the genetic information to dark variants of biomolecules at the magnetic flux tubes formed in Pollack effect.

4. In TGD framework biochemistry would have gradually learned to mimic dark variants of basic processes as a kind of shadow dynamics. Lipid membranes could have formed spontaneously in water already during prebiotic phase when only dark variants of DNA, RNA, AAs and tRNA, water, and lipids and some simple bio-molecules could have been present. The dark variants of replication, transcription and translation would have been present from the beginning and would still provide the templates for these processes at the level of biochemistry.

   Dark-dark pairing would rely on resonant frequency pairing by dark photons and dark-ordinary pairing to resonant energy pairing involving transformation of dark photon to ordinary photon. The direct pairing of basic biomolecules with their dark variants by resonance mechanism could have led to their selection explaining the puzzle of why so few biomolecules survived.

   This is in contrast with the usual view in which the emergence of proteins would have required the emergence of translation machinery in turn requiring enzymes as catalyzers so that one ends up with hen-or-egg question: which came first, the translation machinery or proteins. In RNA life option similar problem emerges since RNA replication must be catalyzed by ribozymes.

5. Gradually DNA, RNA, tRNA, and AA would have emerged by pairing with their dark variants by resonance mechanism. The presence of lipid membranes could have been crucial in catalyzing this pairing. Later ribozymes could have catalyzed RNA replication by the above mentioned mechanism during RNA era: note however that the process could be only a shadow of much simpler replication for dark DNA. One can even imagine membrane RNAs as analogs of membrane proteins serving as receptors giving rise to ionic channels. Note however that in TGD framework membrane proteins could have emerged very early via their pairing with dark AA associated with the membrane. These membrane proteins and their RNA counterparts could have evolved into transcription and translation machineries.

   DNA molecules would have emerged through pairing with dark DNA molecules. The difference between deoxi-ribose and ribose would correspond to the difference between dark RNA and dark DNA manifesting as different cyclotron frequencies and energies making possible the resonant pairing for frequencies and energies. Proteins would have emerged as those proteins able to pair resonantly with dark variants of amino-acid sequences without any pre-existing translational machinery. It is difficult to say in which order the basic biomolecules would have emerged. They could have emerged even simultaneously by resonant pairing with their dark variants.

The communication between dark ordinary variants of biomolecules involves resonance mechanism and would also involve genetic code represented as 3-chords, music of light, and it is interesting to see whether this model provides additional insights.

1. The proposal is that 3-chords assignable to nucleotides as music of light with allowed 64 chords defining what I have called bio-harmony is essential for the resonance [L64, L67, L63](see `http://tinyurl.com/ydhxen4g`, `http://tinyurl.com/yd5t82gq`, and `http://tinyurl.com/y9jxyjns`). The 3 frequencies must be identical in the resonance: this is like turning 3 knobs in radio. This 3-fold resonance would correspond to the analytic mode. The second mode could be holistic in the sense that it would involve only the sum only the sum of the 3 frequencies modulo octave equivalence assigning a melody to a sequence of 3-chords.

2. The proposal is that amino-acids having no triplet decomposition are holistic and couple to the sum of 3 frequencies assignable to tRNA and mRNA in this manner. Also the RNAs in

tRNA could couple to mRNA in this manner. One could perhaps say that tRNA, mRNA and amino-acids codons sing whereas DNA provides the accompaniment proceeding as 3-chords. The couplings of DNA nucleotides to RNA nucleotides would rely on the frequencies assignable to nucleotides.

3. If the sum of any 3 frequencies associated with mRNA codons is not the same except when the codons code for the same amino-acids, the representation of 3-chords with the sum of the notes is faithful. The frequencies to DNA and RNA nucleotides cannot be however independent of codons since the codons differing only by a permutation of letters would correspond to the same frequency and therefore code for the same amino-acid. Hence the information about the entire codon would be needed also in transcription and translation and could be provided either by dark DNA strand associated with DNA strand or by the interactions between the nucleotides of the DNA codon.

4. The DNA codon itself would know that it is associated with dark codon and the frequencies assignable to nucleotides could be determined by the dark DNA codon. It would be enough that the frequency of the letter depends on its position in the codon so that there would be 3 frequencies for every letter: 12 frequencies altogether.

   What puts bells ringing is that this the number of notes in 12-note scale for which the model of bio-harmony [L11, L64] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/ydhxen4g`) based on the fusion of icosahedral (12 vertices and 20 triangular faces) and tetrahedral geometries by gluing icosahedron and tetrahedron along one face, provides a model as Hamiltonian cycle and produces genetic code as a by-product. Different Hamiltonian cycles define different harmonies identified as correlates for molecular moods.

   Does each DNA nucleotide respond to 3 different frequencies coding for its position in the codon and do the 4 nucleotides give rise to the 12 notes of 12-note scale? There are many choices for the triplets but a good guess is that the intervals between the notes of triplet are same and that fourth note added to the triplet would be the first one to realize octave equivalence. This gives uniquely $CEG\sharp$, $C\sharp FA$,$DF\sharp B\flat$, and $DG\sharp B$ as the triplets assignable to the nucleotides. The emergence of 12-note scale in this manner would be a new element in the model of bio-harmony.

   There are 4!=24 options for the correspondence between $\{A,T,C,G\}$ as the first letter and $\{C,C\sharp,D,D\sharp\}$. One can reduce this number by a simple argument.

   (a) Letters and their conjugates form pyrimidine-purine pairs T,A and C,G. The square of conjugation is identity transformation. The replacement of note with note defining at distance of half-octave satisfies this condition (half-octave - tritonus - was a cursed interval in ancient music and the sound of ambulance realizes it). Conjugation could correspond to a transformation of 3-chords defined as

   $$CEG\sharp \leftrightarrow DF\sharp B\flat \quad , \quad C\sharp FA \leftrightarrow D\sharp GB \quad .$$

   (b) One could have

   $$\{T,C\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \quad , \quad \{A,G\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \quad ,$$
   $$\text{or}$$
   $$\{T,C\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \quad , \quad \{A,G\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \quad .$$

   .

   (c) One can permute T and C and A and G in these correspondences. This leaves 8 alternative options. Fixing the order of the image of (T,C) to say $(C,C\sharp)$ fixes the order of the image of (A,G) to $(D,D\sharp)$ by the half-octave conjugation. This leaves 4 choices. Given the bio-harmony and having chosen one of these 4 options one could therefore check what given DNA sequence sounds as a sequence of 3-chords [L11].

That the position the frequency associated with the nucleotide depends on its position in the codon would also reflect the biochemistry of the codon and this kind of dependence would be natural. In particular, different frequencies associated with the first and third codon would reflect the parity breaking defining orientation for DNA.

What disharmony could mean?

Harmonies - also those, which are sad (consider only passions of Bach) - are usually thought of as something beautiful. Could negative emotions really correspond to any bio-harmonies characterized by symmetries. In a discussion with Sini Kunnas I realized that also the notion of disharmony could make sense. There are indeed 6 Hamiltonian cycles without any symmetries [A7, A12, A5]. I neglected them in the model of harmony because they would represent which one might call disharmony. Could one of the contributing 3 Hamiltonian cycles in bio-harmony correspond to this kind of dis-harmony and bring in 20 3-chords without any symmetries? If so the relationship between geometry and aesthetics would become very concrete. The alternative view would be that there are several harmonies realized simultaneously and thi creates disharmony.

The faces of the icosahedron belonging to the orbits of the symmetries of the harmony correspond to DNA codons coding for the same AA assignable to the orbit. The fact that there are no symmetries for these 6 bio-disharmonies, suggests one-to-one correspondence between DNA and AAs if also stop codon corresponds to ordinary AA.

How to concretely realize emotions as music of light?

Music expresses emotions and also create higher level emotions. As all art, it also induces experience of beauty. Since $h_{eff}/h = n$ [K22, K23, K24, K25, K61] serves as a kind of IQ in the evolutionary hierarchy, there are good reasons to expect that the emotions/feelings induced by music and other art forms are assignable to MB.

The dynamics of MB involves oscillations characterized by frequencies and in EEG frequencies are of key importance for the part of MB outside biological body. The communications from cell membrane to MB involve modulation of EEG frequencies identified as generalized Josephson frequencies by nerve pulse patterns [K68] and would define a coding of sensory data to higher level emotions. The control signals from MB via DNA inducing gene expression would use dark photons at cyclotron frequencies to control BB. How to realize the music of genes represented as sequences of 3-chords of dark light as a communication tool between dark and ordinary DNA/RNA and possibly even dark and ordinary variants of tRNA and amino-acids?

1. Communication between ordinary and dark matter levels must be possible. This is guaranteed if the transition energy spectra at different levels of $h_{eff}/h = n$ hierarchy contain common transition energies so that a resonant interaction by exchange of dark photons becomes possible. This condition is extremely demanding and could explain why basic bio-molecules are selected amongst numerous alternatives [L58] - this is indeed one of the hen-egg problems of pre-biotic evolution.

2. A hypothesis worth of studying is that the cyclotron transition energies of both ordinary DNA and RNA nucleotides and their dark variants represented as dark proton sequences are same [L58]. Cyclotron transition energies should cover several octaves and the natural proposal is that magnetic field strength associated with the flux tube codes for the notes. In music experience roughly 10 octaves are needed corresponding to the range of audible sounds.

3. The cyclotron frequencies of DNA nucleotides A, T, C, G are very nearly the same and near 1 Hz for $B = B_{end} = .2$ Gauss since their masses do not differ much. Since the nucleotides are negatively charged, also the cyclotron energies for codons and codon sequences are around 1 Hz. $h_{eff} = h_{gr}$ hypothesis states that the cyclotron energies of DNA are in the energy range of bio-photons in visible and UV [K61, K13, K18] [L63].

There should be correspondences between a) the 64 ordinary DNA codons and allowed 3-chords and b) 64 dark variants of DNA codons and allowed 3-chords. These correspondences fix that between ordinary and dark codons. One would have triality.

1. To realize music of genes one the value of B must have values in a range of several octaves. The magnetic field strengths B associated with the flux tubes accompanying DNA strand should have a spectrum given by 12-note scale. Both 64 dark DNA codons and $4^3 = 64$ ordinary DNA codons should correspond to $20 + 20 + 20 + 4 = 64$ allowed 3-chords formed from the notes of 12-note scale.

2. Dark codons correspond to entangled states of 3 dark protons. The positions of dark protons are different so that ermutations of the positions of dark protons are involved. The invariance of 3-chord under permutations of notes would correspond to fermionic statistics. These permutations are lifted to braidings if dark protons are connected by flux tubes to some other system, for instance ordinary DNA.

   If the dark protons are ordered linearly along flux tube, it would seem that these these positions correspond to those of ordinary code letters. This does not make sense. If the letters of codon are connected to the dark protons by flux tubes, the permutations of dark codons induce braiding of the flux tubes but do not affect the order of the letters of the ordinary codon. Braiding would become an essential part of the correspondence between ordinary and dark codons.

3. One should understand the correspondence of dark codons with the allowed 3-chords of a given harmony and also with the ordinary DNA codons. Bio-harmony is defined as a composite of 3 harmonies with 20 allowed 3-chords and having symmetries Z_6, Z_4, and Z_2 and of tetrahedral harmony with 4 chords. Tetrahedron can be regarded as disjoint object or attached to DNA, and this gives two variants of code.

   How could these the icosa-tetra-hedral Hamilton cycles relate to the physical realization of dark proton triplets? Each icosahedral cycle should give rise to 20 dark proton triplets. Why the icosahedral geometry with Hamiltonian cycle should make itself manifest in the quantum physics of dark proton triplet?

4. Could icosahedral geometry quite concretely correspond to a tensor network? The vertices of the icosahedron would be connected by a sequence of flux tubes connecting nearest neighbors to form a Hamiltonian cycle. Dark proton triplets would quite concretely be localized at the triangular faces of the icosahedron.

   Braided triplet of flux tubes would emerge from the vertices of an icosahedral triangle defining 3-chord and would connect it to the nucleotides of the corresponding ordinary DNA codon. Magnetic field strengths at these flux tubes would correspond to the notes of 12-note scale as defined by the Hamiltonian cycle in question. The permutations of the dark proton states at the vertices of the triangle would induce braidings of the flux tube triplet actually defining minimal braid in topological quantum computation (sic!) The braiding accompanying the states of 3 dark protons would make the correspondence with ordinary ordered DNA codons possible.

   Note that each dark proton triplet could be also connected (without braiding) to its conjugate dark proton triplet by a triplet of flux tubes so that one would obtain closed flux loops and one could speak of knots instead of braids.

   Remark: Braiding brings strongly in mind the many TGD inspired proposals for DNA as topological quantum computer [K4, K87]: maybe DNA as topological quantum computer could be (also?) realized in this manner.

   What physical objects could the 20 vertices of icosahedron correspond to? Hydrogen bonded water clusters give rise to both tetrahedral and icosahedral structures. Could one associate dark proton triplets to the dark parts of these structures? Could one try to experimentally identity possible sequence of icosahedral water molecule clusters with vertices connected by hydrogen bonds associated with the DNA sequence? If the hydrogen bonds correspond to flux loops as suggested, they can be rather long (proportional to $h_{eff}/h = n$) so that even distant water molecules can become hydrogen bonds and one could have a fractal hierarchy of icosahedra.

5. Resonance condition suggests that at the level of ordinary DNA double strand the cyclotron energies of dark protons associated with the hydrogen bonds connecting DNA nucleotides

correspond to those of flux tube triplets connecting ordinary and dark DNA codons. The magnetic field strengths associated with the dark flux tubes accompanying hydrogen bonds would correspond to those associated with the triangles of icosahedral triangle. This would make possible communication between the two dark sectors by dark-photon triplets as music of genes.

This leaves unanswered questions.

1. Why the 20+20+20=60 3-chords from 3 harmonies with different icosahedral symmetries (Z_6, Z_4, Z_2) and 4 chords from tetrahedral harmony would combine to form single bio-harmony with 64 chords? This requires the presence of 3 Hamiltonian cycles with different symmetries. Why all three different symmetry types for DNA and RNA? Could the 20 amino-acids correspond to single symmetry type? Could tRNA codons correspond to two symmetry types?

2. How the 3-chords of dark photons could be played? 3-chord should be a collective effect affecting both dark and ordinary codon by inducing emission of 3-photon state like - like playing a chord by string instrument. The notes of the light chord need not emerge simultaneously but as arpeggios. Could there be a pulse travelling along the Hamiltonian cycle and picking all the cyclotron notes at the vertices containing dark proton and sending a cyclotron signal along flux tubes to ordinary DNA codon. This pulse would travel along dark DNA and play the music defined by dark DNA sequence.

4.5.3 Can one imagine a modification of bio-harmony?

The model for how one can understand how 12-note scale can represent 64 genetic codons has the basic property that each note belongs to 16 chords. The reason is that there are 3 disjoint sets of notes and given 3-chord is obtained by taking 1 note from each set. For bio-harmony obtained as union of 3 icosahedral harmonies and tetrahedral harmony note typically belongs to 15 chords. The representation in terms of frequencies requires 16 chords per note.

If one wants consistency one must somehow modify the model of icosahedral harmony. The necessity to introduce tetrahedron for one of the 3 fused harmonies is indeed an ugly looking feature of the model. The question is whether one of the harmonies could be replaced with some other harmony with 12 notes and 24 chords. If this would work one would have 64 chords equal to the number of genetic codons and 5+5+6 =16 chords per note. The addition of tetrahedron would not be needed.

One can imagine toric variants of icosahedral harmonies realized in terms of Hamiltonian cycles and one indeed obtains a toric harmony with 12 notes and 24 3-chords. Bio-harmony could correspond to the fusion of 2 icosahedral harmonies with 20 chords and toric harmony with 24 chords having therefore 64 chords. Whether the predictions for the numbers of codons coding for given amino-acids come out correctly for some choices of Hamiltonian cycles is still unclear. This would require an explicit construction of toric Hamiltonian cycles.

Previous results

Before discussing the possible role of toric harmonies some previous results will be summarized.

1. Icosahedral bio-harmonies

The model of bio-harmony [L11, L69] starts from a model for music harmony as a Hamiltonian cycle at icosahedron having 12 vertices identified as 12 notes and 20 triangular faces defining the allowed chords of the harmony. The identification is determined by a Hamiltonian cycle going once through each vertex of icosahedron and consisting of edges of the icosahedral tessellation of sphere (analog of lattice): each edge corresponds to quint that is scaling of the frequency of the note by factor 3/2 (or by factor $2^{7/12}$ in well-tempered scale). This identification assigns to each triangle of the icosahedron a 3-chord. The 20 faces of icosahedron define therefore the allowed 3-chords of the harmony. There exists quite a large number of icosahedral Hamiltonian cycles and thus harmonies.

The fact that the number of chords is 20 - the number of amino-acids - leads to the question whether one might somehow understand genetic code and 64 DNA codons in this framework. By combining 3 icosahedral harmonies with different symmetry groups identified as subgroups of the icosahedral group, one obtains harmonies with 60 3-chords.

The DNA codons coding for given amino-acid are identified as triangles (3-chords) at the orbit of triangle representing the amino-acid under the symmetry group of the Hamiltonian cycle. The predictions for the numbers of DNAs coding given amino-acid are highly suggestive for the vertebrate genetic code.

By gluing to the icosahedron tetrahedron along common face one obtains 4 more codons and two slightly different codes are the outcome. Also the 2 amino-acids Pyl and Sec can be understood. One can also regard the tetrahedral 4 chord harmony as additional harmony so that one would have fusion of four harmonies. One can of course criticize the addition of tetrahedron as a dirty trick to get genetic code.

The explicit study of the chords of bio-harmony however shows that the chords do not contain the 3-chords of the standard harmonies familiar from classical music (say major and minor scale and corresponding chords). Garage band experimentation with random sequences of chords requiring conservability that two subsequent chords have at least one common note however shows that these harmonies are - at least to my opinion - aesthetically feasible although somewhat boring.

2. Explanation for the number 12 of notes of 12-note scale

One also ends up to an argument explaining the number 12 for the notes of the 12-note scale [L69]. There is also second representation of genetic code provided by dark proton triplets. The dark proton triplets representing dark genetic codons are in one-one correspondence with ordinary DNA codons. Also amino-acids, RNA and tRNA have analogs as states of 3 dark protons. The number of tRNAs is predicted to be 40.

The dark codons represent entangled states of protons and one cannot decompose them into a product state. The only manner to assign to the 3-chord representing the triplet ordinary DNA codon such that each letter in {A,T,C,G} corresponds to a frequency is to assume that the frequency depends on the position of the letter in the codon. One has altogether $3 \times 4 = 12$ frequencies corresponding to 3 positions for given letter selected from four letters.

Without additional conditions any decomposition of 12 notes of the scale to 3 disjoint groups of 4 notes is possible and possible chords are obtained by choosing one note from each group. The most symmetric choice assigns to the 4 letters the notes $\{C, C\sharp, D, D\sharp\}$ in the first position, $\{E, F, F\sharp, G\}$ in the second position, and $\{G\sharp, A, B\flat, B\}$ in the third position. The codons of type XXX would correspond to $CEG\sharp$ or its transpose. One can transpose this proposal and there are 4 non-quivalent transposes, which could be seen as analogs of music keys.

Remark: $CEG\sharp$ between C-major and A-minor very often finishes finnish tango: something neither sad nor glad!

One can look what kind of chords one obtains.

1. Chords containing notes associated with the same position in codon are not possible.

2. Given note belongs to 6 chords. In the icosahedral harmony with 20 chords given note belongs to 5 chords (there are 5 triangles containing given vertex). Therefore the harmony in question cannot be equivalent with 20-chord icosahedral harmony. Neither can the bio-harmony with 64 chords satisfy the condition that given note is contained by 6 3-chords.

3. First and second notes of the chords are separated by at least major third as also those second and third notes. The chords satisfy however octave equivalence so that the distance between the first and third notes can be smaller - even half step - and one finds that one can get the basic chords A-minor scale: Am, Dm, E7, and also G and F. Also the basic chords of F-major scale can be represented. Also the transposes of these scales by 2 whole steps can be represented so that one obtains A_m, $C\sharp_m$, F_m and corresponding major scales. These harmonies could allow the harmonies of classical and popular music.

These observations encourage to ask whether a representation of the new harmonies as Hamiltonian cycles of some tessellation could exist. The tessellation should be such that 6 triangles meet at given vertex. Triangular tessellation of torus having interpretation in terms of a

planar parallelogram (or perhaps more general planar region) with edges at the boundary suitable identified to obtain torus topology seems to be the natural option. Clearly this region would correspond to a planar lattice with periodic boundary conditions.

Is it possible to have toric harmonies?

The basic question is whether one can have a representation of the new candidate for harmonies in terms of a tessellation of torus having $V = 12$ vertices and $F = 20$ triangular faces. The reading of the article "Equivelar maps on the torus" [A22] (see `http://tinyurl.com/ya6g9kwe`) discussing toric tessellations makes clear that this is impossible. One however have $(V, F) = (12, 24)$ (see `http://tinyurl.com/y7xfromc`). A rather promising realization of the genetic code in terms of bio-harmony would be as a fusion of two icosahedral harmonies and toric harmony with $(V, F) = (12, 24)$. This in principle allows also to have 24 3-chords which can realize classical harmony (major/minor scale).

1. The local properties of the tessellations for any topology are characterized by a pair (m, n) of positive integers. m is the number of edges meeting in given vertex (valence) and n is the number of edges and vertices for the face. Now one has $(m, n) = (6, 3)$. The dual of this tessellation is hexagonal tessellation $(m, n) = (3, 6)$ obtained by defining vertices as centers of the triangles so that faces become vertices and vice versa.

2. The rule $V - E + F = 2(1 - g) - h$, where V, E and F are the numbers of vertices, edges, and faces, relates $V - E - F$ to the topology of the graph, which in the recent case is triangular tessellation. g is the genus of the surface at which the triangulation is im eded and h is the number of holes in it. In case of torus one would have $E = V + F$ giving in the recent case $E = 36$ for $(V, F) = (12, 24)$ (see `http://tinyurl.com/y7xfromc`) whereas in the icosahedral case one has $E = 32$.

3. This kind of tessellations are obtained by applying periodic boundary conditions to triangular lattices in plane defining parallelogram. The intuitive expectation is that this lattices can be labelled by two integers (m, n) characterizing the lengths of the sides of the parallelogram plus angle between two sides: this angle defines the conformal equivalence class of torus. One can also introduce two unit vectors e_1 and e_2 characterizing the conformal equivalence class of torus.

   Second naïve expectation is that $m \times n \times sin(\theta)$ represents the area of the parallelogram. $sin(\theta)$ equals to the length of the exterior product $|e_1 \times e_2| = sin(\theta)$ representing twice the area of the triangle so that there would be $2m \times n$ triangular faces. The division of the planar lattice by group generated by $pe_1 + qe_2$ defines boundary conditions. Besides this the rotation group Z_6 acts as analog for the symmetries of a unit cell in lattice. This naïve expectation need not of course be strictly correct.

4. As noticed, it is not possible to have triangular toric tessellations with $(V, E, F) = (12, 30, 20)$. Torus however has a triangular tessellation with $(V, E, F) = (12, 36, 24)$. An illustration of the tessellation can be found at `http://tinyurl.com/y7xfromc`. It allows to count visually the numbers V, E, F, and the identifications of the boundary edges and vertices. With good visual imagination one might even try to guess what Hamiltonian cycles look like.

   The triangular tessellations and their hexagonal duals are characterized partially by a pair of integers (a, b) and (b, a). a and b must both even or odd (see `http://tinyurl.com/y7xfromc`). The number of faces is $F = (a^2 + 3b^2)/2$. For $(a, b) = (6, 2)$ one indeed has $V = 12$ and $F = 24$. From the article [A22] (see `http://tinyurl.com/ya6g9kwe`) one learns that the number of triangles satisfies $F = 2V$ for $p = q$ at least. If $F = 2V$ holds true more generally one has $V = (a^2 + 3b^2)/4$, giving a tight constraints on a and b.

   Remark: The conventions for the labelling of torus tessellation vary. The above convention based on integers (a, b) used in the illustrations at `http://tinyurl.com/y7xfromc` is different from the convention based on integer pair (p, q) used in [A22] . In this notation torus tessellation with $(V, F) = (12, 24)$ corresponds to $(p, q) = (2, 2)$ instead of $(a, b) = (6, 2)$. This requires $(a, b) = (3p, q)$. With these conventions one has $V = p^2 + q^2 + pq$.

1. The number of triangles in the 12-vertex tessellation is 24: curse or blessing?

One could see as a problem that one has $F = 24 > 20$? Or is this a problem?

1. By fusing two icosahedral harmonies and one toric harmony one would obtain a harmony with 20+20+24 =64 chords, the number of DNA codons! One would replace the fusion of 3 icosahedral harmonies and tetrahedral harmony with a fusion of 2 icosahedral harmonies and toric harmony. Icosahedral symmetry with toric symmetry associated with the third harmony would be replaced with a smaller toric symmetry. Note however that the attachment of tetrahedron to a fixed icosahedral face also breaks icosahedral symmetry.

   This raises questions. Could the presence of the toric harmony somehow relate to the almost exact $U \leftrightarrow C$ and $A \leftrightarrow G$ symmetries of the third letter of codons. This does not of course mean that one could associated the toric harmony with the third letter. Note that in the icosa-tetrahedral model the three harmonies are assumed to have no common chords. Same non-trivial assumption is needed also now in order to obtain 64 codons.

2. What about the number of amino-acids: could it be 24 corresponding ordinary aminoacids, stopping sign plus 3 additional exotic amino-acids. The 20 icosahedral triangles can corresponds to amino-acids but not to stopping sign. Could it be that one of the additional codons in 24 corresponds to stopping sign and two exotic amino-acids Pyl and Sec appearing in biosystems explained by the icosahedral model in terms of a variant of the genetic code. There indeed exists even third exotic amino-acid! N-formylmethionine (see `http://tinyurl.com/jsphvgt`) but is usually regarded as as a form of methionine rather than as a separate proteinogenic amino-acid.

3. Recall that the problem related to the icosa-tetrahedral harmony is that it does not contains the chords of what might be called classical harmonies (the chordds assignable to major and minor scales). If 24 chords of bio-harmony correspond to toric harmony, one could obtain these chords if the chords in question are chords obtainable by the proposed construction.

   But is this construction consistent with the representation of 64 chords by taking to each chord one note from 3 disjoint groups of 4 notes in which each note belongs to 16 chords. The maximum number of chords that note can belong to would be 5+5+6=16 as desired. If there are no common chords between the 3 harmonies the conditions is satisfied. Using for instance 3 toric representations the number would be 6+6+6=18 and would require dropping some chords.

4. The earlier model for tRNA as fusion of two icosahedral codes predicting 20+20=40 tRNA codons. Now tRNAs as fusion of two harmonies allows two basic options depending on whether both harmonies are icosahedral or whether second harmony is toric. These options would give 20+20=40 or 20+24=44 tRNAs. Wikipedia tells that maximum number is 41. Some sources however tell that there are 20-40 different tRNAs in bacterial cells and as many as 50-100 in plant and animal cells.

2. A more detailed model for toric harmonies

One can consider also more detailed model for toric harmonies.

1. The above discussed representation in terms of frequencies assigned with nucleotides depending on their position requires the decomposition of the notes to 3 disjoint groups of 4 notes. This means decomposition of 12 vertices of Hamiltonian cycle to 4 disjoint groups such that within given group the distances between the members of group are larger than one unit so that they cannot belong to same triangle. There are $Bin(12,4) \times Bin(8,4)$ decomposition to 3 disjoint groups of for vertices, where $Bn(n,k) = n!/(n-k)!k!$ is binomial coefficient.

2. Once the Hamiltonian cycle has been fixed and is one assumes that single step along cycle corresponds to quint, one knows what the notes associated with each vertex is and given the note of the 12-note scale one knows the number$0 \leq n < 12$ of quint steps needed to obtain it. For instance, for the proposed grouping $\{C, C\sharp, D, D\sharp\}$ and its two transposes by 2 hole steps one can assign 4 integers to each group. The condition is that within each group the notes labelled by the integers have minimum distance of 2 units between themselves.

3. One could try to understand the situation in terms of the symmetries of the system.

   (a) Could the triplet $\{C, E, G\sharp\}$ and its four translates be interpreted as Z_3 orbits. Could suitable chosen members from 4 disjoint quartets quite general form Z_3 orbits.

   Remark: Particle physicists notes the analogy with 4 color triplets formed by u and d quarks having spin 1/2. Z_4 would correspond to spin and color spin and Z_3 to color.

   (b) Z_4 acts as symmetries of the tessellation considered and these symmetries respect distances so that their action on a quartet with members having mutual distances larger than unit creates new such quartet. Could the triplet $\{C, E, G\sharp\}$ and its four translates by an $n-$multiple of half note, $n = 0, 1, 2, 3$ correspond to an orbit Z_4?

   Could the groups of 4 notes quite generally correspond to the orbits of Z_4? This can be true only if the action of non-trivial Z_4 elements relates only vertices with distance larger than one unit.

4. The group of isometries of the toric triangulation acts as symmetries. $Z_{24} = Z_6 \times Z_4$ is a good candidate for this group. Z_6 corresponds to the rotations of around given point of triangulation and should leave the tessellation invariant. The orbit of given triangle defining the set of DNA codons coding the amino-acid represented by the orbit would correspond to orbit of subgroups of Z_{24}. Only orbits containing orbits containing $1, 2, 3, 4$ or 6 triangles are allowed by the degeneracies of the genetic code. These numbers would correspond to degeneracies that is the numbers of codons coding for given amino-acid. All these numbers appear as degeneracies.

3. What one can say about toric Hamiltonian cycles?

First some basic notions are in order. The graph is said to be equivelar if it is a triangulation of a surface meaning that it has 6 edges emanating from each vertex and each face has 3 vertices and 3 edges [A22]. Equivelarity is equivalent with the folllowing conditions;

1. Every vertex is 6-valent.
2. The edge graph is 6-connected.
3. The graph has vertex transitive automorphism group.
4. The graph can be obtained as a quotient of the universal covering tessellation (3,6) by a sublattice (subgroup of translation group). 6-connectedness means that one can decompose the tessellation into two disconnected pieces by removing 6 or more vertices
5. Edge graph is n-connected if the elimation of $k < n$ vertices leaves it connected. It is known that every 5-connected triangulation of torus is Hamiltonian [A43] (see `http://tinyurl.com/y7cartk2`). Therefore also 6-connected $(6, 3)_{p=2,q=2}$ tessellation has Hamiltonian cycles.
6. The Hamiltonian cycles for the dual tessellation are not in any sense duals of those for the tessellation. For instance, in the case of dodecahedron there is unique Hamiltonian cycle and for icosahedron has large number of cycles. Also in the case of $(6, 3)$ tessellations the duals have different Hamilton cycles. In fact, the problem of constructing the Hamiltonian cycles is NP complete.

Can one say anything about the number of Hamiltonian cycles?

1. For dodecahedron only 3 edges emanates from a given vertex and there is only one Hamiltonian cycle. For icosahedron 5 edges emanate from given vertex and the number of cycles is rather large. Hence the valence and also closely related notion of n-connectedness are essential for the existence of Hamilton's cycles. For instance, for a graph consisting of two connected graphs connected by single edge, there exist no Hamilton's cycles. For toric triangulations one has as many as 6 edges from given vertex and this favors the formation of a large number of Hamiltonian cycles.

2. Curves on torus are labelled by winding numbers (M, N) telling the homology equivalence class of the cycle. M and M can be any integers. Curve winds M (N) times around the circle defining the first (second) equivalence homology equivalence class. Also Hamiltonian cycles are characterized by their homology equivalence class, that is pair (M, N) of integers. Since there are only $V = 12$ points, the numbers (M, N) are finite. By periodic boundary conditions means that the translations by multiples of $2e_1 + 2e_2$ do not affect the tessellation (one can see what this means geometrically from the illustration at `http://tinyurl.com/y7xfromc`). Does this mean that (M, N) belongs to $Z_2 \times Z_2$ so that one would have 4 homologically non-equivalent paths.

   Are all four homology classes realized as Hamiltonian cycles? Does given homology class contain several representatives or only single one in which case one would have 20 non-equivalent Hamiltonian cycles?

It turned out that there exist programs coding for an algorithm for finding whether given graph (much more general than tessellation) has Hamiltonian cycles. Having told to Jebin Larosh about the problem, he sent within five minutes a link to a Java algorithm allowing to show whether a given graph is Hamiltonian (see `http://tinyurl.com/y7y9tr5t`): sincere thanks to Jebin! By a suitable modification this algorithm find all Hamiltonian cycles.

1. The number N_H of Hamiltonian cycles is expected to be rather large for a torus triangulation with 12 vertices and 24 triangles and it is indeed so: $N_H = 27816$! The image of the tessellation and the numbering of its vertices are described in figure below (see **Fig. 4.1**). Incide matrix A characterizes the graph: if vertices i and j are connected by edge, one has $A_{ij} = A_{ji} = 1$, otherwise $A_{ij} = Aji = 0$ and is used as data in the algorithm finding the Hamiltonian cycles.

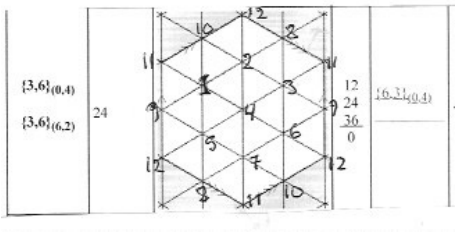

Figure 4.1: The number of the vertices of $(V, F) = 12, 24)$ torus tessellation allowing path $(0, 1, 2, 3, 4, 6, 5, 8, 10, 7, 11, 9, 0)$ as one particular Hamiltonian cycle.

   The cycles related by the isometries of torus tessellation are however equivalent. The guess is that the group of isometries is $G = Z_{2,refl} \rtimes (Z_{4,tr} \rtimes Z_{n,rot})$. $Z_{n,rot}$ is a subgroup of local $Z_{6,rot}$. A priori $n \in \{1, 2, 3, 6\}$ is allowed.

   On basis of [A22] I have understood that one has $n = 3$ but that one can express the local action of $Z_{6,rot}$ as the action of the semidirect product $Z_{2,refl} \times Z_{3,rot}$ at a point of tessellation (see `http://tinyurl.com/ya6g9kwe`). The identity of the global actions $Z_{2,refl} \times Z_{3,rot}$ and $Z_{6,rot}$ does not look feasible to me. Therefore $G = Z_{2,refl} \rtimes (Z_{4,tr} \rtimes Z_{3,rot})$ with order $ord(G) = 24$ will be assumed in the following (note that for icosahedral tessellation one has $ord(G) = 120$ so that there is symmetry breaking).

   Z_4 would have as generators the translations e_1 and e_2 defining the conformal equivalence class of torus. The multiples of $2(e_1 + e_2)$ would leave the tessellation invariant. If these arguments are correct, the number of isometry equivalence classes of cycles would satisfy $N_{H,I} \geq N_H/24 = 1159$.

2. The actual number is obtained as sum of cycles characterized by groups $H \subset Z_{12}$ leaving the cycle invariant and one can write $N_{H,I} = \sum_H (ord(H)/ord(G))N_0(H)$, where $N_0(H)$ is the number of cycles invariant under H.

What can one say about the symmetry group H for the cycle?

1. Suppose that the isometry group G leaving the tessellation invariant decomposes into semi-direct product $G = Z_{2,refl} \rtimes (Z_{4,tr} \rtimes Z_{3,rot})$, where $Z_{3,rot}$ leaves invariant the starting point of the cycle. The group H decomposes into a semi-direct product $H = Z_{2,refl} \rtimes (Z_{m,tr} \times Z_{3,rot})$ as subgroup of $G = Z_{2,refl} \rtimes (Z_{4,tr} \times Z_{3,rot})$.

2. $Z_{n,rot}$ associated with the starting point of cycle must leave the cycle invariant at each point. Applied to the starting point, the action of H, if non-trivial - that is $Z_{3,rot}$, must transform the outgoing edge to incoming edge. This is not possible since Z_3 has no idempotent elements so that one can have only $n = 1$. This gives $H = Z_{2,refl} \rtimes (Z_{m,tr}$. $m = 1, 2$ and $m = 4$ are possible.

3. Should one require that the action of H leaves invariant the starting point defining the scale associated with the harmony? If this is the case, then only the group $H = Z_{2,refl}$ would remain and invariance under Z_{refl} would mean invariance under reflection with respect to the axis defined by e_1 or e_2. The orbit of triangle under $Z_{2,refl}$ would consist of 2 triangles always and one would obtain 12 codon doublets instead of 10 as in the case of icosahedral code.

   If this argument is correct, the possible symmetry groups H would be Z_0 and $Z_{2,refl}$. For icosahedral code both Z_{rot} and Z_{2_refl} occur but $Z_{2,refl}$ does not occur as a non-trivial factor of H in this case.

   The almost exact $U \leftrightarrow C$ and $A \leftrightarrow G$ symmetry of the genetic code would naturally correspond to $Z_{2,refl}$ symmetry. Therefore the predictions need not change from those of the icosahedral model except that the 4 additional codons emerge more naturally. The predictions would be also essentially unique.

4. If H is trivial Z_1, the cycle would have no symmetries and the orbits of triangles would contain only one triangle and the correspondence between DNA codons and amino-acids would be one-to-one. One would speak of disharmony. Icosahedral Hamiltonian cycles can also be of this kind. If they are realized in the genetic code, the almost exact $U \leftrightarrow C$ and $A \leftrightarrow G$ symmetry is lost and the degeneracies of codons assignable to 20+20 icosahedral codons increase by one unit so that one obtains for instance degeneracy 7 instead of 6 not realized in Nature.

What can one say about the character of toric harmonies on basis of this picture.

1. It has been already found that the proposal involving three disjoint quartets of subsequent notes can reproduce the basic chords of basic major and minor harmonies. The challenge is to prove that it can be assigned to some Hamiltonian cycle(s). The proposal is that the quartets are obtained by Z^3_{rot} symmetry from each other and that the notes of each quartet are obtained by $Z_{4,tr}$ symmetry.

2. A key observation is that classical harmonies involve chords containing 1 quint but not 2 or no quints at all. The number of chords in torus harmonies is $24 = 2 \times 12$ and twice the number of notes. The number of intervals in turn is 36, 3 times the number of the notes. This allows a situation in which each triangle contains one edge of the Hamiltonian cycle so that all 3-chords indeed have exactly one quint.

3. By the above argument harmony possesses Z_2 symmetry or no symmetry at all and one has 12 codon doublets. For these harmonies each edge of cycle is shared by two neighboring triangles containing the same quint. A possible identification is as major and minor chords with same quint. The changing of the direction of the scale and the reflection with respect to the edges the Hamiltonian cycle would transforms major chords and minor chords along it to each other and change the mood from glad to sad and vice versa.

   The proposed harmony indeed contains classical chords with one quint per chord and for $F, A, C\sharp$ both minor and major chords are possible. There are 4 transposes of this harmony.

4. Also Hamiltonian cycles for which n triangles contain two edges of Hamiltonian path (CGD type chords) and n triangles contain no edges. This situation is less symmetric and could correspond to a situation without any symmetry at all.

5. One can ask whether the classical harmonies corresponds to 24 codons assignable to the toric harmony and to the 24 amino-acids being thus realizable using only amino-acids. If so, the two icosahedral harmonies would represent kind of non-classical exotics.

Appendix: Some facts about toric tessellations

Genus $g = 1$ (torus) is unique in that it allows infinite number of tessellations as analogs of planar lattices with periodicic boundary conditions. $g = 0$ allows only Platonic solids as tessellations and $g > 1$ allows very few tessellations. The article [A22] gives a nice review about toric tessellations.

1. Toric tessellations correspond to tessellations of plane by periodic boundary conditions. Torus tessellation allows a universal covering identifiable as counterpart of infinite lattice in plane. There are infinite number of coverings of given tessellation labelled by two integers (m, n) since the homology group of torus is $Z \times Z$. The tessellation is obtained by dividing $Z \times Z$ by its normal subgroup. Also the rotation group Z_6 acts as group leaving the tessellation invariant and correspond to the rotation leaving invariant the lattice cell consisting of 6 vertices around given vertex.

2. The tessellation is called decomposable if there is a k-sheeted covering map (map corresponds to a collection of charts) characterized by the subgroup of the isometries of the covering of the tessellation which corresponds to a sub-tessellation. This subgroup is charactrized by a pair (p, q) of integers being generated by the translation $pe_1 + qe_2$ and $2\pi/6$ rotation. The unit vectors can be chosen to be $e_1 = (1, 0)$ and $e_2 = (1, \sqrt{3})/2$ for triangular tessellation (presumably this tessellation is regular tessellation with the conformal equivalence class of torus fixed by the angle between e_1 and e_2). Line reflection transforms $(3, 6)_{p,q}$ to $(3, 6)_{q,p}$ (see Fig 1 of `http://tinyurl.com/ya6g9kwe`). The tessellation is invariant under reflections - regular -if $pq(p - q) = 0$. The peculiar looking form of the conditions follows from the identitity $(3, 6)_{q,p} = (3, 6)_{p+q,-q}$ (also $p = 0$ or $q = 0$ is possble) Note that the tessellation $(3, 6)_{2,2}$ is invariant under reflection and thus non-chiral.

3. The number V of vertices of the triangular itessellation is given by $V = p^2 + q^2 + pq$. The regular tessellation $(p, q) = (2, 2)$ has 12 vertices and is the interesting one in the recent case. It is the smallest regular tessellation. For given (p, q) one can have several non-equivalent pairs (p, q) defining combinatorially non-equivalent tessellations. My interpretation is that they correspond to different conformal equivalence classes for torus: the intuitive expectation is that this should not affect the topology of tessellation nor Hamiltonian cycles. For $(6, 3)_{p,q} = (6, 3)_{2,2}$ with s $(V = 12, F = 24)$ there are 1+6 =7 combinatorially non-equivalent tessellations: one non-chiral and 6 chiral ones.

   Quite generally, the tessellations with V vertices with $V\ mod\ 4 = 0$ (as in the case of $V = 12$) allow one map (chart consisting of faces) with isotropy group of order 2 and 6 maps with isotropy group of order 4. These variants are labelled by an SL(2,Z) matrix $(a, b; 0, c)$ with determinant equal to $V = ac$. For $V = 12$ one has decompositions $12 = 1 \times 12$, $12 = 2 \times 6$, $12 = 3 \times 4$. $-c < b < a - c$ is unique modulo a. In the recent case one as $ac = 12$ allowing $(a, c) \in \{(1, 12), (2, 6), (3, 4)\}$ and pairs obtained by permuting a and c. These matrices need not define combinatorially different tessellations since modular transformations generate equivalent matrices.

4.5.4 Icosa-tetrahedral and icosa-dodecahedral bioharmonies as candidates for genetic code

Both the icosa-tetrahedral [L11] and icosa-dodecahedral harmony to be discussed below can be considered as candidates for bio-harmony as also the harmony involving fusion of 2 icosahedral harmonies and toric harmony [L60]. The basic reason is that the third harmony corresponds to doublets. One cannot exclude the possibility of several equivalent representations of the code.

Icosa-tetrahedral harmony

Icosahedral harmonies can be characterized by a subgroup of icosahedral isometries A_5 having 60 elements. If reflections are included the isometry group, oneas $A_5 \times Z_2$ with 120 elements. The group of symmetries is Z_6, Z_4, or Z_2. There are two choices for Z_2 and the interpretation has been that Z_2 correspond to either reflection or rotation by π. A_5 however allows also $Z_2 \times Z2$ as subgroup. AAs correspond to orbits of the symmetry group and DNA codons coding for the AA correspond to triangles (3-chords) at the orbit. In purely icosahedral model on obtains 20+20+20 codons. A fusion with tetrahedral harmony gives 64 codons.

1. Z_6 gives rise to 3 AAs coded by 6 codons each (leu,se,arg) and 2 AAs coded by 2 codons: the choice of the doublet would require additional conditions. One option is ile doublet.

2. Depending on whether one includes reflection or not, one can have either $Z_4 \subset A_5$ ($60 = 4 \times 15$) or $Z_4 = Z_{2,rot} \times Z_2 \subset A_5 \times Z_2$. I have assumed that $Z_4 = Z_{2,rot} \times Z_2$ but the recent argument suggests the first option. This does not have any implications for the earlier model. Icosahedral Z_4 gives rise to 5 AAs coded by 4 codons each ($5 \times 4 = 20$). This leaves 11 AAs and 3 "empty" AA formally coded by stop codons.

3. Icosahedral Z_2 gives rise to 10 dublets. These 4-plets would correspond to (phe, tyr, his, gln, asn, lys, asp, glu, cys, stop-doublet) This leaves (stop,trp) double and (ile,met) doublet with broken Z_2 symmetry.

   The fusion with tetrahedral code with 4- codons and 4 AAs should explain these 4 AAs. Tetrahedral isometries form group S_3 and reduce to group Z_3 for tetrahedral cycle.

   (a) One could argue that ile-triplet and met correspond to 3-element orbits with 1-element orbit. (stop,trp) would be formed by Z_2 symmetry breaking from trp doublet and there is no obvious mechanism for this.

   (b) If one tetrahedral face is fixed as a face shared with icosahedron, the symmetry group of tetrahedral cycle reduces to Z_1. This would give 4 singlets identifiable as (ile,met) and (stop,trp) symmetry broken doubles. Since ile appears also in doublet, tetrahedral 1-orbit and icosahedral 2-orbit must have a common doubled triangle identifiable as the common face of icosahedron and tetrahedron. The doubling of the common triangle replaces ile-doublet with ile-triplet. This option looks rather reasonable.

Dodecadedral harmony

Dodecahedral harmony correspond to the unique Hamilton cycle at dodecahedron. Dodecahedral harmony as 20 notes and 12 5-chords. If one assumes that the octave divides to 20 notes, this brings in mind "eastern" view about harmony.

The obvious objection against dodecahedral harmony is that dodecahedral faces are pentagons so that dodecahedral chords would be 5- rather than 3-chords so that the correspondence between chords and DNA codons would be lost. The situation changes if 3 notes - 3-chord - determine the 5-chord completely and one can assign a unique 3-chord to each pentagon. This is indeed the case!

1. 3-edges meet in every dodecahedral vertex (this makes the dodecahedral cycle unique apart from rotations) and each edge pair in the vertex belongs to same pentagon (in the case of icosahedron there are 5 edges per vertex so that this is not true). Therefore each pentagon must contain at least 2 edges of Hamilton's cycle.

   The cycle must visit all vertices of pentagon, and the visit to the vertex means that the cycle shares at least one edge with pentagon. Since all vertices of the pentagon must be visited, there are two options. For option a) given pentagon shares with the cycle disjoint 2-edge with 3 vertices and 1-edge with two vertices. For option b) the pentagon shares with the cycle 4-edge with 5 vertices.

2. The numbers n_a of pentagons with 4-edges and $n_b = 12 - n_a$ 2-edge+ 1-edge (making 3 edges) can be deduced easily. Cycle has 20 edges. Pentagon of type a) shares 3 edges with the cycle and the edge is shared by 2 pentagons. This gives $3n_a/2$ edges. Pentagon of type b) shares 4 edges with the cycle. This gives $2n_b = 2(12 - n_a)$ edges. The total number of edges is $3n_a/2 + 2n_b = 20$, which gives $n_a = 8$ and $n_b = 4$. Dodecahedral Hamilton's cycle can be found from web (see `http://tinyurl.com/y5woajcb`). The structure is as deduced here.

   For case a) the 3-chords correspond naturally to the 3 vertices of the 2-edge shared with the cycle. Therefore it is possible to assign unique 3-chords to the dodecahedral harmony and to obtain connection with codons in this case. One however obtains also 12 2-chords: could they have some genetic counterpart?

   What about 5-chords for pentagons of type b)? Hamiltonian cycle can be oriented and this is induces orientation of the pentagons. One can say that the first vertex in the 4-edge is the vertex at which cycle arrives to the pentagon and identify the 3-chord as the first three vertices. It turns out that for the replacement of quint cycle this is not actually necessary.

Is icosa-dodecahedral harmony consistent with the genetic code?

One must check whether icosa-dodecahedral harmony is consistent with the degeneracies of the genetic code.

1. A fusion of 2 icosahedral harmonies and 2 copies of dodecahedral harmony would be in question. As in the case of icosahedral harmony already discussed, the two icosahedral harmonies would have symmetry groups Z_6 and Z_4 and give the codons coding for 3 6-plets and 1 doublet+ 5 4-plets + two copies of dodecahedral harmony.

2. Can the model predict correctly the numbers of codons coding for AAs? It is known that dodecahedral Hamilton cycle divides dodecahedron to two congruent pieces related by Z_2 symmetry (see `http://tinyurl.com/yy6pcogt`). Also the Hamiltonian cycle defining the common boundary has Z_2 symmetry. A good guess is that these Z_2:s corresponds to reflection symmetry and rotation by π but I am not able to exclude $Z_4 \subset G_0$, where G_0 consists of 60 orientation preserving isometries. In this case some orbits - presumably all 3 of them - could contain 4 pentagons. This is not consistent with the condition that one has doublets and singlets.

   If the second symmetry corresponds to reflection, it can be excluded by simply assuming that reflections change the orientation of the cycle.

3. Rotation by π has two fixed points corresponding to opposite poles so that one has 5 2-orbits and 2 1-orbits giving 12 triangles for each copy. Two copies of dodecahedral harmony would give 5+5=10 doublets and 2+2=4 singlets. A possible interpretation would be as (ile,met) and (stop,trp).

   Consider now objections against dodecahedral harmony.

1. Why two copies of dodecahedral code? What distinguishes between them? If imirror symmetry leaves the cycle invariant apart from orientation the copies could be mirror images and consist of same faces. The second option is that they related by a rotation?

2. The number of dodecahedral AAs is 24 rather than 20. Could the additional 4 AAs as orbits have interpretation as AAs in some sense. Could the "empty" AAs coded by stop codons be counted as AAs exceptional in some sense. In TGD framework one can consider the possibility that although AA is "empty", there is analog of AA as physical signature for the end of protein telling what stopping codon it corresponds. The magnetic body of protein is a good candidate.

   Genetic code has several slightly differing variants. Could the 2 additional exotic AAs Pyl and Sec correspond in some situations to the additional AAs?

3. Essential for the bio-harmony as a fusion of harmonies is that one can select from each orbit single face as a representative of the AA it codes - kind of gauge choice is in question - and that the orbits corresponding to different AAs can be chosen to be disjoint. Otherwise codons belonging to the orbits of different Hamilton cycles can code for the same AA if the AA can be chosen to be in intersection. If not, the same codon can code for 2 different AAs - this can indeed occur in reality [L67]!

   The condition that orbits of different cycles do not interesect seems quite stringent but has not been proven. But what if it is actually broken? Indeed, in the case of icosahedral harmony with Z_1 symmetry tetrahedron and icosahedron could have common a doubled face the breaking of this condition would geometrically explain why ile belongs to both icosahedral and tetrahedral orbit.

   Ile is the problem also in the case if icosa-dodecahedral harmony. Dodecahedral singlet codes for ile as also icosahedral doublet. Could one talk about doubling of ile face so that it corresponds to a pair of triangle and pentagon (in 1-1 correspondence with triangle as chord).

4. The two copies of the dodecahedral code should correspond to 5 doublets and 2 singlets each. One expects that together they give rise to 10+2 +10+2 =24 faces. Do they? Mirror symmetry and rotation by π act as symmetries of the cycle so that neither can map the two cycles to each other. Dodecahedral (equivalently icosahedral) rotations give rise to new equivalent cycles. The action on pentagons corresponds to the action on vertices of icosahedron so that it easy to understand what happens.

   Each symmetry corresponds to a rotation around some axis and has opposite icosahedral vertices at this axis as fixed points. Hence any two cycles obtained in this manner have 2 common pentagons. This means reduction $24 \to 22$ unless one interprets the situation in terms doubled faces? Could the disappearing doublet correspond to stop-doublet? What about the remaining stop of the vertebrate code pairing with trp? Why does second singlet correspond to empty AA and not something else such as exotic AA.

5. There is also further problem. Suppose that an intersection of orbits takes place at single triangle. Suppose that one cannot choose this triangle to be "AA" triangle for both orbits. In this case it is not clear to which AA the codon codes. This kind of phenomenon actually takes place in some cases and is known as homonymy [L67]. It is associated with the deviations of the code from the vertebrate code and involves exotic AAs Pyl and Sec. Codons can serve as a stop codon or code for an exotic AA.

Clearly, the notion of bio-harmony involves many unclear aspects but my strong feeling is that there is very beautiful mathematics involved.

4.6 Appendix

4.6.1 Chord tables for some harmonies and their inverses

The formula for inversion of the harmonic keeping note X as fixed can be represented as a product of translation takin X to C, inversion keeping C fixed, and translation taking C back to X. The inversion maps the chord having C as basic note to its mirror image so that the order of notes can change and basic note can change. For instance, the major chord $CM = CEG$ goes to minor chord $CG\sharp F = Fm$ so that $k = 0$ goes to $k \equiv \Delta k_{inv} = 11$. This delicacy must be taken into account. If X remains fixed inversion is just the transformation

$$k \to k_{inv} = (2 \times k(X) - \Delta k_{inv}) \ \ mod \ \ 12 \ . \tag{4.6.1}$$

Table 4.7 gives the inversion of the scale leaving C (and also $F\sharp$) invariant:
The inversion for the types of the chords does not depend on the basic note as is clear from the distance preserving character of the inversion. **Table 4.8** gives the inversion of for the types of the chords leaving C fixed. The elements of the rows give the type of the chord and the number

C	G	D	A	E	H	F+	C+	G+	D+	B-	F
C	F	$B\flat$	D+	G+	C+	F+	H	E	A	D	G

Table 4.7: Inversion of the scale leaving C (and also $F\sharp$) invariant.

M, 0	m, 0	sus4, 0	aug, 0	4, 0	9, 0	4+, 0	9-, 0	6-, 0	maj7, 0
m, 11	M, 11	sus, 0	aug, 0	4, 0	9, 10	9-, 11	4+, 11	maj7, 11	6-, 11
6, 0	7, 0	ex1, 0	ex2, 0	ex3, 0	ex4, 0	ex5, 0	ex6, 0	ex7, 0	ex8, 0
7, 11	6, 11	ex1, 10	ex3, 3	ex2, 3	ex4, 8	ex6, 8	ex5, 80	ex8, 6	ex7, 6

Table 4.8: Table gives the transformation of inversion leaving C invariant on the basic chords having C as basic note.

of quints k corresponding to it. For chords having C as basic note one has $k = 0$. It is easy to deduce the transformation formula in more general case from the table.

The following tables give the chords and corresponding inverse chords for the 11 icosahedral harmonies.

4.6.2 Calculation of incidence matrices

The most stringent definition of harmonic chord progression is as a chord sequence in which two subsequent chords have at least one common note: the distance between subsequent chords defined as the minimal distance between triangles representing them vanishes. Some general comments are in order.

1. Incidence matrices can be computed by using expressions of chords as sets of three notes (possible in Python) and just counting the number of common notes defining the value of the element of the incidence matrix. The quint distance between the chords vanishes if they have common notes. More general incidence matrices would correspond to a larger quint distance.

2. In the case of genetic code and amino-acids one Hamilton cycle from each class labelled by Z_n, $n \in \{6, 4, 2\}$ is involved.

   (a) There are $N = 1 \times 3 \times 8 = 24$ cycle combinations if one does not allow the inverse harmonies. Allowing them gives $N = 8 \times 24$ combinations. If transitions between all representations are possible, there are $M = N^2$ 20×20-dimensional incidence matrices to be calculated for the icosahedral restriction of the code. Incidence matrices are symmetric so that only $D(D+1)/2 = 20(20+1)/2 = 210$ independent matrix elements need to be calculated for given 20×20-D incidence matrix.

   (b) Equivalently, one can calculate the incidence matrix for a space with $N \times 20$ points which is Cartesian product of N amino-acid spaces with 20 points. N has values 24 and 8×24. Remarkably, the magic number 24 of also stringy mathematics appears.

   (c) If the transitions can be restricted to single triplet of cycles, one must calculate 6 20×20-dimensional incidence matrices. This situation could be realistic for portions of the genetic code if the transitions between different cycle triplets are analogous to phase transitions. The number of incidence matrices (one can also use single 60×60 incidence matrix) is still reasonably small and can be documented in written form. In a model for random chord sequences one must specify the probabilities for the transitions between chords with different n for Z_n. Simplest starting point assumption is that the probabilities are identical.

ro6	iro6	re41	ire41	re42	ire42	ro21	iro21
F.aug	F.aug	D.7	A.6	C.ex3	A.ex2	E.m	F.M
G.aug	D+.aug	D.6	A.7	E.ex2	F.ex3	B-.m	B.M
C.m	F.M	G+.7	D+.6	F+.ex3	D+.ex2	C.m	A.M
D.m	D+.M	G+.6	D+.7	B-.ex2	B.ex3	F+.m	D+.M
E.m	C+.M	G.4+	E.9-	D.maj7	B.6-	G.6	D.7
F+.m	B.M	A.9-	D.4+	E.9-	A.4+	C+.6	G+.7
G+.m	A.M	C+.4+	B-.9-	A.7	E.6	A.6	C.7
B-.m	G.M	D+.9-	G+.4+	A.6	E.7	D+.6	F+.7
F.6	C.7	E.maj7	G.6-	G+.maj7	F.6-	D.4+	G.9-
G.6	B-.7	G.maj7	E.6-	B-.9-	D+.4+	G+.4+	C+.9-
A.6	G+.7	B-.maj7	C+.6-	D+.7	B-.6	B.4+	B-.9-
B.6	F+.7	C+.maj7	B-.6-	D+.6	B-.7	F.4+	E.9-
C+.6	E.7	C.9-	B.4+	F.9	D+.9	C.maj7	A.6-
D+.6	D.7	A.9-	D.4+	C.9	G+.9	F+.maj7	D+.6-
C.9	C.9	F+.9-	F.4+	G.9	C+.9	G.6-	D.maj7
D.9	B-.9	D+.9-	G+.4+	E.9	E.9	C+.6-	G+.maj7
E.9	G+.9	B.9	G.9	B.9	A.9	D.9	D.9
F+.9	F+.9	E.9	D.9	F+.9	D.9	G+.9	G+.9
G+.9	E.9	F.9	C+.9	C+.9	G.9	E.9	C.9
B-.9	D.9	B-.9	G+.9	B-.9	B-.9	B-.9	F+.9

Table 4.9: Pairs "X" and "iX" of columns give the chords of the bio-harmonies and their inversions depicted in figures **??**, **??**, **??**, **??**.

ro22	iro22	ro23	iro23	re21	ir21	re22	ir22
A.ex4	G.ex4	A.ex2	B-.ex3	F+.ex3	D+.ex2	D.ex4	E.ex4
D+.ex2	C.ex3	H.ex8	B-.ex7	H.ex4	B-.ex4	H.ex4	F+.ex4
A.m	B-.M	D+.ex2	E.ex3	A.m	E.M	F.M	E.m
D+.m	E.M	F.ex8	F.ex7	D+.M	B-.m	F.m	E.M
G.9-	C.4+	D.7	A.6	A.6	E.7	C.6-	A.maj7
C+.9-	F+.4+	G+.7	D+.6	D+.7	B-.6	B-.maj7	B.6-
C.4	C.4	A.maj7	D.6-	D.7	B.6	C.9-	A.4+
F+.4	F+.4	D+.maj7	G+.6-	B-.6	D+.7	D.7	G.6
E.4+	D+.9-	A.4+	D.9-	G.6-	F+.maj7	G+.6	C+.7
B-.4+	A.9-	D+.4+	G+.9-	F.maj7	G+.6-	G.maj7	D.6-
D.maj7	F.6-	E.7	G.6	D.4+	B.9-	D+.6-	F+.maj7
G+.maj7	B.6-	B-.7	C+.6	B-.9-	D+.4+	C+.4	C+.4
B.maj7	G+.6-	B-.9	G+.9	G+.4+	F.9-	A.4+	C.9-
F.maj7	D.6-	G.9	B.9	E.9-	A.4+	E.4+	F.9-
C.9	D.9	C+.9	F.9	C.9	G+.9	F+.6	D+.7
F+.9	G+.9	A.9	A.9	F.9	D+.9	D+.9	C+.9
A.9	F.9	B.9	G.9	B.9	A.9	C+.9	D+.9
D+.9	B.9	F.9	C+.9	F+.9	D.9	E.9	C.9
D.9	C.9	E.9	D.9	E.9	E.9	B.9	F.9
G+.9	F+.9	D+.9	D+.9	C+.9	G.9	D+.9	C+.9

Table 4.10: Pairs "X" and "iX" of columns give the chords of the bio-harmonies and their inversions depicted in figures **??**, **??**, **??**, **??**.

re23	ire23	re24	ire24	re25	ire25		
F.ex1	F.ex1	H.ex3	G.ex2	F+.ex2	F.ex3		
D+.ex3	G+.ex2	E.ex7	F+.ex8	F.ex3	F+.ex2		
G+.ex1	D.ex1	D.7	A.6	F.M	B-.m		
A.ex2	D.ex3	G+.6	D+.7	B-.m	F.M		
E.7	B.6	G-.M	B.m	C.7	D+.6		
E.6	B.7	D+.m	G+.M	G+.6	G.7		
A.maj7	F+.6-	F.M	F+.m	A.maj7	F+.6-		
B.9-	E.4+	F.m	F+.M	B.9-	E.4+		
G.M	G+.m	C.6-	B.maj7	E.6	B.7		
C+.m	D.M	B-.maj7	C+.6-	E.7	B.6		
D.7	C+.6	A.9-	D.4+	G.M	G+.m		
F+.6	A.7	C+.4+	B-.9-	C+.m	D.M		
B-.9	C.9	E.7	G.6	D.7	C+.6		
D.9	G+.9	F+.6	F.7	B.6	E.7		
B.9	B.9	C.9	F+.9	D+.9	G.9		
C.9	B-.9	D+.9	D+.9	C.9	B-.9		
F.9	F.9	D.9	E.9	C+.9	A.9		
G+.9	D.9	C+.9	F.9	B-.9	C.9		
D+.9	G.9	E.9	D.9	D.9	G+.9		
C+.9	A.9	B.9	G.9	H.9	B-.9		

Table 4.11: Pairs"X" and"iX" of columns give the chords of the bio-harmonies and their inversions depicted in figures **??**, **??**, **??**.

3. For the extended genetic code the most natural assumption is that the extension of the code to icosa-tetrahedral code take places place only in Z_2 sector meaning the extension of amino-acid space by 4 amino-acids and the increase of the number of DNA codons from 60 to 64. There are two kinds of transitions between icosahedral and tetrahedral codons. Tetrahedral codon can correspond to a codon, which is outside the icosahedron having at least one common vertex with the icosahedral codon: this allows 3+3 transitions. Tetrahedral codon can correspond also to punct. Unless the codon/amino-acid contains at least one of these notes, it cannot precede stopping codon. These chords extend the harmony by the counterparts of CM and Am and punct corresponds to $C6 = CGA$.

4. Also the situation in which tetrahedral and icosahedral codes are disjoint must be considered. In this case there are no transitions between tetrahedral and icosahedral sectors. In tetrahedral sector the distances between faces always vanish so that the calculation of this part of the incidence matrix is trivial. Icosa-tetrahedral part of the incidence matrix can be readily written. The difficult part of the calculation of incidence matrices reduces to that for the icosahedral case such that the common face corresponds to either punct or Sec/Pyl. This gives selection rules telling which codons/amino-acids can precede stopping codon/punct in given bio-harmony.

4.6.3 Simulation of harmonic DNA sequence

The following sequence represents a random harmonic sequence based on zero quint distance between neighboring chords (at least one common note). The harmony if combination 3 harmonies **??**, **??**, and **??** extended by adding chords $B\flat$, Gm and $G7$ and associated $B\flat 6$ representing stopping codon and punct in tetra- icosahedral codeandSec or Pyl in their unfused variants. These three harmonies correspond to groups of 20, 20, and 24 DNA codons at orbits of Z_6, Z_4, and Z_2 which is now taken to be Z_2^{refl}. To deduce DNA sequence one must assume detailed correspondence between the codons at the orbits and corresponding chords.

It is assumed that all transitions between neighboring DNAs occurs with the same probability and induce the transitions between amino-acids.

```
Faug, A6, Dm, G6, G6, G6, Em, G6, Cm, G6, F6, Faug, F+m, Dm, G6, G6,
Gaug, G+m, Cm, F6, Dm, Dm, F+m, Dm, F6, F6, B-m, C+6, B-m, F6, Dm, G6,
G6, G6, Gaug, G+m, Cm, Gaug, G6, Dm, B-m, F6, Faug, A6, G6, Gaug, G+m,
```

```
Cm, F6, Faug, F6, Cm, F6, G6, Gaug, Gaug, B6, Gaug, G6, Gaug, Em, Gaug,
Em, A6, F+m, B-m, F6, Cm, Gaug, Em, A6, Faug, B-m, B-m, Faug, F6, G6,
G6, F6, Faug, F6, Dm, G6, F6, Dm, F+m, Dm, F+m, A6, Faug, F6, Faug, Dm,
Dm, B-m, B-m, C+6, C+6, G+m, B6, A6, F+m, Faug, B-m, Dm, B-m, C+6, B-m,
F+m, B6, Gaug, Cm, G+m, Cm, F6, F6, B-m, Dm, F6, F6, G6, Dm, G6, G6, Em,
A6, G6, Cm, Cm, G+m, B6, G+m, C+6, C+6, C+6, Faug, B-m, Dm, Dm, G6, Cm,
Gaug, Cm, F6, Cm, G6, Gaug, G6, F6, Dm, F6, Faug, Faug, Faug, A6, Em,
Em, G6, Dm, Faug, F6, B-m, F6, Cm, F6, B-m, F+m, Dm, G6, F6, F6, Cm, Cm,
Em, G+m, Em, A6, Em, A6, F+m, B-m, B-m, B-m, F+m, B6, A6, Em, G+m, B6,
B6, Em, G6, Dm, B-m, Dm, Dm, B-m, Dm, Faug, Faug, F6, Cm, G6, Gaug, B6,
G+m, Em, G6, G6, Dm, Faug, Faug, F6, Cm, Gaug, G+m, Gaug, B6, F+m, A6,
G6, Em, Cm, F6, Dm, Dm, Dm, G6, Em, Em, A6, Em, Gaug, Em, Cm, Cm, Gaug,
G6, G6, Cm, F6, Dm, Faug, A6, Faug, A6, Faug, F+m, F+m, B-m, C+6, G+m,
Em, Gaug, G6, Gaug, G6, G6, Dm, G6, Dm, Dm, F6, B-m, F6, G6, Cm, G+m,
Em, G+m, B6, G+m, Cm, Cm, F6, Faug, Faug, Faug, F6, Dm, G6, Dm, F+m,
Faug, Faug, B-m, C+6, G+m, C+6, Faug, F+m, B-m, Faug, Faug, A6, G6, Em,
Cm, F6, G6, Cm.
```

4.6.4 Illustrations of icosahedral Hamiltonian cycles with symmetries

The figures below illustrate the Hamiltonian cycles involved. Quite generally, the Z_n symmetry acts by a shift by $12/n$ quints along the cycle and the orbits of chords consist of at most n chords of same type as the reader is encouraged to verify.

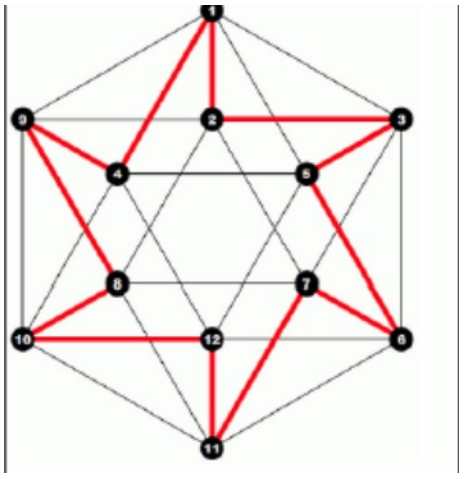

Figure 4.2: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 6-fold rotation symmetry acting shifts generated by a shift of 2 quints.

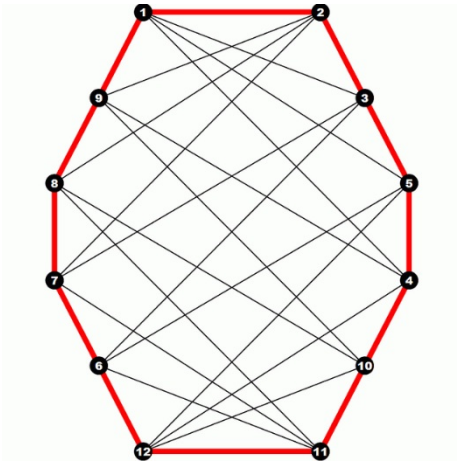

Figure 4.3: $(n_0, n_1, n_2) = (0, 16, 4)$ Hamiltonian cycle with 4 reflection symmetries generated by reflections in vertical and horizontal directions.

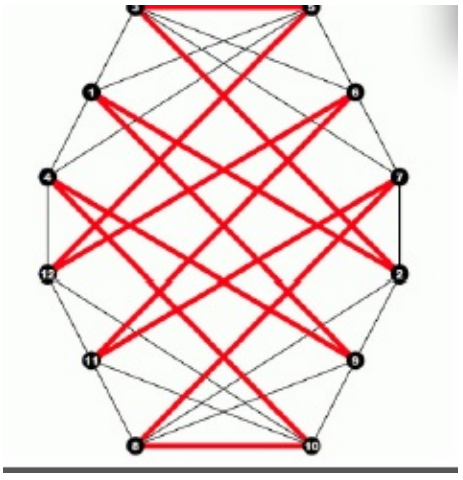

Figure 4.4: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 4 reflection symmetries.

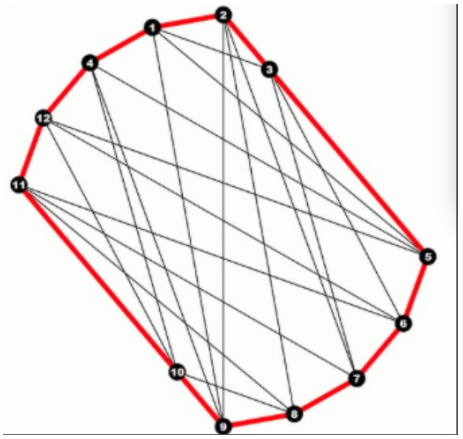

Figure 4.5: $(n_0, n_1, n_2) = (0, 16, 4)$ Hamiltonian cycle with 2-fold rotational symmetry realized as 6-quint shift along the cycle.

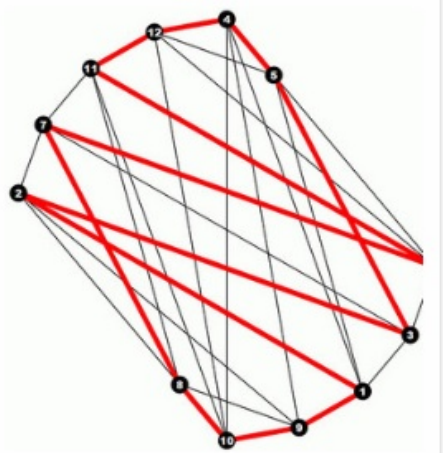

Figure 4.6: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold rotation symmetry.

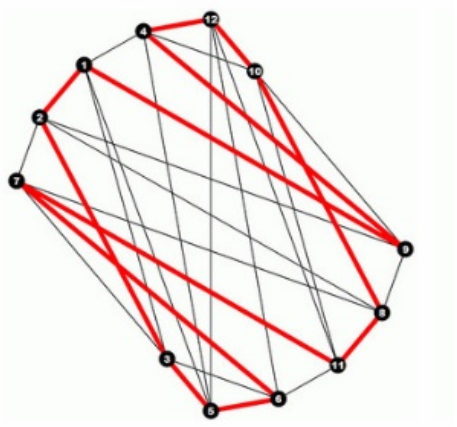

Figure 4.7: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold rotation symmetry.

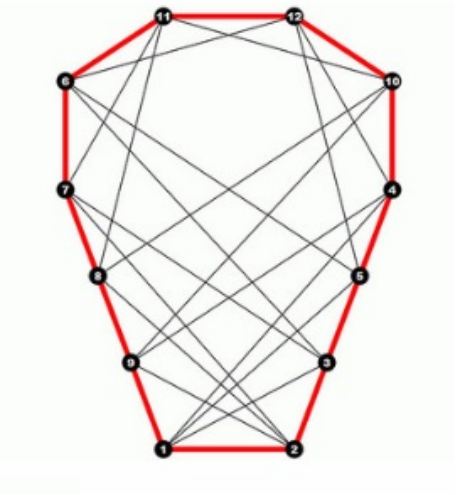

Figure 4.8: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry realized as horizontal reflection

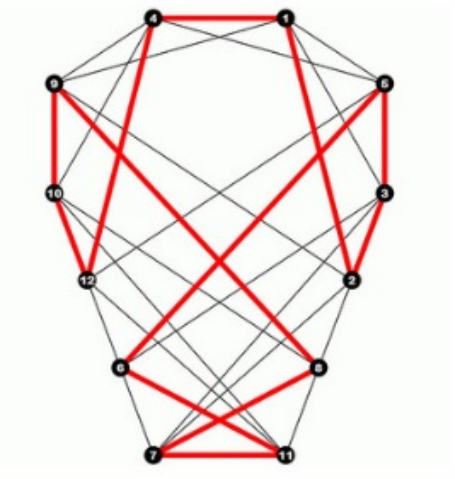

Figure 4.9: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

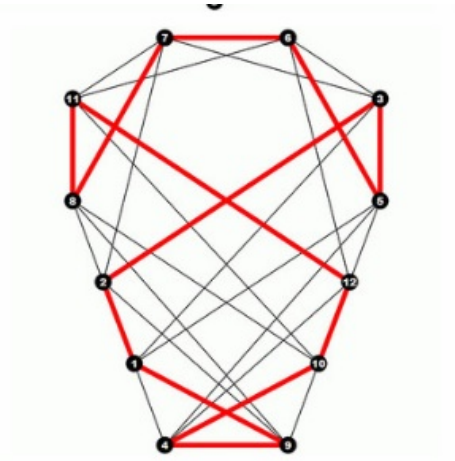

Figure 4.10: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold reflection symmetry.

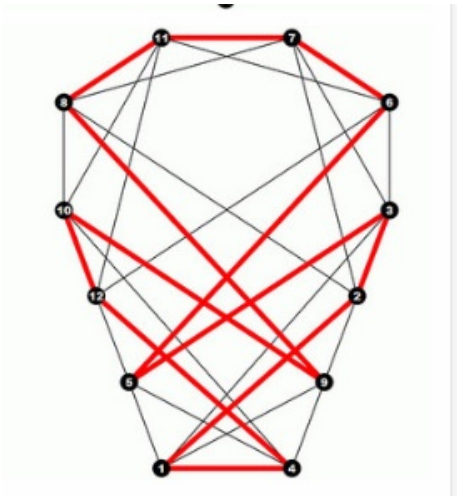

Figure 4.11: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

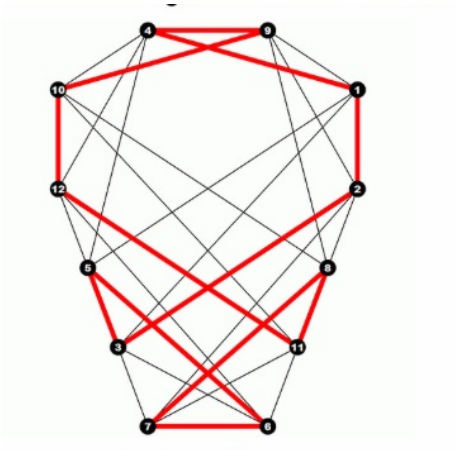

Figure 4.12: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

Chapter 5

An Overall View about Models of Genetic Code and Bio-harmony

5.1 Introduction

During last years kind of brain storming period has occurred in the model of bio-harmony [L11]. A lot of ideas, some of them doomed to be short lived, have emerged, and it seems that now it its time for a thorough cleanup and integration with the general ideas of TGD inspired quantum biology.

TGD leads to 3 basic realizations of genetic code: this is now relatively well established part of TGD inspired quantum biology. One can also consider 3 realization also for bio-harmony. The question is which of them is the realistic one or whether several options can be considered.

5.1.1 3 basic realizations of the genetic code

In TGD Universe there are at least 3 realizations of the genetic code.

Besides biochemical realization one has a realization in terms of dark nuclei realized as dark proton sequences and possibly in terms of more general sequences involving effective dark neutrons. The states of 3 dark protons defining the dark codon have multiplet decomposition 64 + 64+ 40 + 20 corresponding to dark variants of DNA, RNA, tRNA, and amino-acids (AA). I will denote these dark variants by DDNA, DRNA, DtRNA, and DAA.

If one allows also dark analogs of neutrons by allowing negatively charged color bonds between protons, the number of code letters doubles: this could relate to the recently constructed Hachimoji DNA [I24] (see `http://tinyurl.com/y2mcjb4r`) discussed from TGD viewpoint in [L83].

Dark photon 3-chords assignable to the realization of bio-harmony with the note scale identified as Hamilton cycle on a polytope with triangular faces gives a third realization coupling dark and ordinary representations together. I have proposed 3 realizations in terms of icosahedral and tetrahedral [L11], icosahedral and toric [L60], and icosahedral and dodecahedral [L83] geometries (for the latter 5-chords would effectively reduce to 3-chords).

If there is DDNA-DNA, DRNA-RNA, DAA-AA pairing, the negative charges of DNA, RNA, and tRNA nucleotides finds explanation in terms of positive charge of dark proton sequence. For AAs the situation is not clear since the charge per unit length for amino-acids varies and depends on pH. DAA-AA pairing would require that dark analogs of neutrons are present in the dark proton sequence.

5.1.2 3 models of bioharmony

There are now 3 models of bioharmony [L11, L60, L83] making very similar pedictions. Harmony for given graph is defined as a Hamiltonian cycle connecting neighboring points and going through all points of the graph without self-intersections. Scale is identified by assigning notes to the

vertices and faces correspond to the chords of the harmony obtained in this way. Bio-harmonies are fusions of 3 or 4 sub-harmonies.

1. The original proposal - icosa-tetrahedral bio-harmony - is based on the fusion of 3 icosahedral harmonies with symmetry groups Z_6, Z_4 and Z_2 permuting the triangles of given orbit of Z_n. Given icosahedral harmony corresponds to an imbedding of 12-note scale as a Hamilton cycle at icosahedron. The 12 vertices of icosahedron are identified as the notes of 12-note scale and 20 triangular faces define the 3-chords of the harmony.

   The distance between nearest vertices is assumed to correspond to quint that is scaling of the frequency by 3/2. Each cycle defines a collection of 20 3-chords defining an icosahedral harmony. Octave equivalence is used to map the 12 frequencies obtained to single octave. There is however a slight inconsistency since 12 quints corresponds to slightly more than 7 octaves as already Pythagoras realized. The addition of tetrahedron to icosahedral harmony is interpreted as an addition of one vertex adding one note which should be very near to one of the 12 notes.

   Icosahedral harmonies are characterized by a symmetry group Z_n, $n = 6, 4, 2, 1$, $n = 1$ corresponds to chaotic cycles, which might serve as correlate for dis-harmony and might relate to the correlates of emotions: at the level of genetic code is AA would be coded by single DNA codon.

   Icosahedron decomposes to orbits of Z_n consisting of triangles or equivalently chords. The chords can be classified further by the frequency ratios correlating with the emotional effect. One has the orbits $3 \times 6 + 2 = 20$ for Z_6, $5 \times 4 = 20$ for Z_4 and 10×2 for Z_2. Z_6 harmony is unique but there are 3 Z_4 and even more Z_2 harmonies for which Z_2 can correspond to rotation by π or reflection. This can be understood as breaking of symmetry splitting the Z_6 orbits to pieces. This gives $60 = 2 + 20 + 20$ 3-chords. The numbers of chords at give orbit rather neatly correspond the numbers of DNA codons coding for given AA.

   4 chords and DNAs and AAs are however missing. Tetrahedral harmony would add $3+1 = 4$ chords: Z_3 would the symmetry group instead of Z_4. This would be due to the symmetry breaking due to gluing of one-tetrahedral face with icosahedral face, which is however counted as separate face and corresponds to 1-triangle orbit under Z_3 permuting its vertices. This gives 64 3-chords corresponding to codons of genetic code.

   $3 + 1$ decomposition would naturally correspond to (ile, ile, ile, met) 4-plet coded by codons AUX. The numbers of codons coding given AA identified as orbit of Z_n come out almost correctly. The only exception is trp-stop doublet for which doublet decomposes to stop and singlet. One must understand the reason for this symmetry breaking - it might just the need to have stop codon and this could be arranged if there is no tRNA coupling to this codon. Note that for some code variants stop codon UAG corresponds to Pyl and UGA to Sec.

   Since music generates and expresses emotions, the interpretation would be in terms of moods. Even molecules would have moods.

2. Also icosa-dodecahedral and icosahedral-toric harmonies contain the Z_6 and Z_4 icosahedral harmonies (20_1 and 20_2) so that one must only add the missing 10 doublets and 3+1 codons assigned to tetrahedron in icosa-tetrahedral case.

   The dodecahedral harmony with 6 chords arranged in doublets is unique from the uniqueness of the Hamiltonian cycle [L83]. The icosa-dodecahedral harmony would give $20_1 + 20_2 + 12_1 + 12_2 = 64$. 12 decomposes into 6 Z_2 doublets so that one has 12 doublets. The realization of scale for dodecahedral harmony would in 20 powers of rational scaling x such that x^{20} is as near to a power of two as possible [L83]. $x = 2^{1/20}$ would correspond to the Eastern variant of well-tempered scale.

   There are objections against icosa-dodecahedral harmony. Chords are 5-chords rather than 3-chords. The 5-chords of dodecahedral harmony however turn out to be equivalent to 3-chords as far as information content is considered [L83]. The number of vertices for dodecahedron is 20, not 12, but one could argue that dodecahedron corresponds to Eastern harmony having micro-intervals. Two copies of the dodecahedral harmony are needed. What could distinguish between these copies will be discussed later. Also 3+1 is missing.

3. The icosahedral-toric harmony [L60] decomposes as $20_1 + 20_2 + 24 = 64$ involving torus with 24 triangles and 12 vertices. Toric harmony has Z_{24} as isometries and gives 12 doublets. One could argue that the fusion of icosahedral and toric harmonies is geometrically un-natural. One must be however cautious if the geometric realization is in extension of rationals. Also now 3+1 is missing.

The considerations in the sequel suggests that the icosa-tetrahedral option is the most realistic if not unique.

5.1.3 About the geometric interpretation of icosahedral and other symmetries

The geometric interpretation of icosahedral and possible other geometries is a challenge. The 60-element group A_5 of rotations - alternating group of 5-letters - acts as orientation preserving isometries of icosahedron.

1. Since Galois group is central in adelic physics, and all finite groups can appear as Galois groups, one can ask whether icosahedral group and tetrahedral groups could act as Galois group for some extension of rationals relevant for biology. Going to web gives an affirmative answer [A37] (see `http://tinyurl.com/y4qsea6h`)! Icosahedral symmetry appears as Galois group of the general quintic equation! The lowest order polynomial equation not allowing closed expressions for the roots.

   Galois theory (see `http://tinyurl.com/y6e955ke`) allows to understand the situation in terms of the discriminant defined as product $D = \prod_{i<j}(r_i - r_j)^2$, where r_i are the roots of the irreducible polynomial considered. S_n is the symmetry group in the generic case and odd permutations of S_n change the sign of D. If D is square of rational number in the field K considered (which can be also extension of rationals now), Galois group reduces to alternating group A_5.

   Remark: For octahedron and its dual cube the group is S_4 and can be realized as Galois group of 4^{th} order polynomials. For tetrahedron the group is A_4 and can be also realized as Galois group of 4^{th} order polynomials for which discriminant is square in K.

2. Icosahedral and dodecahedral geometries having the same isometry group are common in biology, and one can wonder whether there could be a gometric realization - perhaps at the level of magnetic body. This might somehow relate also to the frequent appearance of Golden mean involving $\sqrt{5}$ in biology and Golden angle rated to the fifth root of unity.

3. $M^8 - H$ duality provides besides the usual formulation of TGD also a formulation in complexified M^8 identified as complexified octonions [L43]. The associativity of the tangent or normal space of space-time surface is assumed as a dynamical principle and implies quaternionicity. Quaternions have $SO(3)$ as automorphism group analogous to Galois group and have the finite isometry groups of Platonic solids as finite subgroups.

   Could quaternionicity give a connection with the geometric picture? In adelic physics discretizations of space-time points as points with coordinates in the extension of rationals are in central role. Could discretizations contain orbits of the Platonic isometries as quaternionic Galois groups? This could also give to the geometric picture although icosahedral symmetries are not obvious in the geometry of say DNA.

4. Is the genetic code really unique as its dark nucleus realization and the fact that the isometry groups of Platonic solids are finite subgroups of quaternionic isomorphisms suggests? Could any Galois group give rise to an analog of bioharmony and of genetic code? Could the recent genetic code correspond to a first step in the process going beyond the solvable polynomial equations?

   What about toric code? The group of toric isometries is Z_{24} and 24 is one of the magic number of mathematics, and dimension 24 is crucial in bosonic string model. Could Z_{24} correspond to the Galois group for 24:th roots of unity defining 24-D algebraic extension of rationals. We cannot sensorily imagine higher dimensions but can do this cognitively. I have

proposed that the ability to imagine higher dimensions could be due to the possibility of higher-dimensional extensions of rationals and p-adics.

Could one realize the icosahedron and 24-torus as imagined object in the algebraic extension of rationals? Could the n-dimensional discrete geometric objects assignable to n-dimensional extensions of rationals have quite generally this kind of representations as a generalized Platonic solid in algebraic extension. Could they define cognitive harmonies as Hamiltonian cycles? Could one imagine also cognitive variant of genetic code whereas as sensory/biological variant of genetic code would be forced by dark proton physics?

5.1.4 Mistracks

In the attempts to understand the connection with standard realization of the genetic code I have also considered the possibility that the frequencies of 3-chord might be mapped to their sum in the interactions. This possibility was considered in the model of homonymy [L67]. In the light of afterwisdom this proposal looks ad hoc.

Also a proposal for how 12-note scale could quite concretely correspond DNA codons was discussed [L69]. The idea was to assign notes with individual letters of the codon such that the note depends on the position of the letter whereas the model of harmony assignment the chord to the entire codon represented as entangled state of 3 dark protons. It is now clear this proposal very probably cannot realize all possible harmonies and is in conflict with the general model which as such fixes the correspondence between chords and codons without any additional assumptions.

5.2 Interactions between various levels

One challenge is to understand how the various realizations of the genetic code interact with each other. There are DX-DY interactions, DX-Y interactions and X-Y interactions and in living matter they should occur in long length scales so that they should be mediated by dark photons.

1. How dark photon triplets assumed to be generated by dark nucleon sequences interact with ordinary DNA? Here one can bring in rather stable ideas of TGD inspired view about quantum biology. Dark matter in TGD sense represents long length scale quantum coherence and bio-chemistry short scale coherence. The interaction is therefore between long and short scales.

2. There are two ways to interact: frequency resonance and energy resonance. Frequency resonance mediates long length scale interactions and if DX-X pairing exists, the exchange of dark photon triplets - 3-chords - allows long range DX-DY interactions. DX-X interaction by energy resonance is short range interaction so that X-(DX-DY)-Y interaction would give rise to long range interaction between X-Y as interaction induced by dark level (MB).

3. DX-X interaction involves energy resonance and transformation of dark photons to ordinary photons with the same energy. Bio-photons would be an outcome of the transition $h_{eff} \to h$. Also the reversal of this transition and more general transitions $h_{eff,1} \to h_{eff,2}$ are of course possible.

   Bio-photons have a universal energy spectrum corresponding to molecular and atomic transition energies. This is possible if they result from dark cyclotron photons if the condition $h_{eff} = h_{gr} = GMm/v_0$ introduced originally by Nottale and implying that the cyclotron energy does not depend on the mass of the charged particle producing the dark cyclotron photons.

5.2.1 The independence of the interaction energy on frequency

Dark matter as a hierarchy phases labelled by $h_{eff}/h_0 = n$ identifiable as a dimension of extension of rationals implies evolutionary hierarchy: n serves as a kind of IQ. This strongly suggests that ordinary matter is controlled by dark matter at MB and mimics its behavior.

Evolution would not proceed by change and necessity but would be a process controlled and guided by MB. MB would be an active intentional agent guiding the evolution. Situation in biology

would be much like that in modern technological society where intentional technical progress leads to more and more refined products. How could this be realized at the level of basic bio-molecules? One should also understand how genetic code evolves gradually to a more refined form.

1. The selection of basic bio-molecules having energy resonance with their dark variants mediated by dark photon 3-chords by change would be extremely in-effective process. MB should have mechanisms of tuning the energies of dark photons to achieve energy resonance.

   This is achieved if the value of h_{eff} at the flux tubes mediating the interaction can be controlled. Since the length of flux tube is proportional to the h_{eff} by Uncertainty Principle, the variation of h_{eff} would mean variation of the length L of the flux tube: a kind of motor action of MB. Cyclotron frequencies are proportional to the value of monopole magnetic field B at flux tube and by flux quantization one has $B \propto 1/S$, S the area of flux tube cross section (which for monopole flux tubes is closed 2-surface). The variation of the thickness/area of the flux tube, second motor action of MB, would allow to vary cyclotron frequencies.

2. The ideal situation concerning the coupling to ordinary matter would be that same chemical transition with fixed energy for given molecule could couple to several frequencies. This would be achieved if the cyclotron energy is constant.

   The condition that the cyclotron energies in a coupling to a given molecule do not depend on the frequency requires that $h_{eff,i}$ at flux tube i compensates this dependence. MB can vary the value of B to vary frequencies and the value of $h_{eff,i}$ to keep energy unaffected. The areas S and length L of flux tubes are varied so that the volume remains unaffected. $B \propto 1/S$ and $L \propto h_{eff}$ by Uncertainty Principle. $E_c \propto \hbar_{eff} B = constant$ implies that L/S is constant. S increases like $S \to x^2 S$ and $L \to x^2 L$ in the scaling changing $f_c \to f_c/x^2$. The magnetic energy $E_{magn} = B^2 SL \propto L/S$ of the flux tube is not changed. Kind of energy criticality would be in question - one would have a large number of flux tube configurations with the same energy and volume ideal for control purposes. Quantum criticality is actually basic dynamical principle of quantum TGD allowing to predict the spectrum of various coupling parameters.

3. Besides cyclotron frequences Josephson energies are central in TGD based model of nerve pulse and EEG. Josephson energy $E_J = ZeV$ and cyclotron frequency $f_c = ZeB/m$ do not depend on h_{eff}. An attractive possibility is that cyclotron photons couple to Josephson junctions meaning that they become Josephson photons and then transform to ordinary photons inducing molecular transitions.

4. In the case of bio-harmony the frequencies would be rational multiples of basic frequency and by separating common numerator they are certain integer multiples $f_i = n_i f_0$ of a basic frequency f_0. The integers n_i have decomposition to products of powers of certain primes: $n_i = \prod p_i^{k_i}$ and each of p_i appears as some maximal power $k_{i,max}$. If one has $n = \prod_i p^{k_{i,max}} n_0$ one can obtain $h_{eff,i} = h_{eff}/n_i$. In this manner one would obtain the desired independence of $E_{c,i}$ on f_i. For Pythagorean scale only primes $p = 2$ and $p = 3$ would be involved.

All codons coding for given AA could have same coupling energy. Unless the values of Planck constants and frequencies associated with flux tubes coupling to given codon are fixed, one could have same transition energy for all letters but this is an unrealistic condition. Transition energies are naturally different and can code for letters if not even codons. For this option only the correct combination of frequencies and values of $h_{eff,i}$ allows resonant coupling.

The 3-chords associated with different harmonies would naturally correspond to the same energy. The physics of emotions would not be directly visible at the level of chemistry: chemist would certainly agree with this. The values of Planck constants would characterize the frequencies: I have indeed speculated that nucleotides could be labelled by values of h_{eff}. Number theory would be essential for the understanding life at the level of genes: Galois groups would characterize the nucleotides. Galois groups code for complexity at the level of dark matter so that the behavior guided by the MB of molecule would depend on the $IQ = n = h_{eff}/h_0$ of MB.

5.2.2 The independence of cyclotron energy on frequency and Nottale hypothesis

Is the independence of interaction energy on frequencies consistent with $h_{gr} = GMm/v_0$ hypothesis [E1] [K75, K61, K12]? Here one might encounter difficulties. The division by n_i should change one of the parameters appearing in the formula. The interpretation has been m corresponds to the dark proton mass at the end of the flux tube connecting it to large mass M. If so m cannot be varied.

Could M be varied?

1. The parameter $v_0 \simeq 2^{-11}$ can be varied by powers of two, which do not affect the notes identified by octave equivalence.

2. Could M correspond to atomic or molecular mass in good approximation equal to sum of atomic numbers A of atoms involved? The divisors of the total atomic number A_{tot} would define the allowed integers n_i characterizing the frequencies of Pythagorean scale in the model of bio-harmony. One must have $h_{gr}/h > 1$ with requires $M > \hbar/Gm = 1.3 \times 10^{19} m_p v_0$. For $v_0 = 2^{-11}$ this corresponds to $M > \hbar/Gm = 6 \times 10^{15} m_p$. The scale of a water blob with $A = 20$ containing this number of protons is about 70 μ, which is of order cell size. One can wonder how A_{tot} could be kept as divisible by n_i characterizing the frequencies of the Pythagorean scale. The problem is that an addition of one proton spoils the divisibility conditions completely.

3. The solution of the problem could be based on a more precise view about h_{eff} [L82]. The understanding of the variation of Newton's constant - too large to be due to experimental errors - led to the realization of the meaning of the fact that space-time surfaces can be regarded simultaneously coverings of n_2-fold M^4 and n_1 fold CP_2 and that one has $n = n_1 n_2$ in $h_{eff}/h_0 = n$ and n_1 would have interpretation as the number of flux tubes which are parallel in M^4 and can be even disjoint. This would give $h_{gr} \propto n_1$ and the factors of n_1 should correspond to the integers characterizing the notes of the 12-note scale. One could perhaps say that effectively single proton is replaced with n_1 protons located at different flux tubes so that also proton mass becomes $n_1 m$. One would have effectively a Bose-Einstein condensate like state of n_1 protons (at different flux tubes).

4. In the Pythagorean representation of octave the notes correspond to powers $(3/2)^k$, $k = 0, 1, ..., 11$, if $3/2)^{12} \simeq 2^7$ is not included. The corresponding integers are $3^k 2^{11-k}$. Only powers of primes $p = 2$ and $p = 3$ are involved and one just have $n_1 \propto 3^{11} 2^{11}$. If one increases the number of octaves involved to 14 to get a representation for chords needed to avoid the mapping of two dark codons to same 3-chords, one must have $n \propto 3^{23} 2^{23} = 6^{23}$. One can consider also simpler representations using integers expressible in terms of powers of primes $p = 2, 3, 5$ but one must give up exact quint cycle in this case. Interestingly, a good guess for the standard value h of h_{eff} is as $h = 6h_0$ [L31, L63].

5. Small p-adic primes $p = 2$, $p = 3$ and perhaps also $p = 5$ (Golden Mean) are expected to be of special importance in TGD inspired biology [K56]. $p = 2$ seems to appear everywhere and there is also support for $p = 3$ in biology [I61, I62] (see `http://tinyurl.com/ycesc5mq`): great evolutionary leaps seem to correspond to time scales coming in powers of 3.

6. The branching of the flux tube bundle to n_i sub-bundles $N_i = n/n_i$ could correspond to the reduction $h_{eff} \to h_{eff}/n_i$. This could be seen as reduction of h_{eff}. One can also consider phase transitions reducing n to n/n_i.

5.3 About the details of the genetic code based on bio-harmony

TGD suggests several realizations of music harmonies in terms of Hamiltonian cycles representing the notes of music scale, most naturally 12-note scale represented as vertices of the graph used. The most plausible realization of the harmony is as icosahedral harmony [L11] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/yyjpm25r`).

1. Icosahedron (see `http://tinyurl.com/l5sphzz`) has 12 vertices and Hamiltonian cycle as a representation of 12-note scale would go through all vertices such that two nearest vertices along the cycle would differ by quint (frequency scaling by factor 3/2 modulo octave equivalene). Icosahedron allows a large number of inequivalent Hamiltonian cycles and thus harmonies characterized by the subgroup of icosahedral group leaving the cycle invariant. This group can be Z_6, Z_4, or Z_2 which acts either as reflection group or corresponds to a rotation by π.

2. The fusion of 3 icosahedral harmonies with symmetry groups Z_6, Z_4 and Z_2 gives 20+20+20=60 3-chords and 3+1 + 5 + 10 =19 orbits of these under symmetry group and almost vertebrate genetic code when 3-chords are identified as analogs of DNA codons and their orbits as amino-acids. One obtains counterparts of 60 DNA codons and 3+1 + 5 + 10 =19 amino-acids so that 4 DNA codons and 1 amino-acid are missing.

3. The problem disappears if one adds tetrahedral harmony with 4 codons as faces of tetrahedron and 1 amino-acid as the orbit of the face of tetrahedron. One obtains 64 analogs of DNA codons and 20 analogs of amino-acids. I call this harmony bio-harmony. The predicted number of DNA codons coding for given amino-acid is the number of triangles at the orbit of given triangle and the numbers are those for genetic code.

4. How to realize the fusion of harmonies? Perhaps the simplest realization that I have found hitherto is based on union of tetrahedron of 3 icosahedrons obtained by gluing tetrahedron to icosahedron along its face which is triangle. The precise geometric interpretation of this realization has been however missing and I have considered several variants. I have proposed that the model could explain the two additional amino-acids Pyl and Sec appearing in Nature.

   There is also a slight breaking of symmetries: ile 4-plet breaks into ile triplet and met singlet and trp double breaks into stop and trp also leu 4-plet can break in leu triplet and ser singlet (see `http://tinyurl.com/puw82x8`). This symmetry breaking should be understood.

5.3.1 Why 3 icosahedral harmonies and 1 tetrahedral harmony?

The following argument suggests a more detailed solution of these problems than proposed earlier.

1. The copies of icosahedron would differ by a rotation by multiples of $2\pi/3$ (Z_3) around axis through the common triangular face. This face unlike the other faces remains un-affected. Also tetrahedron remains un-affected so that it is counted only once.

   If the 3 copies of the icosahedral common face are counted as separate (this is important!), one obtains 20+20+20 faces from icosahedron. If also tetrahedral shared faces is counted as separate, tetrahedron gives 4 faces: 64 codons altogether as required. One obtains 19 orbits from the 3 icosahedra and 1 orbit from tetrahedron: 20 orbits as counterparts of amino-acids altogether.

2. But can one really counter the 4 common faces as separate? One must do so. Could these faces be interpreted as somehow special codons? Maybe as stop codons or start codons for the vertebrate genetic code which also corresponds to the realization of DNA, RNA ,tRNA, and amino-acids as dark proton triplets so that DNA sequences would correspond to dark proton sequences. Could the shared codons be assigned with various modifications of the vertebrate code involving also exotic amino-acids Pyl and Sec.

3. Consider first the tetrahedral face. If the common face is removed from the 4-face orbit of tetrahedron, the orbit has only 3 faces and correspond to an amino-acid coded by 3 DNA codons. ile is the only such amino-acid and the interpretation could be that one ile corresponds to the 3 tetrahedral faces and met acting as start codon to the fourth shared face.

4. Also 3 icosahedral amino-acids corresponding to orbits containing the shared face can lose 1 codon each. To nake this more concrete, one can look for the deviations from the vertebrate code.

(a) There are 10 doublets if the doublet UAA, UAG acting as stop codons is counted as doublet coding for stop regarded formally as amino-acid.

(b) The second member in the doublet UGA, UGG coding for tyr in code table could correspond to a common face and act as a stop codon.

(c) For the modifications of genetic code UAG coding for stop can code for Pyl and UGA coding for stop can also code for Sec. UGA can also code for trp so that there would not be any symmetry breaking in this case. Could UAG and UGA correspond to common faces for two icosahedra?

(d) There is also third icosahedral shared face. CUG coding for leu can also code for ser. Could this correspond to the third exceptional codon associated with the icosahedral part of the code?

5. If the answers to the questions are affirmative, all basic deviations from the vertebrate code can be understood. The translation of the codons associated with shared face would be unstable for some reason.

   (a) 3-chord representation is more fundamental than the chemical one. This could mean that the chords associated with the shared faces are very near to each other so that the correspondence between 3-chord representation and chemical representation of codons becomes unstable if based on triple resonance.

   (b) The proposal has indeed been that the 13th vertex implied by tetrahedron corresponds to a note very near to one of the notes of 12-note scale - this note is necessary since the 12-note scale defined by quints gives 12th note slightly more than octave under octave equivalence as discovered already by Pythagoras.

   If this picture is correct, the symmetry breaking of the genetic code would be due to the presence of the face common to icosahedron and tetrahedron and reflect the problem discovered already by Pythagoras. The rational number based Pythagorean scale defined by quints is special: people with absolute pitch prefer it over the well-tempered scale involving powers of irrational number $2^{1/12}$ requiring extension of rationals.

5.3.2 Could stop codons correspond to dissonant 3-chords?

One can approach the situation also from the point of view of harmony - or rather, dis-harmony: could dissonance 3-chords act as stop codons. The 3-chords of icosahedral harmonies can be classified to three groups depending on whether the triangle representing the chord contains 0, 1, or 2 sides [L11]: in in other words, whether the chord contains 0 , 1, or 2 quints. The harmonies can be labelled by the triplet (n_0, n_1, n_2) telling the numbers of chords with 0, 1, and 2 quints.

1. The unique Z_6 harmony necessarily present in the bio-harmony has $(2, 12, 6)$. It has two augmented chords (transposes of $C_{aug} = CDG\sharp$) containing two major thirds and defining the 3-chord of a harmony assignable to triangle). This beautiful chord to which finnish tangos so often end, cannot be regarded as dissonance.

2. The 2 Z_4 harmonies have $(n_0, n_1, n_2) = (0, 16, 4)$ and $(4, 8, 8)$. For the latter harmony one has genuine dissonances since the highest and lowest note of 3-chord are separated by major or minor third. The chords with 0 quints labelled by script "ex1","ex2",...,"ex6" (for the notation see [L11]) are dissonances in this sense. "ex7" and "ex8" ($CDF\sharp$ and $CDG\sharp$) cannot be regarded as dissonances in this sense.

3. The 3 $Z_{2,rot}$ harmonies have $(0, 16, 4)$, $(2, 12, 6)$, and $(4, 8, 8)$. Both 2-plets and 4-plets contain 2 dissonances.

4. There are 3 $Z_{2,refl}$ harmonies with $(2, 12, 6)$ and 1 with $(4, 8, 8)$. These harmonies have genuine dissonances. Interestingly, $(2, 12, 6)$ corresponds to a doublet for which only the second member corresponds to dissonance.

5. For tetrahedral harmony single step should correspond to 1/4:th of octave (using suitable power of 3/2 as a rational approximation) so that the notes at the vertices of tetrahedron should correspond to $CE\flat F\sharp$ defining C_{dim}. This does not appear in the icosahedral code table as 0-quint chord. Although the triangles of tetrahedron and icosahedron would be shared in some sense, the chords cannot be same. This support the idea that ile triplet and met are coded by tetrahedral faces.

The chords containing 0 quints appearing in Z_4 and Z_2 harmonics can be regarded as dissonant. The minimization of dissonance would give a fusion of the unique Z_6 harmony $(2, 12, 6)$, unique Z_4 harmony $(0, 16, 4)$ and unique $Z_{2,rot}$ harmony $(0, 16, 4)$. Bio-harmony would be unique and contain no dissonances. Recall however that the proposal is that bio-harmonies serve as correlates for moods realized even at the level of basic bio-molecules.

For other options one would have dissonant chords. $Z_{2,refl}$ harmony $(2, 12, 6)$ has only single dissonant chord. Since stop codons would naturally correspond to dissonances, this observation raises some questions.

1. Could the dissonant chord of $Z_{2,refl}$ harmony $(2, 12, 6)$ correspond to the triangle shared by tetrahedron and icosahedron? Could this correspond to (stop,trp) pair with stop coded by dissonant chord "ex"7 ($CDF\sharp$ defining part of D7 chord). This would fix the code to contain Z_6 harmony $(2, 12, 6)$, unique Z_4 harmony $(0, 16, 4)$ and unique $Z_{2,refl}$ harmony $(2, 12, 6)$. There would be single dissonance coding for stop in stop,trp doublet.

2. The doublet coding for stop should formally code for amino-acid. One cannot realize this doublet as a doublet of dissonances with "ex"n, with $n \in \{1, .., 6\}$ for single bio-harmony. The second member of this doublet could however correspond to the shared triangle.

This tentative picture should be of course checked. There are also cycles without any symmetries. Could these chaotic cycles be interpreted as disharmonies.

5.3.3 How could the representations of genetic code as dark 3-chords and nucleotide triplets relate?

One of the poorly understood aspects of the model is how the various representations of the code relate.

Frequency coding of nucleotides is not possible

Frequency coding of nucleotides would look natural but it is easy to see that it is in conflict with bio-harmony.

1. The representations as dark proton triplets and dark photon triplets do not involve decomposition to ordered triplet of letters as the ordinary chemical representation does. Dark protons are entangled and one cannot order them and there is no obvious ordering of the frequencies of dark photons.

   This is not a problem for the correspondence between dark proton triplets and dark photon triplets and one can even imagine assignment of dark cyclotron photons with 3 parallel flux tubes acting as wave guides. This could mediate the interaction between dark variants of basic biomolecules with same value of h_{eff} as frequency resonance.

2. The interaction between ordinary DNA/RNA/tRNA and its dark variant should involve the transformation of dark photon triplet associated with flux tube triplet emanating from dark bio-molecule to ordinary photons (possibly bio-photons) and energy resonance would be involved. Is the energy resonance involved with the formation of the dark-ordinary pairs or with the sustainment of these pairings? The example of benzene suggests sustainment.

3. The assumption that energy resonance is involved with dark-ordinary pairing indeed leads to problems. The first guess would be that ordinary photon triplet somehow carries information about the position of nucleotide in the codon. The 4 nucleotides would correspond to 4 frequencies with frequency scale depending on the position inside the codon. There are indeed

12 frequencies in the 12-note scale so that 3 frequency scales with 4 frequencies associated with each of them would give 64 combinations of frequencies.

Frequency coding of nucleotides however leads to a problem. The first two letters of the codon are known to determine the amino-acid coded by it to a high degree since the third letter typically distinguishes between 1 or 2 amino-acids only, and labels codons at the orbit of DNA codon defining amino-acid. Therefore for DNA codons coding same amino-acid the first two frequencies should be same. This is not the case for bio-harmony for the simple reason that the frequencies of 3-chords along the orbit defining amino-acids are different. Only the frequency ratios defining the type of the chord are same along the orbit.

The frequency ratios determine the correspondence so that the correspondence can be only between *entire* dark and ordinary codons, and cannot be reduced to correspondence between frequencies and letters. Holism does not reduce to reductionism.

Does the impossibility of frequency coding of nucleotides lead to problems with the models of replication and transription?

This becomes a potential problem in the model for DNA replication and transcription to RNA.

1. The basic picture about bio-catalysis in TGD framework is following. U-shaped magnetic flux tubes emanate from the reactants and can reconnect to form a pair of flux tubes connecting the reactants. The shortening of the flux tube pair by a reduction of h_{eff} brings the reactants together and liberates the energy needed to kick the reactants over the potential wall making the reaction rate extremely low otherwise.

   The U-shaped flux tubes or flux tube triplets would be associated with dark codons of dark DNA accompanying DNA strand, and would be formed as the flux tube pair(s) connecting the strands split by the reversal of reconnection. The h_{eff} associated with resulting U-shaped flux tubes associated with replicating strands would increase requiring metabolic energy. They would get longer and could act as tentacles scanning the environment to spot similar flux tubes assignable to nucleotides or codons by resonance.

2. In the standard picture one assumes that nucleotides defining the letters of the codons appear as non-correlated molecules in the environment, and that each codon is built by a stepwise process in which letters attach to it. The letters can respond only to single frequency and cannot "know" which position to attach to. Thefrequency coding is not consistent with the idea that dark photon triplet assigned with the dark codon gives rise to energy resonance with the letters one by one.

   Could the triple resonance occur as single step and attach all 3 nucleotides in single step? Or could the triple resonance be a collective frequency resonance with dark codon already attached to the ordinary codon in the environment. Ordinary-dark pairing by energy resonance would sustain rather than generate DNA strand since otherwise the Coulomb repulsion due to the large negative charge of DNA does not allow stability.

3. The problem is that it is nucleotides seem to appear in the environment rather than codons. Could the nucleotides of the environment actually form loose codons connected to dark codons by long flux tubes with large value of h_{eff}? Could the reduction of h_{eff} bringing nucleotides together induce the reduction of flux tube lengths giving rise to ordinary codon? If the reduction of h_{eff} for flux tubes occurs nucleotide-by nucleotide, one would have consistency with the standard picture. The simplest picture is following.

   Dark codons are paired with the loose variants ordinary codons. The opening of DNA double strand leads to the splitting of the flux tube pairs connecting the ordinary codons of strands to U-shaped flux tubes, which reconnect with U-shaped flux tubes coming dark codons paired with loose ordinary codons. The reduction of h_{eff} d pairs nucleotides of loose codons with those of ordinary codons.

4. The pairs of dark codons and loose codons would be analogous to tRNA molecules. One can imagine even pre-tRNA molecules with loose coupling of RNA and amino-acid so that

replication and transcription would be very similar topological processes. Also RNA transcription and translation of RNA to amino-acids would rely on similar mechanism. The only difference would be that only the second - active - strand would form U-shaped flux tubes connecting with dark RNA codons.

What about remote DNA replication

This model could also explain remote replication of DNA for which Montagnier *et al* have reported evidence [I48]. Also remote transcription is predicted to be possible. I have already earlier considered a model of remote replication [K96] in an article written together with Peter Gariaev who has reported this kind phenomenon already earlier. I have discussed the findings of Montagnier *et al* in [L4].

1. The experiment involves two vessels, call them A and B. A contains genes and B only nucleotides - at least according to the standard picture. There is irradiation using 7 Hz frequency not far from the lowest Schumann frequency having a nominal value of 7.8 Hz. What happens is that the replicas of genes appear in B. It is also reported that the DNA generates em radiation possibly responsible for the information transfer.

2. The proposed model for the ordinary DNA replication generalizes easily to describe also remote replication. The new element would be that the U-shaped flux tubes from A would extend to B - here 7 Hz radiation could be essential - , would be parallel to each other, and have same average length, which is natural if they have same value of h_{eff}. Also the experimental arrangement could favor parallel flux tubes. In B the dark codons paired with loose codons formed from ordinary nucleotides would be present, and their U-shaped flux tubes would reconnect with those coming from A. Remote replication could take place: here it is essential that the U-shaped flux tubes are parallel and have very nearly the same length.

   The TGD interpretation would be that the Earth's magnetic body is involved and generates quantum coherence in the length scale at least the size of the system studied. The reported em radiation would naturally relate to the dark photon triplets representing the codons.

Is ZEO needed to understand the replication?

In TGD one must give up thinking in terms of standard ontology of bio-chemistry in which the process is a kinetic process governed by differential equations for the populations of molecules and proceeding in step-wise manner nucleotide by nucleotide. ZEO suggests temporal holism - at least at the level of single dark codon, which cannot be built building brick by building brick.

1. An open question is in which time scale this temporal quantum holism holds true: in the time scale of addition of single codon or in the time scale of replication of gene or something else? In the following the possibility that temporal holism holds in the time scale for the pairing of dark codons.

2. In ZEO one could have state function reduction in which initial state corresponds to dark codon plus population of nucleotides and final state to dark codon paired with the ordinary codon formed from 3 nucleotides in energy resonance with the codon formed from nucleotides. What matters are only the initial and final states.

3. If "big" state function reduction (BSFR) is in question, the final state would correspond to a superposition of deterministic time evolutions leading from the outcome of the reduction to geometric past, possibly but not necessary to a state in which nucleotides do not form codon paired with the dark codon.

4. The process would create strong correlations between the position of nucleotides of the codon and between the positions of codon and its dark variant and therefore a generation of entanglement. Unitary evolutions followed by "small" state function reductions (SSFRs) would generate a state as a superposition of the states satisfying the criteria of the desired final state and other states and BSFR would select the desired final state. It could be followed by BSFR returning the original arrow of time but doing nothing for the state.

5.4 How to compose beautiful music of light in bio-harmony?

The topic of this section is the detailed definition of the notion of bio-harmony [L18, L19, L98]. A sequence of 3-chords of bio-harmony defines a music piece: what rules guarantee that this piece is beautiful? This question is interesting because the chords of bio-harmony correspond to DNA codons.

Bio-harmony as a realization of genetic code

TGD leads to a notion of bio-harmony in terms of icosahedral and tetrahedral geometries and 3-chords made of light assigned to the triangular faces of icosahedron and tetrahedron [L18, L19, L98]. Bio-harmonies are associated with the so-called Hamiltonian cycles , which go through every vertex of Platonic solid once. For icosahedron the number of vertices is 12, the number of notes in 12-note scale. The 64 codons of bio-harmony represented as light 3-chords formed by dark photon triplets are formed from 3 20-chord harmonies associated with icosahedron and the unique 4-chord harmony associated with tetrahedron.

The surprise was that vertebrate genetic code emerged as a prediction: the numbers of DNA codons coding for a given amino acid are predicted correctly. DNA codons correspond to triangular faces and the orbit of a given triangle under the symmetries of the bio-harmony in question corresponds to DNA codons coding for the amino acid assigned with the orbit.

Codon corresponds to 6 bits: this is information in the usual computational sense. Bio-harmony codes for mood: emotional information related to emotional intelligence as ability to get to the same mood allowing to receive this information. Bio-harmony would be a fundamental representation of information realized already at molecular level and speech, hearing and other expressions of information would be based on it. For emotional expression at RNA level possibly involved with conditioning at synaptic level see [L62].

About generalizations of the notion of bio-harmony

One can consider several generalizations for the notion of bio-harmony.

1. All Platonic solids, in particualr tetrahedron, cube, octahedron and dodecahedron are possible and one can consider the possibility that they also define harmonies in terms of Hamiltonian cycles. Dodecahedron would have 5-chords (pentagons as faces) as basic chords and there is only single harmony. Same mood always, very eastern and enlightened as also the fact that scale would have 20 notes.

   Also octahedron gives 3-chords (triangular faces) whereas cube gives 4-chords (squares as faces). One can of course speculate with the idea that DNA could also represent this kind of harmonies: sometimes the 3N rule is indeed broken, for instance for introns.

2. Galois confinement [L110] allows the possibility to interpret dark genes as sequences of N dark proton triplets as higher level structures behaving like a single quantal unit. This would be true also for the corresponding dark photon sequences consisting of 3N dark photons representing the gene in bio-harmony as an analog of a music piece consisting of 3-chords and played by transcribing it to mRNA.

   Basic biomolecules (DNA, RNA, tRNA, amino acids) would have names represented as a sequence of light 3-chords representing a piece of music and dark biomolecules with the same name could recognize and communicate with each other in 3N-resonance. Dark-ordinary communications could transform dark 3N-photon to single bio-photon so that resonance would be possible when the sum of energies coincides with a transition energy of the ordinary biomolecule. The resonance condition would very effectively select survivors in the fight for survival.

3. The picture can be viewed even more generally. Any discrete structure, defining graph, in particular cognitive representation providing a unique finite discretization of space-time surface as points with the coordinates of the 8-D embedding space coordinates in the extension of rationals, defines harmonies in terms of Hamiltonian cycles. Could also these harmonies make sense? The restrictions of the cognitive representations to 2-D partonic 2-surfaces would

define something analogous to bio-harmony as Hamiltonian cycle of 2-D graph (Platonic surfaces solids can be regarded as 2-D graphs). The interpretation as representations of Galois groups and the notion of Galois confinement is possible although one loses the symmetries of the Platonic solids allowing to identify genetic code.

During years I have indeed considered some modifications of the original bio-harmony base on the fusion of 3 icosahedral harmonies and tetrahedral harmony in partcular so called E_8 harmony and toric harmony [L30, L60] but the overall conclusion [L78] is that the original model is the most plausible candidate.

The challenges of the model

The model of bio-harmony is far from complete and this article discusses a more detailed definition. Also the question about the rules defining beautiful music by posing rules on chord sequences are considered. These aesthetic rules are also rules for the corresponding DNA and amino-acid sequences.

1. The fusion of the three harmonies having symmetry groups Z_n, $n = 6, 4, 2$ has been considered but not in the required detail. The Hamiltonian cycles of icosahedron are fixed only modulo isometries of icosahedron preserving the shape of the cycle, scalings of the cycle by a power of quint forming group Z_{12} leaving the cycle of invariant but inducings transponation (change of the key), and the change of the cycle orientation possibly related to minor-major dichotomy correlating with joyful-sad dichotomy. For a single icosahedral cycle these transformations do not change anything but for the fusion of 3 cycles realized at the same icosahedron the situation changes, and the number of harmonies increases dramatically.

   Are all combinations of icosahedral harmonies allowed or are there some natural restrictions on them? I have considered this question but it seems that there is no good reason for posing any restrictions. The spectrum of harmonies determined by dark genetic codons and therefore the spectrum of emotions at the molecular level would be surprisingly rich.

2. Is it possible to reproduce the basic harmonies of the western music based on the 12-note system which inspired icosahedral harmonies? In particular, can one understand the chords C, F, G of C-major scale? By octave equivalence the nearest neighbors of the Hamiltonian cycle are related by quint scaling scaling frequency by factor 3/2 scaling C to G. The 3-chords containing at least one cycle edge contain quint (C$\rightarrow$ G) and quint is the basic aspect of bio-harmony. For harmonies with opposite orientation quints become perfect fourths (C$\rightarrow$ F) and FCG corresponds to transponantion of F by two quints.

   For a single icosahedral harmony the chord-pairs analogous to C-F or C-G do not appear in any obvious manner. If the 3 icosahedral harmonies are related by quint scalings (FCG) the analogs of these chord pairs become natural. Could this be the solution to the problem?

3. What are the rules producing aesthetically satisfying music? I experimented with the ultraconservative assumption that only chord pairs containing common quint are allowed: the result was not ugly but it was boring. Already the transitions of CFG major scale are too radical for this option!

   An attractive idea is that the sequence of 3-chords is continuous in some sense. Could the sense be strictly geometric: could chord pairs be nearest neighbors in some sense. For Option I nearest neighbors have a common edge (3 nearest neighbours). For Option II they have a common vertex (10 nearest neighbors). These options do not allow all 3-chord pairs and thus not all possible DNA pairs and all possible amino-acid pairs. A more abstract definition identifies the nearest neighbors with the orbits of nearest neighbors for Option I or II under the symmetry group Z_n ($n = 6, 2$). Codon is replaced with the codons coding for the same amino-acid. For Option II this allows to have all possible chord pairs and therefore DNA and amino-acid pairs.

4. Also the role of tetrahedral harmony and its relation to start and stop codons is interesting. One wants also to understand why the genetic code at the bio-chemical level is not quite complete and why there are several variants of it.

Symmetry	$\#(class)$	$\#(repr)$
Z_6	1	8
Z_4	2	12
$Z_{2,rot}$	3	24
$Z_{2,refl}$	5	24

Table 5.1: The number $\#(class)$ of equivalence classes of Hamiltonian cycles ad the number $\#(repr)$ of representatives in the class for icosahedral Hamiltonian cycles. If the orientation is not taken into account the number of representatives reduces to $\#(repr)/2$

5.4.1 About bio-harmonies

The set of allowed 3-chords define music harmony. The 12-note scale is essential for the western view about harmony. The TGD inspired geometric model for music harmony identifies bio-harmony as a fusion of 3 icosahedral harmonies with 12-note scale represented geometrically as a Hamiltonian cycle at icosahedron and 1 tetrahedral harmony represented as a unique Hamiltonian cycle of tetrahedron. Each icosahedral harmony has 20 3-chords identifiable as triangular faces of the icosahedron whereas tetrahedral harmony 4 3-chords. This gives 20+20+20+4=64 chords - the number of genetic codons.

Symmetries of icosahedral harmonies

There are 3 types of icosahedral harmonies with symmetries characterized by a subgroup of icosahedral isometries, which is Z_6, Z_4 or Z_2 acting either as a rotation by π or as a reflection. The orbits of triangles are identified as counterparts of amino-acids coded by the DNA codons assigned with the triangles of the orbit.

1. For Z_6 given triangle gives rise to 3 6-orbits with 6 triangles and 1 2-orbit: Z_3 subgroup of icosahedral group permutes the 3 6-orbits and acts trivially to 2-orbit.

2. For Z_4 there are 5 4-orbits and Z_5 permutes these orbits.

3. For Z_2 there are 10 2-orbits and Z_{10} permutes them. Z_2 can act either as reflections or rotations.

There are also 6 cycles without any symmetries perhaps identifiable as dis-harmonies. They will not be considered in the sequel. For them the number of amino-acids coded by codon would be one.

Table 5.1 summarizes the numbers of equivalence classes of cycles and under icosahedral rotation group for various symmetry groups as well as the numbers of representatives in the class. These numbers allow to deduce the number of bio-harmonies by fixing one of the icosahedral harmonies, most naturally the Z_6 harmony for which one has only one class.

Remarkably, the combination of 3 icosahedral cycles with symmetries Z_k, $k = 6, 4, 2$ with the tetrahedral Hamiltonian cycle gives 64 codons and the model correctly predicts the numbers of DNA codons coding for a given amino acid. Could there be a connection between music and genetic code? Could one speak of bio harmonies as correlates of emotions at the molecular level?

The natural expectation is that the symmetries Z_n of a given harmony leave the ratios of frequencies of 3-chords invariant. This is true if the edge connecting nearest neighbors along Hamiltonan cycle corresponds to a quint that is scaling of frequency by 3/2 and projection to the basic octave (octave equivalence). Therefore the chords at the orbit of a given chord coding for the same amino-acid are replaced by a scaling by power of 3/2 so that the scalings are mapped to unitary rotations.

The factors of 12 include indeed 6, 4, and 2 so that the 12-element group of scalings modulo octave equivalence can be mapped to Z_{12} rotations. There is however a problem with rational quints due to the fact that - as already Pythagoras found - $(3/2)^{12} = 129.746...$ does not correspond exactly to $2^7 = 128$. One reason for introducing icosahedron could be that this brings additional note allowing to get rid of the problem. One can also construct the notes by powers of $2^{1/12}$ applied

to the basic frequency but now the frequencies are not rational. Furthermore, people with absolute pitch favor rational frequency ratios, which suggests that rational numbers and roots of unitary assignable with adelic physics as physics of cognition are really important.

Fusion of 3 icosahedral harmonies and tetrahedral harmony to bio-harmony

There is quite a large number of icosahedral Hamiltonian cycles and therefore of bio-harmonies. Although the isometries of icosahedron and their transponations do not matter for given icosahedral harmony, they matter when one has 3 icosahedral harmonies. A simple example from physics helps to understand this: although rotations are symmetries of an N-particle system the rotations of a single particle are not symmetries anymore and represent new degrees of freedom.

1. Bio-harmony assigns to the same icosahedron 3 Hamilton cycles with symmetries Z_k, $k = 6, 4, 2$. This means assigning to the same icosahedron 3 Hamiltonian cycles giving rise to 3 representations of 12-note scale each giving 20 chords so that one 20+20+20 chords coding 3 classes of amino acids. Tetrahedron gives the remaining 4 chords.

   There are N_i, $i = 1, 2, 3$ cycles corresponding to $Z_{k(i)}$, $k(i) = 6, 4, 2$: for the values of N_i and detailed 3-chord contents of icosahedral harmonies see [L11]. From the table **Table 5.1** one has for $(Z_6, Z_4, Z_{2,rot})$ $\#(class) = (\#(class)_1, \#(class)_2, \#(class)_3) = (1, 2, 3)$ giving 6 different classes and $(Z_6, Z_4, Z_{2,refl})$ $(\#(class)_1, \#(class)_2, \#(class)_3) = (1, 2, 5)$ giving 8 different classes. This gives $N = 14$ different icosahedral Hamiltonian cycles.

   The numbers of reresentatives for given equivalence class are for both $(Z_6, Z_4, Z_{2,rot})$ $(Z_6, Z_4, Z_{2,rot})$ $\#(repr) = (2, 12, 24)$.

2. The 3 cycles go through all points of the icosahedron. This means that for each point of icosahedron there are 3 cycles going through that point. There can be however situations in which there are common edges. 5 edges arrive at given icosahedral vertex. There are 3 cycles entering and leaving the vertex: this makes 6 cycle edges. There is necessarily one edge shared by two cycles. If the edge is shared by 3 cycle edges, one edge has no cycle edge. This kind of situation - 3-edge - is achieved by performing a suitable Z_5 rotation for the third cycle.

   Do all bioharmonies have 3-edges? Could 3-edges have a special role concerning bio-harmony and music experience? Could they define chords with preferred quints such as chords C, F, G in C major scale? The bio-harmonies having chord(s) with 3-edge could give rise to simple CFG type harmonies. Fusion of 3 icosahedral harmonies differing by quint scalings gives a CFG type situation, and one could assign all these 3 types of chords with a triangle with 3-edge. Geometrically the chord progression would reduce to a repetition of the same triangle! Allowing also the triangle at the other side of the 3-edge, the chord progression involving only these 2 triangles consists of 3+3=6 chords.

3. One can assume that the 3 Hamiltonian cycles start at the same almost arbitrarily chosen vertex of the icosahedron. As a special case one can assume that it corresponds to the same basic note (C). Since Z_6 allows only a single cycle, it is natural to fix it: the fact this cycle has 2 orientations gives degeneracy factor 2.

   The other other cycles are determined apart from the rotation group Z_5 leaving the base point invariant. Therefore the Z_4 and Z_2 harmonies give rise to an additional $5^2 = 25$-fold degeneracy of bio-harmonies $N \to 25N$. If the cycles are required to have a common first edge besides the base point, one does not obtain the degeneracy factor. This argument shows that common edges are possible and the vertices associated with them are definitely special.

   Fixing the cycle types and the Z_6 cycle one can calculate the number of bioharmonies for a given equivalence classes as the number $\#(repr(Z_4)\#(repr(Z_2)$ One obtains 12×24 representatives for both choices of Z_2. For r $Z_2 = Z_{rot}$ the total number of bioharmonies is

$$N(harmony, rot) = 2 \times 2 \times 12 \times 3 \times 24 = 2^7 \times 3^2$$

$$N(harmony, refl) = 2 \times 2 \times 12 \times 5 \times 24 = 2^7 \times 3 \times 5 \ .$$

The first factor of 2 comes from the two orientations for the fixed Z_6 cycle.

4. The transponations realized as scalings along the Hamiltonian cycle define 1-to-1 map of icosahedral vertices which is however not an isometry but preserves the harmony. This gives a degeneracy factor 12^2 and one has

$$N(harmony, ...) \to 12^2 \times N(harmony, ...) \ .$$

The formula for the total number of bioharmonies is

$$\begin{aligned} N(harmony) &= N(harmony, rot) + N(harmony, refl) = 2^{14} \times 3^3 \ , \\ N(harmony, rot) &= 2^{11} \times 3^4 \ , \\ N(harmony, refl) &= 2^{11} \times 3^3 \times 5 \ . \end{aligned} \tag{5.4.1}$$

(5.4.2)

How to understand the tetrahedral code and symmetry breaking of the perfect code?

The precise understanding of the relationship between tetrahedral and icosahedral codes has been a long standing challenge andI have considered several scenarios. The geometric idea has been that tetrahedron is somehow glued to icosahedron along on faceand selects a unique codon of the icosahedron defining the basic chord. As found, another manner to fix this chord as a chord to which one can assign 3 cycle edges. There might be other faces with the same property.

One can get information about the situation by looking at the code table.

1. There are 10 unbroken icosahedral Z_2 doublets containing (stop,stop) plus 1 symmetry broken doublet (stop,tyr). What could cause the symmetry breaking? The energy resonance condition associated with the pairing of dark mRNA codons with dark tRNA codons could explain the presence of stop codons: translation would stop when no tRNA in energy resonance is found.

   Dark 3-photon representing the dark stop codons could not couple to tRNA codon in energy resonance since there would not be tRNA with cyclotron resonance energy triplet resonating with that of dark stop codon. This would be the case for the (punc,punc) doublet and also for punc member of (puc,trp) doublet. The mimicry of dark level by biochemical level would not be complete. For the variants of the code it would be even less complete.

2. From the table one learns that both Z_6 and Z_4 codons are realized completely for the vertebrate code. This leaves only one conclusion: (ile,ile,ile,met) must correspond to a Z^4 symmetry breaking for tetrahedral rather than icosahedral 4-plet. The AGG coding for met, which is unique in the sense that it serves as a mark for the beginning of genes, would correspond to a tetrahedral face.

   The failure of energy resonance could force the splitting of unbroken tetrahedral ile 4-plet to (ile,ile,ile,met). Fourth codon in Z_4 4-plet would be in energy resonance with tRNA associated with met. Note that icosahedral code gives rise to 4+5+10=19 amino-acids and met provides the 20^{th} amino acid. Symmetry breaking would be necessary to mark the starting and stopping points of transcription and translation.

   3-chords also depend on the icosahedral harmony and for some icosahedral harmonies energy resonance could fail so that the emotional state of at dark matter level would reflect itself at the biochemical level. The number of icosahedral harmonies is (1,2,3,5) for $(Z_6, Z_4, Z_{rot,}, Z_{2,refl})$. For Z_4 and Z_2 the failure of energy resonance is possible.

   Remark: I must confess that many earlier texts about the problem contain a stupid error. I have considered the proposal that (ile,ile,ile,met) could correspond to symmetry broken icosahedral 4-plet. Vertebrate code has however 5 unbroken 4-plets corresponding to (val,pro,thr,ala,gly) as also 3 unbroken 6-plets (leu,ser,arg)! For vertebrate code the symmetry breaking can therefore occur only for icosahedral Z_2 doublets and tetrahedral Z_4 4-plet.

Variations of the genetic code

There exists also as many as 31 genetic codes (see http://tinyurl.com/ydeeyhjl) and an interesting question is whether this relates to the context dependence. Mitochondrial codes differ from the nuclear code and there are several of them. The codes for viruses, prokaryotes, mitochondria and chloroplasts deviate from the standard code. As a rule, the non-standard codes break U-C or A-G symmetries for the third code letter.

In the proposed framework the failure of energy resonance conditions could be at the level of tRNA. The dark tRNA analog of RNA could be in energy resonance with "wrong" amino acid.

Some examples are in order (see http://tinyurl.com/puw82x8).

1. UUU can code Leu instead of Phe (symmetry breaks for Phe doublet) and CUG can code Ser rather than Leu (symmetry breaks for leu 6-plet). In this case it seems that the "problem" is at the level of tRNA. The dark RNA codon could couple with a "wrong" amino acid.

2. In bacteria the GUG and UUG coding for Val and Leu normally can serve as Start codons. In this case symmetry breaking for Z_4 4-plet would be in question. The problem could be also at tRNA level. Note however that both tetrahedral codons and icosahedral Z_4 codons have the same symmetry group. Could tetrahedral codons correspond to a different frequency scale and correspond to Leu and Val 4-plet instead of symmetry broken ile 4-plet.

3. UGA can code to trp rather than punc: in this case the broken symmetry would be restored since also UGG codes for trp. Both codons for (trp,trp) doublet would be in resonance: this supports the explanation for the emergence of the third stop codon.

4. There is variation even in human mitochondrial code (see http://tinyurl.com/puw82x8). In 2016, researchers studying the translation of malate dehydrogenase found that in about 4 per cent of the mRNAs encoding this enzyme the UAG Stop codon is naturally used to encode the AAs trp and arg. This phenomenon is known as Stop codon readthrough [I45]. Also this phenomenon could be understood at tRNA level.

5. There is also a variant of genetic code in which there are 21st and 22nd AAs Sec and Pyl coded by Stop codons. UGA in (punc,trp) doublet can code for Sec and punc in the same organism. UAG can code for (punc,punc) doublet Pyl instead of punc and UAG. This introduces additional breaking of A-G symmetry for the third letter of codon. Energy resonance at the level of tRNA could explain these deviations from the vertebrate code.

Peter Gariaev has introduced the notion of homonymy of genetic code meaning that the same codon can code for several amino-acids and the coding depends on context. I have considered this phenomenon from the TGD point of view in [L67]. Resonance could explain this phenomenon.

Dark mRNA codon could be in frequency resonance with dark tRNAs coding for different amino acids. The fraction of particular synonymous amino-acid produced in translation would naturally depend on how well the energy resonance condition is satisfied. Homonymy could also reduce to the level of tRNA: this happens if the coupling of the tRNA analog of RNA codon has energy resonance with several amino-acids.

5.4.2 How to produce beautiful bio-music?

Music expresses and produces emotions and harmonies in music correspond to emotions. Chemical representation of the genetic code should be the same irrespective of the emotional state of the gene represented at the magnetic body in terms of dark proton triplets also representing genetic codons and by music of light represents 3-chords of light with frequency ratios determined by one of the bio-harmonies.

This is achieved naturally. The correspondence between the chords of harmony and DNA and amino-acids does not depend on what vertex of icosahedron the base note (C for definiteness in the sequel) corresponds to. It also depends only on the shape of the Hamiltonian cycle invariant

under isometries of the icosahedron. Furthermore, transponations of the scale by power of 3/2 plus projection to the basic octave do not affect the Hamiltonian cycle and therefore leave the correspondence with DNA codons and amino acids invariant.

The sequences of 3-chords would correspond to sequences of DNA codons mapped to sequences of amino-acids. Genes would be like music pieces. These music pieces would also serve as kind of names of passwords in 3N-fold resonance in communications between dark variants of basic biomolecules and between them and ordinary basic biomolecules. They would be like theme songs of TV series catching the attention or names essential for symbolic dynamics at the level of the basic biomolecules. The basic biomolecules in the same emotional state - that is having the same bio-harmony - could resonate and therefore couple.

What the rules for a beautiful bio-music could be? Could these rules select particular bioharmonies and/or particular DNA sequences as allowed chord progressions and allow a deeper understanding of why particular genes are selected? Note that the condition that the chords of bio-harmony define 3N-resonances assignable to transitions of the basic biomolecules could lead to the selection of both harmony and biomolecules. A weaker condition is that ordinary biomolecules couple only to the sum of frequencies appearing in 3N-frequency assignable to dark codon.

Are beautiful chord sequences continuous in some sense?

The original model discussed in [L11, L78] started from a very conservative idea for what harmonic change of chord could be. The two chords should have at least a single quint. This fails for the chords with no quints. The resulting music pieces were also boring which is not a surprise: for instance, the transitions between basic chords C, F, G of C major scale are not possible.

This suggests that one should not start from music but from geometry. Let us consider isohedral geometry for simplicity and the proposed picture for the bio-harmonies.

1. Continuity in some sense is a natural requirement. The natural definition of continuity is that the sequence of 3-chords of progression should define a sequence of neighbouring triangles at the icosahedron. But how should one define neighborhood?

2. Concerning the notion of nearest neighbor, there are 3 options to consider.

   Option I: The strong form of continuity is that neighboring triangles have at least one common edge. This allows 4 different chord pairs. This would mean 4 possible DNA codon pairs for a given Hamiltonian cycle. For bio-harmony the symmetry of icosahedral harmony determined by Z_n ($n = 6, 4, 2$) can change and one would have 4+4+4=12 codon pairs. This kind of correlation for codon sequences would have been observed.

   Option II: For a weaker option the neighboring triangles would have at least 1 common vertex. A given triangle would have 4+3+2+1 =10 neighbors ("1" corresponds to the triangle itself as a neighbor). This would give 10+10+10 =30 possible codon pairs.

   Tetrahedral harmony gives further pairs but since one triangle of tetrahedron should correspond to a fixed triangle of icosahedron, this can change the situation for only a single chord. It is known that the minimum of 32 two codons are needed to code amino acids. The optimum situation very probably not reached for all bio-harmonies (if any), would be that the amino acid associated with the next codon can be any aminoacid. It should be easy to demonstrate by studying a sample of genes or more general DNA codon sequences to find that this prediction is wrong.

   Option III: For the weakest option the nearest neighbors would correspond to triangles at the orbits of the nearest neighbors in the sense of **Option II** or perhaps even **Option I** under the symmetry group Z_n of a given cycle. For instance, the transitions which would not change the codon would be replaced with all codons coding for the same amino-acid. The notion of nearest neighbor would reduce to the level of amino-acids: only the transitions to codons coding for the same amino-acid would be possible.

   For the generalization of **Option I** Z_6 cycle would give 4 orbits of which several must be identical so that there are no problems. Z_4 cycle would give 4 orbits with 4 codons so that one amino acid is missing. For the Z_2 option one obtains only 4 2-origi so that 6 amino-acids are missing.

For the generalization of **Option II** 10+10+10 nearest neighbours would be replaced with their orbits. For the Z_6 cycle there are nearest neighbor 10 orbits and since there are only 4 orbits, there are no problems. For the Z_4 cycle one there are 5 4-orbits so that the minimal degeneracy of a given orbit is 2.

For the Z_2 cycle there are 10 2-orbits, and this number is obtained unless some 2-orbit occurs more than once. The 10 nearest neighbor triangles must correspond to different amino-acids: whether this is possible for all bioharmonies, remains an open question. In any case, it is plausible **Option III** can produce all possible codon pairs although this need not be the case for all bioharmonies. Could preferred bioharmonies be selected by the condition that all codon pairs are possible?

What about melody?

Melody is also an important part of music. A rough rule of thumb is that a beautiful melody tends to contain notes of the chord accompanying it. Dissonance is of course what makes music really interesting. This can be understood as a resonant coupling of the notes of the melody with the notes appearing in the accompanying chords.

Can one apply this picture to the music of light? Could the dark 3-photon states bound to a single unit by Galois confinement tend to decay to ordinary 3-photon states (bio-photons) and could melody represented as a sequence of single photon states couples resonantly to these photons? Could melody correspond to as sequence dark photons 1-plets decaying to ordinary bio-photons coupling to the decay products of dark photon triplets representing genetic codons?

Summary

The basic results of the article are a precise definition of bio-harmony allowing to obtain the analogs of ordinary simple harmonies as special cases and a proposal that the 3-chord sequence defines a beautiful music piece if it corresponds to a continuous sequence for icosahedral faces. In principle this criterion allows bio-harmonies for which all possible codon pairings appear in chord sequences but some bio-harmonies might be excluded.

5.5 Is genetic code part of fundamental physics in TGD framework?

5.5.1 3 basic realizations of the genetic code

Topological Geometrodynamics (TGD) proposes 3 basic realizations of the genetic code [L78]. The first realization is the standard chemical realization. The second realization is in terms of dark proton sequences (dark nuclei) with proton triplet representing a codon. Ordinary DNA strands would be accompanied by dark magnetic flux tubes carrying the dark proton triplets. Also RNA, amino-acids and tRNA would have dark proton analogs.

The third realization is in terms of dark photon triplets and involves the notion of bio-harmony described in terms of icosahedral and tetrahedral geometries with 3-chords of light (perhaps also sound) assigned to the triangular faces of icosahedron and tetrahedron. 12-note scale is realized as a Hamiltonian cycle for icosahedron with the step between nearest neighbor vertices for the cycle realised as quin (scaling of frequency by factor 3/2). The 3-chords correspond to the triangular faces of the icosahedron. Also tetrahedral realization of 4-note scale is necessary in order to obtain genetic code. DNA codons correspond to triangular faces and the orbit of a given triangle under the symmetries of the bio-harmony corresponds to DNA codons coding for the amino acid assigned with the orbit. Vertebrate genetic code emerges as a prediction.

The 3-chords of dark photon triangles are assigned with the triangular faces of icosahedron and tetrahedron [L11, L78, L106] such that their corners are labelled by the notes of the 12- and 4-note scales realized as a icosahedral and tetrahedral Hamiltonian cycles, which are closed paths connecting vertex to neighboring vertex and going through every vertex once.

Genetic code corresponds to a fusion of tetrahedral harmony with 4 chords and of 3 icosahedral harmonies with 20 3-chords having as group of symmetries Z_6, Z_4 and Z_2 - Z_2 can correspond

either to reflection or rotation by π. There are also 6 disharmonies without any symmetries (Z_1) with single DNA codon coding for single amino-acid. There is a considerable number of different icosahedral harmonies and the 3 icosahedral harmonies can be in different key so that a large number of bio-harmonies is possible [L106]. The details of the model of bio-harmony are not completely fixed. In particular, the understanding of stop codons is not completely satisfactory. The small deviations from the vertebrate code (say bacteria and mitochondria) could be understood as being due to the incomplete mimicry of the dark code by chemical code in accordance with the idea that the mimicry has gradually evolved more complete.

Dark photon 3-chords mediate interaction between various realizations. Both dark proton and dark photon triplets would be dynamical units analogous to protons as color confined states of 3 quarks and in the adelic vision the notion of color confinement is replaced with Galois confinement [L106, L165]. Also genes could be seen as Galois confined states of 3N dark protons and dark photons. 3N-photon exchange would be realized as 3N-fold frequency - and energy resonance (mere energy resonance) between dark levels with the same value (different values) of h_{eff} . The possibility to modify the value of h_{eff} for flux tube makes it possible to have for a given codon single resonance energy [L165, L163, L164].

There are several questions relating to the bio-harmony.

1. The gluing of icosahedron and tetrahedron along the face looks ugly in the original model. Why both icosahedron and tetrahedron and why the gluing? The recent progress with M^8-H duality [L101, L102] suggests an answer. The tessellations (honeycombs) of hyperbolic 3-space H^3 appear at the fundamental level and induce sub-tessellations of the magnetic flux tubes. One of these honeycombs- tetrahedral-icosahedral honeycomb (TIH)- involves all Platonic solids with triangular faces - tetrahedron, octahedron, and icosahedron. Could genetic code relate to TIH?

   Cognitive representation [L54, L88, L96] as a set of points of space-time surface in the space of complexified octonions O_c with points having O_c coordinates in extension of rationals associated with the polynomial defining the space-time surfaces are central for for both quantum TGD and TGD inspired theory of cognition leading to adelic physics [L50]. The cognitive representation is mapped to $H = M^4 \times CP_2$ by $M^8 - H$ duality [L101, L102].

   Could the genetic code be realized at the level of fundamental physics as a TIH in H^3 emerging as a cognitive representation [L54, L88, L96, L110] for the space-time surfaces in M^8 and by $M^8 - H$ duality also in $H = M^4 \times CP_2$. If so, the biological realization could be only one particular realization of the code.

2. Why there should ber 3 icosahedral harmonies and one tetrahedral harmony? There is a partial answer to this question. The correspondence with 64 dark proton triplets representing codons and triangles requires 3 icosahedral harmonies. What distinguishes stop codons from other codons? It turns out that stop codons could be dark proton triplets for which the corresponding triangle does not exist in THI realization! The lack of dark proton triplet would mark the end of the gene.

It should be possible to unify various TGD inspired models of genetic code to a single unified description. Is the time ripe for this?

1. The realizations in terms of dark protons and dark photons are related: dark photon 3N-plets would be emitted by dark proton 3N-plets in 3N-proton cyclotron transitions. In the 3N-resonance interaction with DNA, RNA, amino-acids, and tRNA the dark photon 3N-plet would transform to ordinary photons (bio-photons). Energy resonance could select the basic information molecules.

2. How the dark level interacts with the ordinary matter? Music expresses and creates emotions. Light 3-chords for a given bio-harmony could therefore represent an emotional state of MB (emotions as sensory perceptions of MB?). Fourier transform in terms of frequencies represents non-local holistic information and emotional information indeed is holistic information. Codons as units of 6 bits would represent ordinary temporily local, reductionistic information.

Each emotional state corresponds to a particular collection of 3-chords as allowed chords of the bio-harmony and therefore the resonance occurs with different biomolecules or induces different transitions of these bio-molecules. Could this serve as a universal mechanism of bio-control? Could epigenesis as a control of DNA transcription rely on this mechanism? As a matter of fact, the model described in this article emerged from an attempt to understand epigenesis in the TGD framework.

3. Is it possible to unify all models of the genetic code to single model so that the representation of a codon as dark proton triplet is assigned to a representation as an "activated" triangle of icosahedron or tetrahedron of TIH containing at it vertices dark protons defining the same codon as the triangle as 3-chord for a given icosahedral harmony. Could these "activated" triangles be selected faces of TIH. Could genes correspond to sequences of these icosahedron-tetrahedron pairs at magnetic flux tubes?

In the sequel the questions raised above are discussed.

5.5.2 Genetic code and hyperbolic tessellations

Why 3 different icosahedral harmonies with symmetries Z_6, Z_4, and Z_2 plus one (there is only one) tetrahedral harmony is needed to get $3 \times 20 = 60 + 4$ chords in correspondences with 64 codons of the genetic code?

Hyperbolic tessellations and genetic code?

What comes into mind, are fundamental lattice like structures - tessellations - having as basic building bricks icosahedron and tetrahedron - at least these. This would make sensical to speak about gluing of tetrahedron to icosahedron, which looks a strange operation in the original formulation of the model.

1. Platonic solids correspond to finite tessellations at 2-sphere or equivalently 3-D solid polyhedrons in 3-D space Euclidian space E^3. Maybe one could answer the question by increasing dimension and by studying 3-D polyhedrons of 4-D space defining tessellations of the hyperbolic space H^3.

   By $M^8 - H$ duality [L101, L102], these tessellations appear at the fundamental level TGD as cognitive representations since the 3-D mass shells with the geometry of H^3 appear naturally in the solutions of dynamical equations as algebraic equations at the level of M^8 identifiable as real section of complexified octonions O_c. The dynamics reduces to the associativity of the normal space of the space-time surface determined as a root for the real part of an octonionic polynomial obtained as an algebraic continuation of a real polynomial. Real part is defined in quaternionic sense by decomposing octonion to two quaternions in the same manner as a complex number is decomposed to its real and imaginary parts.

   The algebraization of the octonionic counterpart of Dirac equation forces its identification as the counterpart of momentum space version of the ordinary Dirac equations and the identification of M^8 as an analog of momentum space so that space-time surface is analog of Fermi ball.

2. The tessellations of H^3 are analogs of lattices in an Euclidian momentum space E^3. In adelic physics they define cognitive representations providing unique discretizations of space-time surface both at the level of M^8 and H. $M^8 - H$ duality maps tessellations to their analogs of $H = M^4 \times CP_2$. Contrary to my long held belief, Uncertainty Principle forces the map to be instead of a direct identification an inversion for $M^4 \subset M^8 \to M^4 \subset H$ [L101, L102]. Mass hyperboloids correspond in H to light-cone proper time constant sections of space-time surface: light-cone proper time defines Lorentz invariant cosmic time.

3. The tessellations of H^3 can have several different analogs of unit cells glued together along their 2-D faces. The positive curvature of sphere forces Platonic solids as tessellations of 2-sphere to be closed and be finite. H^3 as a negative curvature space does not allow a closure. This implies a large number of tessellations as infinite analogs of regular solid polyhedra.

Both icosahedron, octahedron and tetrahedron have triangular faces so that they might allow gluing together for the simplest tessellations. Also more complex tessellations are possible.

Details about hyperbolic tessellations

Consider now in more detail some tessellations of H^3 possibly relevant for the bio-harmony [L11, L78, L106] involving icosahedral and tetrahedral geometries.

Some basic concepts and notations are necessary to help the reader to understand the Wikipedia articles, which give detailed explanations and illustrations.

1. Regular polytopes are tessellations consisting of single polytope. There are subtle differences between tessellations and honeycombs: tessellations are more general than honeycombs. These differences are not relevant for what follows so that I will use both terms interchangeably.

2. Schläfli symbol [A11] `https://cutt.ly/7jagV1T` $(p, q, r, ..)$ characterizes regular polytopes in both Euclidian spaces and hyperbolic spaces locally but does not tell anything about the object globally. For a 3-D regular polytope (p, q, r) in 4-D space (say tessellation of H^3 the faces have p vertices, q identical faces meet at given vertex, and r identical 3-cells meet along given edge. For instance, $(3, 5, 3)$ characterizes a regular tessellation having icosahedron as fundamental cells with 3 icosahedrons meeting along given edge.

3. Vertex figure [A15] `https://cutt.ly/yjagMQn`) represents the neighboring vertices as seen from a given vertex. Formally it is defined by contracting all edges emanating from the vertex to their middle points and connecting these points by lines along faces. For a n-D polytope (p,r,s,..) the vertex figure is n-1-D polytope (r,s,...). For instance, for icosahedron (3,5) the vertex figure is (5) telling that 5 edges meet at vertex. For the regular honeycombs in H^3 the vertex figure is a regular polyhedron. For instance, for $(3, 5, 3)$ it is (5,3) identifiable as dodecahedron. Second notation for the vertex figure is as the list of numbers of edges meeting at the vertices of the face: For icosahedron this list is 3.3.3.3.3 telling that the faces of the edge figure has 5 vertices at which edges meet.

4. Edge figure [A15] (`https://cutt.ly/djag9Q9`) is the vertex figure of the vertex figure of the polytope. For D-dimensional polytope it is polytope of dimension D-2. For a regular polytope $(p, q, r, ..., s)$ the edge figure is $(r, ..., p)$: for Platonic solids (r,s) edge figure is () telling that two faces meet along a given edge. For the regular polytope (r,s,p) the edge figure tells the number of identical 3-cells meeting at given edge. For cubic lattice it is 4. For semiregular honeycombs the 3-cells need not be identical.

5. The notion of dihedral angle (see `https://cutt.ly/vjs2OBI`) is very useful in trying to understand whether a given tessellation of E^3 and H^3 is possible. Dihedral angle is defined as the angle between the faces of the polytope meeting along a given edge. For tetrahedron it is 120 °, for octahedron 90 ° and for icosahedron 138.19 °. Since at least 3 polyhedra must meet at a given edge, the sum of these angles must be smaller than 360 degrees in E^3. This prevents icosahedral tessellations in E^3.

   In H^3 negative curvature allows the sum to be larger than 360 ° (think of polygons at a saddle surface as a visualization) so that 3 icosahedra might meet at a given edge as indeed occurs for $(3, 5, 3)$ tessellation. The sum of the dihedral angles of T, O, and I assignable to to tetrahedral-icosahedral honeycomb in H^3 is 348.19 ° and smaller than 360 ° but rather near to it.

6. An important notion is Coxeter group [A3] (`https://cutt.ly/FjdEJeG`) acting as the symmetry group of the honeycomb. Coxeter group is generated by reflections meaning that honeycombs can be generated by reflections in suitable mirror planes. Honeycomb is constructed kaleidoscopically: a concretization of Leibniz's monadology is in question. Coxeter group and therefore also the honeycomb is characterized by Coxeter diagram [A2] (`https://cutt.ly/SjdEZiH`) having as its nodes the mirrors and connected by edges labelled by the dihedral angles $\phi = \pi/n$ between the mirror planes. The value of n is written explicitly to the diagram except when it is the minimal value $n = 3$. For instance, the

sequence [(5,3,3,3,3)] characterizing tetrahedral-icosahedral honeycomb in H^3 tells that the dihedral angles between the 5 mirror planes are $(\pi/5, \pi/3, \pi/3, \pi/3, \pi/3)$.

Consider now honeycombs in hyperbolic space H^3.

1. The simplest tessellations - regular honeycombs - of H^3 consist of icosahedra and dodecahedra having the same isometry group. That 3 of the 4 most symmetric honeycombs in H^3 have icosahedral symmetries whereas the fourth has cubic symmetries, is a highly encouraging sign. These 4 regular honeycombs are icosahedral honeycomb $\{3, 5, 3\}$ with 3 icosahedrons meeting along edge; order-5-cubic honeycomb $\{4, 3, 5\}$ with 5 cubes (rather than 4 as in E^3) meeting along a given edge; and dodecahedral honeycombs of order 4 (5) with 4 (5) dodecahedra meeting along edge. In all these cases the sum of the dihedral angles is larger than 360 ° so that the negative curvature of H^3 is essential for the existence of these honeycombs.

2. What about the combinations of Platonic solids having triangles as faces - tetrahedron, octahedron, and icosahedron? From Wikipedia article [L122] (`https://cutt.ly/cjaheWC`) one learns that there exists honeycombs of H^3 characterized by Schläfli symbol $\{(3, 3, 5, 3)\}$ and Coxeter group with symbol $[(5, 3, 3, 3)]$ consisting of reflections and generating the honeycomb. The regular honeycombs are characterized by 3 integers (say $(3, 5, 3)$) and the meaning of the code is not quite clear to me but must reflecs the fact that the honeycomb is semiregular.

   Tetrahedron corresponds to (3,3) and icosahedron to (3,5) and octahedron (3,4) as a rectified tetrahedron obtained by contracting edges to their middle points and expanding vertices to faces, has symbol $r(3, 3)$. Perhaps (3,3) in (3,3,5,3) refers tCoxetergroupo both tetrahedron and its rectification and (3,5) in (3,3,5,3) to icosahedron. The last "3" tells that 3 identical solid icosahedra, tetrahedra, or octahedra meet at given edge.

   In particular, the tetrahedral-icosahedral honeycomb (TIH) is a compact uniform but not a regular honeycomb, having icosahedra, tetrahedra, and octahedra, all of which have triangular faces, as analogs of unit cells [A8, A6, A14] (see `https://cutt.ly/xhBwTph`, `https://cutt.ly/lhBwPRc`, and `https://cutt.ly/0hBwUOO`)). The Wikipedia article [L122] contains beautiful illustrations of these honeycombs.

   One can wonder why "tetrahedral-icosahedral honeycomb" does not involve octahedron. This is said to reflect the fact that only tetrahedral and icosahedral cells of the tessellation are regular 3-cells. All these polyhedra are regular as Platonic solids, and it remains unclear to me what the lacking regularity of the octahedron as 3-cell means in the recent context.

   For TIH $\{(3, 3, 5, 3\}$ the vertex figure is rhombicosidodecahedron (RID) [A10] (`https://cutt.ly/yjahitS`) discovered already by Kepler. Kepler talked about Harmonices Mundi and I cannot but smile as I recall how I read as a young man a book having fun with Kepler's medieval belief on celestial harmonies and laughed also! Maybe the celestial harmonies are making a glorious comeback!

   RID is an Archimedean solid [A1] (`https://cutt.ly/njahaGN`) having 60 vertices corresponding to 12 disjoint pentagons and 20 disjoint triangles with 60 vertices both. RID has as faces 20 triangles assignable to icosahedron, 12 pentagons assignable to dodecahedron plus 30 squares - 62 faces altogether. RID is obtained by radially scaling the distance of icosahedral and dodecahedral faces from origin but keeping the area of the spherical faces the same: this yields squares as additional faces. Triangles and pentagons have only squares as edge neighbors.

   Edge figure tells the number of edges meeting at given edge. For TIH it is 3. Regular and single-ringed Coxeter diagram uniform polytopes to which also TIH belongs have a single edge type. Therefore icosahedron, tetrahedron, and octahedron must meet at given edge. That vertex figure contains 3 types of faces (triangles, and squares, and pentagons) presumably reflects this. Recall that the sum of the dihedral angles of T,O, and I is 348.19 °.

One can try to build a more concrete picture about how the Platonic solids are glued together along their triangular faces in the icosahedral-tetrahedral honeycomb.

1. Must to make this concrete, one can regard Platonic solid as a kind of mini Earth with two other Platonic solids glued to its surface like mountains. In all cases one has Platonic analog of a planar lattice of triangles at this mini Earth. To minimize typing call the 3 different Platonic solids T, O, and I.

2. Due to the symmetries one expects that for O and I the triangles correspond to different Platonic solids if they are edge neighbors. For T this is not possible since all faces are edge neighbours. All 6 2+2 configurations of B and C are however related by a rotational symmetry. This already gives a rather satisfactory picture about what the situation looks like at the surface of each mini Earth (I cannot avoid the analogy with inner planets, the living Earth as the largest one would correspond to I!).

3. The radius R of circumscribed inner or or outer sphere gives an idea about the size scales of these Platonic solids when the edge length a is the same for them as it is in the recent case. The following gives the radii of the outer sphere.

$$\begin{array}{lll} \text{tetrahedron} & \frac{R_{T,out}}{a} = \sqrt{\frac{1}{2}} \ , & \frac{R_{T,in}}{a} = \sqrt{\frac{1}{24}} \\ \text{octahedron} & \frac{R_{O,out}}{a} = \sqrt{\frac{3}{4}} \ , & \frac{R_{O,in}}{a} = \sqrt{\frac{1}{6}} \ , \\ \text{icosahedron} & \frac{R_{I,out}}{a} = \frac{1}{2}\sqrt{\phi\sqrt{5}} \ , \phi = \frac{(1+\sqrt{5})}{2} \ , & \frac{R_{I,in}}{a} = \frac{\sqrt{3}}{12}\sqrt{3+\sqrt{5}} \ . \end{array} \tag{5.5.1}$$

4. The ratios of the outer radii are given by $R_{I,out} : R_{O,out} : R_{T,out} = \sqrt{\phi\sqrt{5}} : \sqrt{\frac{3}{4}} : \sqrt{\frac{1}{2}} \simeq 1.9021 : 0.8660 : 0.7071$. The ratios of the inner radii are given by $R_{I,in} : R_{O,in} : R_{T,in} = \sqrt{\phi\sqrt{5}} : \sqrt{\frac{3}{4}} : \sqrt{\frac{1}{2}} \simeq .756 : 0.408 : 0.2041$. That icosahedron has the largest size, is natural since the total solid angle defined as a sum of the solid angles of the 20 triangles is $4/pi$ and the contribution of an individual triangle is smallest for I and largest for the 4 triangles of T.

Could TIH allow to unify the models of genetic code?

Does this picture help to say anything interesting about the model of bio-harmony and even to unify the models of genetic code?

1. tessellations define in a natural manner discretizations of MB defining cognitive representations suggested to relate to the geometric representations for the states of the brain at MB and more generally, for the states of various parts of the biological body at MB. There is evidence for an effective hyperbolic geometry of brain realized in a statistical sense [J11] (`http://tinyurl.com/ybghux6d`) : functionally similar neurons are near to each other in this effective hyperbolic geometry. This evidence is discussed from TGD point of view in [L103]: one ends up with a proposal that the MB of the brain provides a geometric representation for the statistical aspects of the brain - kind of abstraction? Information from the brain would be sent by dark Josephson radiation from similar neurons to positions of MB near to each other. This model could generalize to other parts of organism. MBs could form a kind of abstraction hierarchy representing more and more abstract data about the state of organism.

2. Could the icosahedral-tetrahedral tessellation allow a justification for the fusion of 3 icosahedral harmonies with the tetrahedral harmony? Why does the octahedral harmony disappear? Octahedral harmony would mean 6 additional notes assignable to the vertices of octahedron and 8 3-chords and this does not fit with facts.

   Remark: In the Wikipedia article about TIH it is said that octahedrons of TIH are not regular, unfortunately in the sense that I do not understand. Note also that tetrahedral and octahedral harmonies are unique because there is only a single Hamiltonian cycle.

3. Geometrically the tessellation means identification of the neighbouring faces, which gives a justification for the strange looking proposal of gluing tetrahedron to icosahedron in order to

fuse 3 icosahedral and one tetrahedral harmony. If also the 3-chords associated with the faces are identified, one can ask whether only icosahedral and tetrahedral harmonies are needed and the chords of the octahedral harmony are determined by them.

2 3-chords of tetrahedral harmony are the same as those for icosahedral harmony but the 2 3- chords associated with the 2 T-O faces are independent. This would give 62 independent chords (amusingly, 62 happens to be the number of faces of RID).

One of the tetrahedral chords is necessary since purely icosahedral harmony allows to get only 19 amino-acids identified as the orbits of the chords under the symmetries of a particular icosahedral harmony with 20 chords: one additional chord is needed for the missing amino-acid. Since two icosahedral triangles facing the tetrahedron "eat" 2 further tetrahedral chords, this leaves 1 tetrahedral chord from 4: 3 chords as tetrahedral codons are missing. Could the 3 missing tetrahedral 3-chords correspond to the ordinary DNA codons acting as stop codons? Could the stop codons lack a representation as dark photon triplets or could their frequencies be such that they do not allow 3-resonance with any tRNA?

4. How genes would be realized in the tessellation? Could dark genes correspond to flux tubes forming 1-D sub-tessellations of H^3 induced to the flux tubes? Could gene correspond to a sequence of icosahedron-tetrahedron pairs such that neighboring codons are associated with icosahedron-tetrahedron pairs as cell-neighbors. Two subsequent icosahedrons would have a tetrahedron between them.

   Could the tessellation induced from H^3 to MB be dynamical involving an "activation" of a particular triangle as a codon inside each icosahedron and tetrahedron? Could dark genes at the flux tubes have these codons as induced dark codon sequences? Could "activation" mean that the triangle representing particular codon is accompanied by 3 dark protons at its vertices and representing the same genetic codon? The representations in terms of dark protons triplets, as triangles of icosahedron and tetrahedron, and as dark photon triplets would fuse to single representation. There could be a representation also for stop codons in terms of 3 dark protons but there would not be no triangle where to locate them so that coding would stop! The missing dark codon would signify the end of the gene.

   This would give the long-sought connection between dark codons realized as dark triplets and dark codons realizing bio-harmony and dark codons realized as dark photon triplets generated in the cyclotron transitions of dark codons. An essential role would be played by Galois confinement [L106] stating that these triplets behave like dynamical units - just like 3 confined quarks forming a baryon. Galois confinement generalizes to the level of genes.

5. This proposal is of course one of the many variations of single theme developed during years. What is new that the proposal would make the roles of the icosahedral and tetrahedral geometries concrete, not at the level of bio-molecules but at the level of their MBs. A profound dramatic generalization of the notion of genetic code from biology to the level of fundamental physics is also suggestive. Even a hierarchy of genetic codes in various scales can be considered.

   The interpretation of various harmonies as correlates of emotions implies that each icosahedral-tetrahedral unit of the tessellation would have its own varying emotional state expressed and affected by biochemical level via different interaction actions with ordinary biomatter realized in terms of dark photon N-resonance with targets depending on the emotional state [L165, L163, L164]. This could serve as a universal mechanism of bio-control by MB applying also to epigenesis.

   There are still several open questions: in particular, what is the deeper reason for the fusion of just 3 icosahedral bio-harmonies. That the number of the dark codons is 64 is a partial reason but is this enough.

6. There are reasons to ask whether the cell membrane and microtubuli could provide a 2-D realizations of the genetic code [L165]. If genes are induced as 1-D sub-tessellations from that of MB, there is no reason to exclude 2-D or even 3-D induced tessellations.

7. I cannot avoid the temptation of mentioning the notion of memetic code [K39], which was my first idea about genetic code and proposed as a generalization of genetic code by starting

from a speculated hierarchy of Mersenne primes, whose members would come as $M(n+1) = M_{M(n)}$, $M_n = 2^n - 1$, ($M(2) = 2$. This gives the Mersenne primes $M(2) = M_2 = 3$, $M(3) = 2^3 - 1 = 7$, $M(4) = M_7 = 2^7 - 1$, $M(5) = M_{127} = 2^{127-1}$. It is not known whether the hierarchy continues. M_7 would correspond to the ordinary genetic code and M_{127} to memetic code with codons realizable as sequences of 20 codons.

Could memetic code be realized by TIH? Could one consider a planar or cylindrical subtessellation with a width of 20 tetrahedral-icosahedral pairs? If the size assignable to single pair is that of DNA codon - 1 nm roughly - the width would be about 20 nm which might relate to the radial scale of the microtubuli.

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5.6 Galois groups and genetic code

Galois groups, in particular simple Galois groups acting on cognitive representations consisting of points, whose coordinates in a number theoretically preferred coordinate system of octonions belong to EQ, play a fundamental role in the TGD view of cognition [L110]. The TGD based model of genetic code [L11, L107] involves in an essential manner the groups A_5 (icosahedron (I)), which is the smallest non-abelian simple group, and A_4 (tetrahedron (T)). Genetic code has as building bricks Hamiltonian cycles of I and T. Genetic code relates to information and therefore to cognition so that the interpretation of these symmetry groups as Galois groups is suggestive.

The most recent step of progress was the realization that genetic code can be represented in terms of icosa-tetrahedral tessellation of a hyperbolic 3-space H^3 [L122] and that the notion of genetic code generalizes dramatically. Also octahedron (O) is involved with the tessellation but plays a completely passive role. The question why the genetic code is a fusion of 3 icosahedral codes and of only a single tetrahedral code remained however poorly understood.

The progress in the understanding of the role of Galois groups inspired by a summary of inverse Galois problem [A44] (`https://cutt.ly/jmjpyDS`) in TGD framework [L117] made it possible to answer this question. The proposal is that the symmetry groups of the I, O, and T can be identified as Galois groups.

Icosa-tetrahedral tessellation can be replaced with its 3-fold covering replacing $I/O/T$ with the corresponding symmetry group acting as a Galois group. Octahedral codons can be regarded as icosahedral and tetrahedral codons so they do not contribute to the code. T has only only a single Hamiltonian cycle and its 3-fold covering behaves as a single cycle. T has only only a single Hamiltonian cycle and its 3-fold covering behaves effectively as a single cycle.

5.6.1 Could the symmetries of icosa-tetrahedral realization of the genetic code correspond to Galois symmetries?

Abelian groups Z_p, p prime, are simple and the alternating group A_5 with order 60 is the smallest non-Abelian simple group. All groups A_n, $n \geq 5$ are simple and have $n!/2$ elements. A_5 corresponds to the icosahedral group isomorphic with the symmetry group of the dodecahedron.

The TGD based model of genetic code [L11, L107, L122] involves in an essential manner the groups A_5 (icosahedron) and A_4 (tetrahedron). Simple groups play a fundamental role in the TGD view of cognition. Could this mean that genetic code represents the lowest level of an infinite cognitive hierarchy?

The TGD inspired model model of genetic code, cognition, and Galois groups

TGD based model of bioharmony [L11, L107, L122] provides a model of genetic code as a fusion of 3 icosahedral Hamiltonian cycles and the unique tetrahedral Hamiltonian cycle (what "fusion" precisely means is far from clear and I have considered several options).

Icosahedral Hamiltonian cycles is a non-self-intersecting path at icosahedron connecting nearest points if icosahedron going through all 12 points of the icosahedron. It is interpreted as a

representation of a 12-note scale with a scaling by quint assigned to a given step along the cycle. For a given Hamiltonian cycle, the allowed 3-chords of icosahedral harmony are identified as chords defined by the triangular faces of the icosahedron.

Remark: In the sequel I will use the shorthands IH, OH, and TH for icosahedral, octahedral, and tetrahedral harmonies. Also the notation $I/O/T$ will be used for icosahedron/octahedron/tetrahedron unless there is a danger of confusing them with their symmetry groups with identical shorthand notations.

Galois groups are essential for cognition in the TGD framework. In particular, simple groups as primes for groups are also primes for cognition [L110]. Genes represent information and Galois groups are crucial for cognition in the TGD framework. Genes would correspond to sequences of 3-chords of bioharmony. This raises several questions.

Could genetic code relate to Galois group A_5 as the smallest simple non-abelian Galois group (and also to the fact that the only polynomials of order smaller than 5 are generically solvable)? Could genetic code correspond to the lowest level in a hierarchy of cognition and of analogs of genetic code?

The order $n = 60$ for A_5 suggests a fusion of 3 icosahedral codes to give 20+20+20 = 60 codons.

1. 3 Platonic solids, - icosahedron (I), tetrahedron (T) , and octahedron (O) - which have triangles as faces so that one can consider the possibility of constructing a lattice like structure by gluing these Platonic solids together along their faces. Hyperbolic space H^3 indeed allows isosa-tetrahedral tessellation, which also involves O:s. I have proposed that this allows a realization of genetic code and also of genes [L122]. The notion of gene generalizes so that genes can also be 2- or 3-D lattice-like structures.

2. A_5 has $A_3 = Z_3$ as a subgroup and I(cosahedron) corresponds to A_5/Z_3. I has several Hamiltonian cycles having as a symmetry group Z_6, Z_4 or Z_2. Z_2 can act either as rotations or reflections.

   Q: Could A_5 as a Galois group as 3-fold covering of I make it possible to understand why the fusion of just 3 icosahedral codes is possible?

3. Tetrahedral group T corresponds to the alternating group $A_4 = S_4/Z_2 = Z_4 \times Z_3$ with 12 elements and tetrahedron identification as A_4/Z_3. The tetrahedral Hamiltonian cycle (4-scale) is unique and has 4 3-chords. The 3-fold copy would correspond to A_4. Information about the unique Hamiltonian cycles of O and T can be found in [A23] (`https://cutt.ly/9mlMiV8`).

   Q: Could the factor that there is only one tetrahedral cycle explain why only a single tetrahedron contributes?

4. Octahedral group O has 24 elements and is the wreath product of Z_3 and Z_2^3 and has also the decomposition $O = S_2 \times S_4$. Octahedron can be identified as O/Z_3. Also octahedral Hamiltonian cycle representing 8-scale with 8 chords is unique.

   Q: Why don't octahedral codons contribute?

A model of the genetic code based on icosa-tetrahedral tessellation of hyperbolic 3-space

TGD leads to a proposal for a geometric representation of the genetic code in terms of icosa-tetrahedral tessellation of the hyperbolic 3-space H^3 (mass shell or light-cone proper time $a =$ *constant* hyperboloids of M^4) [L122]. Both I, O, and T having triangular faces appear in the tessellation. Recall that the corresponding harmonies are denoted by IH, OH and TH.

I do not completely understand the details of the icosa-tetrahedral tessellation. The following picture satisfies the constraints coming from the notion of harmony but I have not proven that it is correct. Here the help of a professional geometrician knowing about tessellations of H^3 would be needed.

1. The analog of the discrete translational symmetry for lattices can be assumed: all I:s , O:s and T:s are equivalent as far as common faces with neighboring Platonic solids are considered.

2. The term icosa-tetrahedral tessellation suggests that all octahedral faces are glued to tetrahedral and icosahedral faces so that octahedral chords reduce to either icosahedral or tetrahedral chords. OH would not be an independent harmony. This requires that the number of common faces between two O:s vanishes: $n_O^O = 0$.

3. T shares at least 1 face with a given I so that the number of tetrahedral chords is reduced to at most 3 for given T. 4 purely tetrahedral faces (not shared with I) are needed. I would have $n_{IT} \leq 4$ purely tetrahedral faces in such a way that the total number of purely tetrahedral 3-chords is 4.

   The simplest possibility is that I shares a common face with 2 T:s. Each T shares 2 faces with O providing 2 purely tetrahedral 3-chords and shares the remaining 2 faces with distinct I:s. One would have $n_T^I = 2$, $n_T^O = 2$, $n_T^T = 0$.

   Since each I defines independently 20 chords, 2 I:s cannot have common faces. One would have $n_I^T = 2$, $n_I^I = 0$ and $n_I^O = 18$ to give $n_I^T + n_I^O + n_I^I = 2 + 18 + 0 = 20$.

4. What remains to be fixed are the numbers n_O^I and n_O^T satisfying $n_O^I + n_O^T = 8$. The conditions $n_O^T \geq 1$ and $n_O^I \geq 1$ must be satisfied since both T and I share faces with Os.

   Music comes to rescue here. The 8 3-chords of OH could define OH sub-harmony of IH. Analogously, the 4 3-chords of TH could define TH as a sub-harmony of OH.

   Could IH sharing 18 3-chords with OH contain 2 transposed copies of OH plus 2 chords of TH? IH cannot of course contain the entire TH as a sub-harmony.

   Could OH contain one copy of TH? This would give $n_O^I = n_O^T = 4$. Could the IH part of OH actually be TH as a sub-harmony of IH so that OH would reduce to 2 copies of TH?

To sum up, if the answers to the questions are positive, the incidence matrix n_i^j, $i, j \in \{I, T, O\}$, telling how many faces i shares with j would be given by

$$\begin{bmatrix} n_I^I & n_I^O & n_I^T \\ n_O^I & N_O^O & n_O^T \\ n_T^I & N_T^O & n_T^T \end{bmatrix} = \begin{bmatrix} 0 & 18 & 2 \\ 4 & 0 & 4 \\ 2 & 2 & 0 \end{bmatrix} \quad . \tag{5.6.1}$$

3-fold cover of the icosa-tetrahedral tessellation

The proposed model does not yet explain the fusion of 3 icosahedral Hamiltomnian cycles. A 3-fold cover of the icosa-tetrahedral tessellation which replaces Platonic solids with their symmetry groups is highly suggestive. This raises a series of questions.

1. How could this representation relate to a possible interpretation in terms of the Galois groups $I = A_5$ and $O = S_2 \times S_4$ and $T = A_4$? Z_3 appears as a sub-group of all these groups and these Platonic solids are coset spaces I/Z_3, O/Z_3, and T/Z_3.

2. Could one lift the icosa-tetrahedral tessellation to a 3-sheeted structure formed by the geometric representations of the Galois groups of this structure acting as symmetry groups? Platonic solids would be replaced with their symmetry groups acting as Galois groups.

3. Could the 3 different icosahedral Hamiltonian cycles correspond to different space-time sheets - roughly CP_2 coordinates as 3-valued functions of M^4 coordinates whereas 20 regions representing icosahedral vertices would correspond to different loci of $E^3 \subset M^4$ just as one intuitively expects?

4. Same should apply to the tetrahedral and octahedral parts of the tessellation. But don't the 3 identical copies of the tetrahedral Hamiltonian cycle give 64+8=72 codons? How can one overcome this problem?

   The following is a possible answer to these questions.

1. $h_{eff} = 60h_0$ corresponds to 60-sheeted space-time (here also $60k$-sheeted space-time is possible if 60-D extension of k-dimensional extension is in question). For T and O an analogous picture would apply. One could say that the projections of I and O and T are in M^4. At each sheet one would have icosa-tetrahedral tessellation.

2. I has 3 types of Hamiltonian cycles with symmetry groups Z_6, Z_4, and Z_2 and can give 3 different copies. However, only a single copy of tetrahedral harmony appears in the model: otherwise the number of codons would be larger than 64. Could the 3 identical Hamiltonian cycles for T and O effectively correspond to a single Hamiltonian cycle?

3. The fusion of Hamiltonian cycles is analogous to a formation of many-boson states. For T and O all Hamiltonian cycles would be identical: one would have only one Hamiltonian cycle effectively. The 3-chords associated with the 3 octahedral and tetrahedral cycles are identical so that only single tetrahedral harmony would be present.

To sum up, the lift of the icosa-tetrahedral complex to that defined by the respective Galois groups could explain why just 3 icosahedral Hamiltomian cycles and effectively only 1 tetrahedral cycle.

5.7 MeshCODE theory from TGD point of view

Benjamin Goult has made an interesting proposal in the article *The Mechanical Basis of Memory the MeshCODE Theory* [J2] (`https://cutt.ly/WzlrmrM`) published in Frontiers of Molecular Neuroscience in 25 February 2021.

The proposal is that the cell or at least synaptic contacts realize mechanical computation in terms of adhesive structures consisting of hundreds of proteins known as talins, which act as force sensors. Talins are connected to integrins in the extracellular matrix, to each other, and to the actins in the cell interior.

This proposal does not conform with the TGD vision but inspires a series of questions leading to a rather detailed general vision for how magnetic body (MB) receives sensory input from biological body (BB) coded into dark 3N-photons representing genes with N codons and as a response activates same but differently realized genes, RNA or corresponding proteins as a reaction [L165, L11, L78, L107, L122]. This would mean a universal response function assigning to sensory input a unique response. Sensory input would code the response to it in terms of dark genes, which also generalize in TGD framework.

5.7.1 Some basic facts

The role of a protein known as talin [I17] (`https://en.wikipedia.org/wiki/Talin_(protein)`) is the topic of the article. Talin is associated with the cell-substratum contact and mechanically couples cytoskeleton and extracellular matrix (ECM) together. Adhesion units formed by integrin coupling to ECM, talin, and actin at cytoskeleton side form adhesion structures consisting of hundreds of adhesion units.

It is good to begin with by listing some basic definitions and facts.

1. Cytoskeleton [I4] (`https://en.wikipedia.org/wiki/Cytoskeleton`) consists of microfilaments (actin), intermediate filaments, and microtubules (MTs) which in neurons are called neurotubules. Neurons contain neurotubules [I13] (NTs)(`https://en.wikipedia.org/wiki/Neurotubule`) generated at MT organizing center (MTOC) and transferred to dendrites and axon, where they are parallel to the neuronal surface.

   The cytoskeleton of an ordinary cell has as basic building bricks MTs and microfilaments and intermediate filaments. Both MTs and NTs are polarized. The + ends of MTs are at MTOC. + ends of NTs point towards the axon terminal and - end to the parent neuron. NTs in dendrites have mixed polarities.

2. ECM [I7] (`https://cutt.ly/5zNYtP6`) is a three-dimensional network consisting of extracellular macromolecules and minerals, such as collagen, enzymes, glycoproteins and hydroxyapatite that provide structural and biochemical support to surrounding cells. Cell adhesion, cell-to-cell communication and differentiation are common functions of the ECM.

3. Integrins [I9] (https://cutt.ly/xzNYk7n) are transmembrane receptors that facilitate cell-cell and cell-extracellular matrix (ECM) adhesion. Upon ligand binding, integrins activate signal transduction pathways that mediate cellular signals such as regulation of the cell cycle, organization of the intracellular cytoskeleton, and movement of new receptors to the cell membrane. The presence of integrins allows rapid and flexible responses to events at the cell surface (e.g. signal platelets to initiate an interaction with coagulation factors).

4. Actins [I2] (https://cutt.ly/LzNYEo9) are a family of globular multi-functional proteins that form microfilaments. It is found in essentially all eukaryotic cells, where it may be present at a concentration of over 100 μM; its mass is roughly 42-kDa, with a diameter of 4 to 7 nm. An actin protein is the monomeric subunit of two types of filaments in cells: microfilaments, one of the three major components of the cytoskeleton, and thin filaments, part of the contractile apparatus in muscle cells.

One can visualizetalin as a spring between cytoskeleton and ECM. Talincouples directly to integrins at ECM side and either indirectly or directly to actin at cytoskeleton side. Talin's role is to be a rope in a "tug-of-war" between integrins at ECM and actin and it acts as a force sensor and could give rise to a molecular sense of touch based on force.

The part of talin subject to forces from the cellular interior and environment consists of 13 proteins domains which can be in two thermodynamically stable states analogous to the opposite magnetizations of ferromagnet and the domain exhibits hysteresis curve under a varying external force. The phases correspond folded and unfolded configuration looking like a straight bar. The two phases can be labelled by a bit and the proposal is that the talin conformations define 13 bits.

The domains are not identical so that each equilibrium state under varying external net force could correspond to a unique configuration in which domains are folded or unfolded. If so, talin would serve as a 13-bit force sensor of external forces with finite resolution corresponding to 13 octaves in linear scale. It will be found that the response could actually be determined by 6 bits and correspond to genetic codon.

The abstract of [I63] summarizes the functions of talin.

> ... Talin forms the core of integrin adhesion complexes by linking integrins directly to actin, increasing the affinity of integrin for ligands (integrin activation) and recruiting numerous proteins. It regulates the strength of integrin adhesion, senses matrix rigidity, increases focal adhesion size in response to force and serves as a platform for the building of the adhesion structure. Finally, the mechano-sensitive structure of talin provides a paradigm for how proteins transduce mechanical signals to chemical signals.

It is clear that talin does not look only a passive sensory receptor. That integrins are not necessary for talins to function implies that they have emerged before integrins in the evolution. It is clear that talins are essential aspect of multicellular life.

5.7.2 Could adhesion structures act as classical computers?

The proposal of the article [J2] relies on computationalism and suggests that talin could be more than a sensory receptor and adhesion structures could act as a computer. The structures formed by the adhesion units consisting of integrin-talin-actin triplets would serve as 13-bit units. Adhesion units would perform mechanical computation based on what authors call MESHcode.

One can argue that mechanical computation requires that adhesion units are isolated from the environment during the computation. This is in conflict with the role as force sensors. A weaker proposal would be that computation occurs only in the synaptic contacts which should be isolated during the computation. The same could take place also in the contacts between neurons and glial cells.

Concerning the synaptic level, a more realistic view to my opinion is that learning as a strengthening of the synaptic strengths corresponds to a development of force equilibrium of adhesion units. Learning could be described as the change of the resting states of the talin units and lead to a higher tension and larger number of unfolded protein domains. Nerve pulse patterns could cause temporary changes of this pattern.

5.7.3 TGD interpretation of adhesion units as quantal force sensors

In the TGD framework all communications and control in biology should rely on genetic code whose fundamental realization would be at the level of dark proton sequences forming dark nuclei with $h_{eff} = nh_0 > h$ and dark photons.

Dark proton triplets - light 3-chords - would represent the counterparts for dark DNA, RNA, tRNA, and aminoacids and dark photon triplets could represent dark DNA codons [L11, L78, L107, L122]. Number theoretic vision [L50, L51] leads to a proposal that not only dark 3-photon 3-proton units act as single particle like units but also dark 3N-photons and 3-N protons do so and represent a gene consisting of N codons. Galois confinement would bind the photons and protons to larger particle units analgous to baryons as composites of 3-quarks.

All communications to MB would use dark 3N-photons coupling to corresponding dark 3N-proton by cyclotron resonances [L165, L163, ?]. Therefore 3N-photon as a dynamical gene with N codons would define its own address. Frequency modulation of frequencies of 3N-photon would give rise to a sequence of resonance peaks and the continuous signal would be transformed to a signal analogous to nerve pulse sequence and could realize motor action as a response.

Magnetic body containing dark matter as the master

MB has a hierarchical onion-like structure with levels labelled by the value of $h_{eff} = nh_0$ giving rise to increasing scales. The dark analogs of DNA, RNA, tRNA, and amino-acids define flux tubes accompanying their ordinary variants with codons realized as dark 3-proton units.

In TGD genetic code in terms of 3-chords would be realized in a universal manner for the simplest tessellation of hyperbolic space known as icosa-tedrahedral honeycomb involving icosahedrons and tetrahedrons (also octahedrons are involved but they would be in passive role) [L122]. This would suggest that genetic code using dark proton- and dark photon triplets is realized at all layers of MB. Chemical realization would represent the lowest level in the hierarchy.

The layers of MB with increasing value of h_{eff} would define a hierarchy of abstractions. There is evidence for an effective statistically determined hyperbolic geometry [J11] in the sense that neurons functionally but not necessarily spatiall near to each other are near to each other in this effective geometry. This hyperbolic geometry would be realized quite concretely at the level of MB [L103] for which hyperbolic geometry of proper time constant hyperboloid of the light-cone gives a concrete meaning.

One particular implication could be that sensory receptors of a given structure (say adhesion units of given cell-environment pair) could communicate their sensory data to neighboring icosa-tetrahedral units of the honeycomb of some layer of MB representing the codons of genetic code. The states of the icosahedrons and tetrahedrons of the honeycomb would be dynamical and selected by the 3-chord (actually pair of 3-chord and conjugate) to actualize genetic codon as 3-quark units assignable to the corresponding triangle of icosahedron or tetrahedron.

This would define sensory representation at MB, and the simplest option is that it automatically determines motor response as a sequence of resonance peaks communicated back to the biological body (BB) where they would initiate gene expression, RNA or protein activity, MT activity, or nerve pulse activity. The feedback would be directly to DNA (or RNA, amino-acid of protein, or even tRNA, microbuli, or cell membrane).

The biochemical motor actions of MB would be realized as bursts of dark cyclotron 3N-photons induced by the cyclotron resonances at MB transforming to ordinary photons (biophotons or IR photons with energy above thermal energy) controlling biochemistry by inducing molecular transitions.

This condition constrains the value of h_{eff} for a layer of MB. The size of the layer should be of the order of wavelengths involved.For valence bonds the values of $h_{eff} = h_{em}$ would be rather small and assignable with small layers of MB. For frequencies in EEG range the large value of gravitational Planck constant $h_{eff} = h_{gr}$ [L59, L165] assignable to the gravitational flux tubes would guarantee that the energies are in the required range.

The following picture about how sensory input induces gene expression or some other activity with communication and control realized in terms of genetic code might apply completely generally, not only in the case of adhesion units.

1. Suppose the sensory receptors of a given structure (say adhesion units of a given cell) are organized into coherent structures in the sense that the signals from them go along flux tubes to nearby cells of icosa-tetrahedral honeycomb at some layer of MB.

   Adhesion structures consting of few hundred adhesion units are indeed connected to each other. Coherence would be forced by the quantum coherence at the level of MB as a forced coherence. One could assume that the cells of the honeycombinvolved are organized linearly but even 2-D and 3-D structures are possible.

   For a structure consisting of N units, the dark 3N-photon signal would define a dark gene of N codons. The nice feature of the representation is that there is no need to organize the sensory receptors (say adhesion units) linearly at the level of the cell. The level of ordinary biomatter would be like RAM with ordering realized at the level of MB.

2. The naive picture is that if the dynamical gene realized in this manner has a dark counterpart at the level of flux tube accompanying DNA, gene expression could be initiated automatically as a feedback signal realized as a sequence of resonance peaks. Also RNA, proteins or MTs could be activated in an analogous manner.

   There would be a one-one correspondence between sensory inputs to MB and corresponding gene expressions and give a meaning for the genetic code. All sensory inputs to MB would be realized as N-genes in terms of generalized Josephson radiation which is frequency modulated and generates a sequence of resonance peaks inducing gene expression or RNA and protein activation.

3. The dynamical gene at MB need not correspond to an existing or expressible gene so that the response is not possible. This would give rise to an evolutionary pressure. Epigenesis controlled by MB could make the gene expressible. Also a suitable mutation for existing gene or emergence of new gene could produce the needed gene. Whether MB is able to induce this kind of mutations is an interesting question. Could a dark gene as a flux tube containing dark proton sequence representing the desired gene pair with ordinary DNA codons and give rise to a new gene?

   Or could MB "use scissors" to replace codon-anticodon pairs in an existing gene: this would mean reconnection of a closed flux tube pair containing the codon-anticodon pairs of the added gene fragment. Could a piece of dark DNA as a flux tube carrying the dark proton sequence pair with ordinary DNA codons and give rise to a new gene? Or could one add to an existing gene a piece represented as a dark DNA paired with the ordinary DNA. Most viruses have single stranded RNA genomes. Bacteriophages have double stranded DNA genomes. They are known to give rise to the modifications of the genome. Could these DNA modifications be induced by a reconnection of darkmagnetic flux tubes.

Universality of the genetic code and its higher dimensional representations

If genetic code at space-time surface is induced from a universal code assignable to the icosa-tetrahedral honeycomb of hyperbolic 3-space, representations of genetic code with dimensions $D = 0, 1, 2, 3$ are possible as induced representations. The codons associated with the cells of honeycombes projected to the space-time surface would define the induced codons [L122].

tRNA would be a 0-D representation and DNA, RNA, amino acids would be 1-D representations of the code. Also higher-dimensional representations are possible and could be associated with the basic biological structures.

1. I have proposed that cell membrane defines a 2-D representation of the genetic code [L122]. Also microtubuli could define a 2-D representation of genetic code. These 2-D representation could be dynamical and independent of genome and make genome dynamical. This would be a biological analog for AI able to write genes as program modules needed in a given situation.

2. Could a 3-D representation of genetic code be associated with the ECM and make it possible for MB to receive sensory input from ECM and control it? This layer of MB could also receive sensory information also from adhesive structures. The frequency range involved would be probably below EEG frequencies or at least below conscious frequencies since we

do not experience the interior of body consciously and the time scale of dynamics is slow as compared to EEG scales.

Hydrozyapatite molecules are present in bones forming a part of ECM. Fisher has proposed that the Posner molecules associated with hydroxyapatite molecules could have important role in quantum biology [J23]. This inspired the proposal that they provide a realization of genetic code [L28]. One cannot exclude the possibility that the code is 3-D. This would fit with the general idea that the genetic code serves as a universal code for communications and control.

Some TGD inspired numerology

If one takes the proposed general picture seriously, one must ask how the 13-bits codons assignable to talins and MTs could reduce to genetic codons. It is good to start with numerology or should one call it physics inspired poor man's number theory.

1. The number of protein domains in talin is 13. Also the number of tubulin dimers in 13-tubulin unit of MT/neurotubule appearing in cytoskeleton is 13. Could one think of communication between MTs and talins using 13 bit code? Or could the code using 13 bits be for some reason special? Could this code somehow reduce to the proposed universal 6-bit code defined by genetic code?

2. There are 4 protein domains consisting of 4 alpha helices and 9 domains with 5 alpha helices. This gives 61 alpha helices altogether. Numerologist might notice that 61 is the number of DNA codons with stop codons excluded. Could one assign to helices genetic codons and could these configurations labelled by 61 bits code for genes with length not longer than 61 units?

3. Numerologist might also notice that both $M_{13} = 2^{13} - 1$ and $M^{61} = 2^{61} - 1$ are Mersenne primes. If one has n bits and does not count the configuration with all bits 0 but assuming that at least single bit is always equal to 1, one has 2^{n-1} full bits.

   For M_{13} this corresponds to 12 full bits which corresponds to 2 genetic codons. To obtain 2 codons, single fixed talin should be unfolded and represent 1. Could this have interpretation in terms of a force threshold? One can argue that there is some minimal force unfolding some fixed talin. If the force is below the threshold, there is no need to communicate. Also in the case of MT the conformation of preferred tubulin, say the first or last one in 13-unit should always correspond to 1.

4. One cannot exclude the possibility that the responses of talin units correspond to two independent codons. This could be true also for13-bit units MTs.

   The alternative option is that both talins and 13-tubulin units of MT correspond to codon-anticodon pairs so that information content would reduce to that of single DNA codon. Half of the bits would serve as check bits. Also the purpose of the conjugate strand of DNA would be to serve as check codons.

   If this is the case, the adhesion unit would have only 2^6 different responses and would represent a genetic codon. The number of talins is few hundred that this would correspond to a DNA sequence of length of order 10^{-7} meters. In the case of MT 6 bits would be check bits.

5. The proposal would have far reaching consequences: the genetic code realized by MTs and talins would be dynamical rather than fixed and could represent a step to a higher evolutionary level.

6. The dynamics of the codon or of a pair of pair of independent codons assignable to the adhesion unit would mean change of the "sensory codon" possibly corresponding to a real codon assignable to it. The slow time variation of the gene assignable to the collection of adhesion units could define varying gene expression or some other activations (of say microtubuline).

These speculations encourage the question whether the codon-anticodon pairs possibly assignable to adhesion units integrate to sequences or perhaps even 2-D structures representing 2-D adhesion structures of DNA codon-anticodon pairs defining genes.

If these 2-D honeycomb structures at the level of MB decompose to piles of 1-D structures as microtubules do, they could even induce the expression of gene groups. Also 2-D gene expression in terms of microtubules modifying the cytoskeleton can be considered. Note that the honeycomb structures are not needed at the level of ordinary biomatter.

A simple model for the adhesion units

In TGD framework magnetic body (MB) containing dark matter controls ordinary living matter. MB receives sensory input from organism in terms of dark Josephson radiation arriving from cell membranes acting as generalized Josephson juctions. Sensory information is coded by the modulation of membrane potential. For ordinary cells only small modulations of membrane potential would induce modulations of Josephson frequency. For neurons nerve pulse patterns introduce more drastic modulation.

1. The two states of the protein domains could correspond to different values of h_{eff}. The reduction of h_{eff} at the magnetic flux tube accompanying the protein would induce the shortening of the flux tube associated with the unfolded protein to the folded configuration.

2. Cohesion units would aserve as sources of sensory information about the net force acting on the cohesion unit and coded by 13 bits unless the bits are independent. For instance, different bits would correspond to different signals, say different frequencies of dark photons. If one takes the interpretation as a pair of codons seriously, the signal could consist of a dark 3-chord and its conjugate 3-chord sent to MB and defining at the MB a representation of gene to be possibly activated.

3. Josephson radiation as dark 3-photons from the part of the cell membrane considered would mediate the 13 bit signal defined coded to a local change of membrane potential with 2^{12} values defining 12 octaves if there is threshold corresponding to activation of a preferred talin. Note that the frequencies audible for humans are in the range 20 Hz- 20 kHz and correspond to 10 octaves.

4. MB would receive the sensory input and react by possibly sending control signal to DNA inducing gene expression or inducing activity of proteins or RNA. This means that talin molecules would not be active but MB receiving the sensory input from adhesion units.

   MB could also send control signal to microtubuli if MT contains a sequence of 13-tubulin units corresponding to the dynamical gene [**?**] [I11] (`https://en.wikipedia.org/wiki/Microtubule`). This would reflect itself in the dynamics of MTs. This control loop would modify the force equilibrium by a modification of the shape of the cell.

5. MTs could represent an evolutionary step making the genome dynamical and independent of genes and extending ordinary genome as the microtubular response possible for eukariotes suggests. Also the long MTs inside axons conform with this interpretation.

6. MTs are highly dynamical. Their lengths are continually varying. According to "search-and-catch" model MTs inside cells are scanning their 3-D environment and whey the find a target attach to it and MT is stabilized. This conforms with general vision about U-shaped dynamical flux tubes serving as tentables and forming a reconnection with a similar U-tube of the target. Immune system would be rely on this mechanism at the fundamental level and allow the system to detect and catch invader molecules on basis of their cyclotron energy/frequency spectrum [K41, L165].

7. The general vision suggests that the feedback loop should involve also microfilaments and intermediate filaments. It would be interesting to see whether the structure of microfilaments and intermediate filaments could allow realization of the counterpart of genetic code. The basic signature are GTP and ATP molecules providing metabolic energy for motor action.

5.7.4 An application to memory and learning

Since the increase of synaptic strengths is believed to be behind the formation of memories as behaviors and habits, it is appropriate to discuss the notion of memory in TGD framework and consider connections with the model for the adhesion units at synaptic contacts.

The major issue with memory is potentiation (repeat of same memory which facilitates memory recall and learning) and amnesia, Alzheimer disease and memory when dreaming. There should be a compatible explanation for these phenomena.

In TGD one distinguishes between two kinds of memories. Episodal-/sensory memories and memories as associations/learned behaviors.

Memories as learned behaviors

Neuroscience explains learned behaviors in terms of strengthening of synaptic contacts and I believe that this is part of the story.

The formation of associations in conditioning is a highly emotional process and here the surprising finding [J10] (see `http://tinyurl.com/ycqxyeqk`) few years ago (roughly) was helpful. The popular article " *Scientists Sucked a Memory Out of a Snail and Stuck It in Another Snail*" tells about the finding (see `http://tinyurl.com/y92w39gs`).

The RNA of a sea snail which had learned by (presumably painful) stimulus a behavior was scattered on the neuronal tissue of another sea snail in a Petri dish. The neuronal tissue learned the same behavior!

The TGD based explanation is following.

1. Emotions are realized already at the molecular level [L64] in terms of music of light - bioharmony [L11, L78, L107, L122]. The emotional stimulus at the MB of RNA induced learning by changing the allowed 3-chords of bioharmony. Also the sequences of 3-chords characterizing 3N-genes and other basic linear biomolecules changed. The resonant couplings to the basic biomolecules changed so that also chemical behavior changed.

2. The emotional state of the conditioned seanail RNA infected the RNAs and probably also DNAs and proteins of neurons and induced learning.

3. Synaptic strengths had to change and the molecular emotions as music of light would have induced this.

   If the idea about mechanical control of synaptic strengths by talin molecules by push and pull from ECM and cytoskeleton is correct, the molecular mood had to induce a strong force changing the talin conformations. Emotion would quite concretely correspond to a force!

   This would have induced a reaction at the level of microtubules with the mediary of MB as a response making the change permanent. Neurotubules of the cytoskeleton in dendrites and axons would be involved in realizing the learning as a permanent change.

Potentiation and two kinds of memories

The notion of potentiation applies to both kinds of memories.

1. The repetition of stimulus generating the learned behavior increases the synaptic strength. Perhapsby inducing a memory recall of the emotional experience at molecular level.

2. Potentiation for sensory memories creates an almost copy of sensory memory mental image at "geometric now": the re-experience and the more one has these almost copies in the geometric future of "geometric now", the higher the probability that the attempt to remember by sending dark photon signals to the future hits the memory mental image are successful. The latest memory recalls create memories mental images nearest to "geometric now" and the probability for memory recall is highest for them.

Why oldest sensory memories are those which survive when one begins to lose memories at old age?

1. There are a lot of almost copies about the oldest memories: does this mean that the memory recall has a higher probability to be successful?

2. One can also argue that the memory mental images of young age have also gone through a long sequenceof re-incarnations which have gradually increased the value of h_{eff}.

   Large h_{eff} means that the frequency f needed to produce a dark photon with energy $E = h_{eff}f$ in biophoton range is lower and therefore the period $T = 1/f$ is longer. Uncertainty Principle says that the time period over which memories are optimally recalled is of order$T = 1/f$.

Amnesia,Alzheimer, and why we forget dreams so fast

Amnesia might relate to the inability to recall sensory memories by sending signals with a correct frequency to the memory mental images. The energy of the dark photons is proportional to h_{eff} and if it is reduced in the recalling end as tends to happen in the absence of metabolic energy feed, the ability to recall memories is weakened or lost. For instance, alcoholism can lead to a loss of memory recall and this could be the reason.

Alzheimer means a loss of memories as behaviors and inability go generate new ones. In TGD framework [L48] the weakening of the synaptic connections would make the build up of connection between magnetic flux tubes associated with presynaptic dendrite and postsynaptic axon and the dark photon signal could not propagate because the connection is broken.

Also the propagation along axonal flux tubes could be impossible or highly attenuated if the value of h_{eff} for them is reduced. Also the energy for a given freqeuency would be reduced below the biophoton energy range.

Why do we forget dreams so fast? We do not remember anything about sleep without dreams. In ZEO this can be understood if sleep corresponds to "small death" for an appropriate layer of MB meaning re-incarnation with an opposite arrow of time. Dreams would correspond to states in which part of the brain is awake and possibly receives information from the sleeping part of the brain realized as a dream. Dream would be due to a communication of virtual sensory input from MB with opposite arrow of time to sensory organs.

This does not yet explain why we forget dreams so fast. As the memory image ages, it shifts to the future of "geometric now" in CD, and the needed frequency as inverse of the age decreases. Could it be that we cannot generate the frequencies of dark photons needed for the memory recall.

Memories change

Episodal memories are not carved in stone. They are modified in memory recalls. In TGD framework, the modification of (episodal) memory mental images is unavoidable. Memory mental images are living entities and evolve re-incarnation by re-incarnation. Memory recalls are basically analogous to quantum measurements of memory mental images induced BSFR and quantum measurement indeed changes the state of the system measured.

1. The sub-selves of self as mental images continue to live at sub-CDs which in the proposed model drift to the geometric future of CD increasing SSFR by SSFR. These sub-CDs experience BSFRs and evolve incarnation by incarnation. In general evolution happens and they become smarter and wiser. Memories are indeed said to grow sweeter in time.

2. Each memory recall must take the memory subself to a state in which it has arrow of time opposite to that of recaller so that the signal about the memory propagates to the geometric past to "geometric now" [the ball at center of CD at which future and past directed cones glued together].

   The BSFR for memory subself with the same arrow of time as recaller induces memory recall. Memory recall is a murderous process. If the memory recall occurs spontaneously, the murder is not not the recaller.

Confabulation

The phenomenon of confabulation relates most probably to episodal/sensory memories, not memories as behaviors and habits. Confabulation could be understood in the following manner. Memory mental images are just glimpses about what happened since only those aspects of the event which receive the attention form memory mental images. Memory recaller builds a logical sounding story around these glimpses so that confabulation is unavoidable.

Even our sensory perception is fabrication of stories [L42]. Sensory organs are seats of primary sensory experience and there is feedback from MB and brain to sensory organs as virtual input. This feedback loop generates standardized mental images by pattern completions and recognition.

If the sensory input is meager the story can be non-realistic as I know as a person with a poor eye sight. REM dreams and hallucinations are an excellent example of this: in this case there is only virtual sensory input present.

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5.8 Appendix: Tables of basic 3-chords for the icosahedral harmonies with symmetries

The tables below give list for the three types of 3-chords for the 11 harmonies possessing symmetries. One must remember that the reversal of the orientation for the cycle induces the transformation $C \leftrightarrow C$, $F\sharp \leftrightarrow F\sharp$, $H \leftrightarrow C\sharp$, $F \leftrightarrow G$, $D \leftrightarrow B\flat$, $E \leftrightarrow G\sharp$, $A \leftrightarrow D\sharp$ and produces a new scale with minor type chords mapped to major type chords and vice versa. Also one must remember that all 3-chords except those which are simple majors or minors lack the third so that their emotional tone remains uncharacterized. For instance, $C6$ does could be replaced with $Cm6$ and $G7$ with $Gm7$. The reader can check the chords by direct inspection of the figures. The convention used is that vertex number one corresponds to C note.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(Faug, Gaug)$	$(Cm, Dm, Em, F\sharp m, G\sharp m, B\flat m)$,	$(C9, D9, E9, F\sharp 9, G\sharp 9, B\flat 9)$.
		$(F6, G6, A6, B6, C\sharp 6, D\sharp 6)$.	

Table 5.2: Table gives various types of 3-chords for harmonies with Z_6 rotational symmetry. Note that half-octave shift is an exat symmetry. Note that $G^{aug} = CEG\sharp, F^{aug}$ act as bridges between the groups related by half octave shift. The chords have been arranged so that they form orbits of Z_6. "Amino-acid chords" correspond to preferred chords at the orbits.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(D7, D6, G\sharp 7, G\sharp 6)$,	$(B\flat 9, B9, E9, F9)$.
		$(G4+, A9-, C\sharp 4+, D\sharp 9-)$,	
		$(Emaj7, Gmaj7, B\flat maj7, C\sharp maj7)$,	
		$(C9-, A9-, F\sharp 9-, D\sharp 9-)$.	
(4, 8, 8)	$(Cex3, Eex2, F\sharp ex3, B\flat ex2)$.	$(Dmaj7, E9-, A7, A6)$,	$(B\flat 9, F9, C9, G9)$.
		$(G\sharp maj7, B\flat 9-, D\sharp 7, D\sharp 6)$.	$(E9, B9, F\sharp 9, C\sharp 9)$.

Table 5.3: Table gives various types of 3-chords for the two harmonies with $Z_4 = Z_2^{rot} \times Z_2^{refl}$ symmetry. 4-plets represent the orbits. First cycle has no harmonic loners. Second cycle gives rise to bio-harmony (4, 8, 8) for which 0-quint chords are dissonant.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(Em, B\flat m), (Cm, F\sharp m),$	$(D9, G\sharp 9),$
		$(G6, C\sharp 6), (A6, D\sharp 6),$	$(E9, B\flat 9).$
		$(D4+, G\sharp 4+), (B4+, F4+),$	
		$(Cmaj7, F\sharp maj7), (G6-, C\sharp 6-).$	
(2, 12, 6)	$(Aex4, D\sharp ex2).$	$(Am, D\sharp m), (G9-, C\sharp 9-),$	$(C9, F\sharp 9),$
		$(C4, F\sharp 4), (E4+, B\flat 4+),$	$(A9, D\sharp 9),$
		$(Dmaj7, G\sharp maj7),$	$(D9, G\sharp 9).$
		$(Bmaj7, Fmaj7).$	
(4, 8, 8)	$(Aex2, Hex8, D\sharp ex2, Fex8).$	$(D7, G\sharp 7), (Amaj7, D\sharp maj7),$	$(G9, C\sharp 9), (A9, D\sharp 9),$
		$(A4+, D\sharp 4+), (E7, B\flat 7).$	$(B9, F9), (E9, B\flat 9).$

Table 5.4: Table gives various types of 3-chords for harmonies with Z_2 rotation symmetry acting as half-octave shift. The doublets represent 2-chord orbits.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(F\sharp ex3, Hex4),$	$(Am, D\sharp), (A6, D\sharp 7),$	$(C9, F9), (B9, F\sharp 9),$
		$(D7, B\flat 6), (G6-, Fmaj7),$	$(E9-, C\sharp 9).$
		$(D4+, B\flat 9-), (E9, G\sharp 4+),$	
(2, 12, 6)	$(Dex4, Hex4).$	$(F, Fm), (C6-, B\flat maj7),$	$(C9, D\sharp 9),$
		$(D7, G\sharp 6), (Gmaj7, D\sharp 6-).$	$(D\sharp 9, C\sharp 9),$
		$(C\sharp 4-, A4+), (E4+, F\sharp 6).$	$(E9, B9).$
(4, 8, 8)	$(Fex1, D\sharp ex3, G\sharp ex1, Aex2).$	$(E7, E6), (Amaj7, B9-),$	$(D9, B9), (C9, C\sharp 9),$
		$(G, C\sharp m), (D7, F\sharp 6).$	$(F9, G\sharp 9), (D\sharp 9, B\flat 9).$
(2, 12, 6)	$(Hex3, Eex7).$	$(D7, G\sharp 6), (G, D\sharp m),$	$(C9, D\sharp 9),$
		$(F, Fm), (C6-, B\flat maj7),$	$(D9, C\sharp 9),$
		$(A9-, C\sharp 4+), (E7, F\sharp 6).$	$(E9, B9).$
(2, 12, 6)	$(F\sharp ex2, Fex3).$	$(F, B\flat m), (C7, G\sharp 6),$	$(B\flat 9, D\sharp 9),$
		$(Amaj7, B9-), (E6, E7),$	$(C9, C\sharp 9),$
		$(G, C\sharp m), (D7, B6).$	$(D9, H9).$

Table 5.5: Table gives various types of 3-chords for harmonies with single reflection symmetry.

Chapter 6

About honeycombs of hyperbolic 3-space and their relation to the genetic code

6.1 Introduction

$M^8 - H$ duality and the realization of holography in M^8 strongly suggests the importance of tessellations of H^3 (analogous to lattices of E^3) in the TGD based physics. These tessellations form a scale hierarchy and can thus appear in all scales. The hierarchy of effective Planck constants labelling dark matter as phases of ordinary matter indeed predicts quantum coherence in arbitrarily long scales and gravitational quantum coherence corresponds to the largest scales of quantum coherence among basic interactions.

The 4 regular honeycombs correspond to cubic, icosahedral, and 2 dodecahedral tessellations. The quasiregular icosa-tetrahedral honeycomb has tetrahedra, octahedra and icosahedra as cells having triangular faces as cells. These honeycombs serve as candidates for physically interesting tessellations. These 5 honeycombs are unique in that they involve only Platonic solids. I have proposed that the icosa-tetrahedral tessellation might define a universal realization of the genetic code as an induced structure so that the genetic code would be much more than a biochemical accident. The details of this realization are discussed in [L122, L78].

These 5 Platonic tessellations (or honeycombs, I will used these terms interchangeably in the sequel) could occur also in astrophysical scales as gravitational tessellations. The recent discovery of gravitational hum might have an explanation as gravitational diffraction in this kind of a tessellation. The unexpectedly large intensity of hum could be due to the concentration of the radiation intensity in discrete directions and due the fact that in diffraction the amplitude of the scattered field is proportional to the square N^2 of the number N of scatterers rather than N.

Icosa-tetrahedral tessellation relates to the TGD based view of the genetic code. The TGD inspired view of genetic code has evolved during decades.

1. The first model of the genetic code was based on the so-called Combinatorial Hierarchy [K39] [L122] and predicted what I called memetic code realized as sequences of 21 DNA codons. Surprisingly, this model made a comeback as I prepared this article.

2. After several stray paths I ended up from a model of music harmony [L11, L27] [L107, L78] based on Hamiltonian cycles at the icosahedron to a model of genetic code also involving the tetrahedral Hamiltonian cycle.

   The basic observation was that the 12-note scale could correspond to a Hamiltonian cycle of icosahedron such that the steps of the cycle define a quint cycle. 12-note scale is obtained from the quint by octave equivalence. There are 3-types of icosahedral Hamiltonian cycles and each cycle defines 20 3-chords assignable to the triangular faces of the icosahedron and defines a musical harmony.

One obtains 20+20+20 chords for the 3 different harmonies with symmetry groups Z_6, Z_4 and Z_2. The orbits of these groups define sets of 3-chords. The surprising finding was that if these sets are identified as amino acids, the numbers of the chords are the same as the numbers of DNAs coding for a given amino acid. By adding a tetrahedral Hamiltonian cycle one obtains 64 3-chords. At the level of molecules the music would be "music of light". Since music expresses and generates emotions, the idea that emotions appear already at the molecular level was natural. Different combinations of 3 Hamiltonian cycles with symmetries Z_6, Z_4 and Z_2 would correspond to different moods at bio-molecular level (why just 3?)

The model made almost correct predictions for the numbers of mRNA codons coding for amino-acids. I have discussed a considerable number of its variants during years and even considered the replacement of icosahedron and tetrahedron with some other geometric object.

The basic problem was that gluing the tetrahedron and icosahedron together looked ugly and would have allowed only 63 codons. At that time I did not yet realize that an icosahedron and tetrahedron could be parts of a bigger structure.

3. Second model was based on the realization of codons as dark proton triplets assumed to reside at the monopole flux tubes parallel to DNA strands [L27, L78]. Dark proton triplets would neutralize the constant negative charge of -3 units per codon. The model suggested that it might be possible to understand the numbers of DNA, RNA, tRNA and amino acids in terms of entangled states of dark proton triplets representing codons. The model had also problems: in particular, one had to assume an additional binary degree of freedom to get the number DNA and mRNA codons correctly and the proposed identifications of this new degree of freedom did not look quite realistic.

4. Icosa-tetrahedral realization [L122] of the code in terms of icosatetrahedral honeycomb of H^3 was the next step in the evolution of ideas. It was made possible only by the dramatic development of understanding of TGD itself, in particular of its number theoretical aspects related to $M^8 - H$ duality [L101, L102].

   The tessellations of the hyperbolic 3-space H^3 represented as possibly complex mass shell in $M^4_c \subset M^8_c$ and as light-cone proper time = constant hyperboloids in $M^4 \subset M^4 \times CP_2$ are central in the the realization of holography in TGD. Icosa-tetrahedral honeycomb is a completely unique tessellation involving only Platonic solids and all possible platonic solids, tetrahedron, icosahedron, and octahedron are present. Kind of a quantum Platonic holy trinity is in question.

   This led to a proposal of the genetic code in terms of icosa-tetrahedral honeycomb induced to the 3-surface by restriction. This realization could be assignable to the magnetic body of the system involving dark matter in the TGD sense. The realization would be universal and would not be restricted to mere biology. Counterparts of codons and genes can be realized also for higher-dimensional objects, say cell membrane and even brain.

   Icosa-tetrahedral realization led to a proposal that the realizations of the code in terms of dark photon triplets and in terms of dark proton triplets are closely related. I did not however really understand the properties of the icosa-tetrahedral honeycomb when I published the first article about it [L122].

   Sequences of N dark cyclotron photon triplets as representations of genes consisting of N dark proton triplets would make possible communications between dark genes by 3N-resonance. Genes would serve as addresses, much like in LISP, and the message would be coded by the modulation of the frequency scale. The details of this picture that were not discussed at that time create problems that are solved by the model based on icosahedral honeycomb.

In this article the properties of hyperbolic honeycombs are considered in detail and also a detailed view about the realization of DNA double strand in terms of the icosa-tetrahedral tessellation is considered. The emerging model is surprisingly quantitative and suggests a lot of new understanding about the dark realization of genetic code. Also a connection with the notion of memetic code [K39] [L29] and the realization of memetic codons in terms of 21 DNA codons are suggested by the model.

I have added to the end of the article a section about the recent progress in the understanding of icosa tetrahedral tessellation (ITT). The improved understanding of the ITT allows us to answer some long standing questions related to the detailed realization of the genetic code. It however turns out that the notion of the super-icosahedron discussed in the original version of this article is not consistent with the improved view. However the 3-D generalization of the vertex figure of the ITT as its inverse image under projection permutes the numbers for the Platonic solids appearing in the super-icosahedron.

6.2 About honeycombs in hyperbolic 3-space

This section, written in 2023, represents some new understanding related to the tessellations of H^3 known as honeycombs.

6.2.1 Some preliminaries

Some preliminaries are needed in order to understand Wikipedia articles related to tessellations in general.

1. Schläfli symbol $\{p,r\}$ (`rb.gy/j36tg`) tells that the possibly existing Platonic solid $\{p,r\}$ has r p-polygons as faces meeting at each vertex. For instance, icosahedron $\{3,5\}$ has 5 triangles as faces meeting at each vertex.

   Schläfli symbol generalizes to higher dimensions. The analog of Platonic solid $\{p,r,q\}$ possibly in 4-dimensions and assignable to 3-sphere has q 3-faces which are Platonic solids $\{p,r\}$. This description is purely combinatorial and is recursive. For instance, one can start from 3-D dimensional Platonic solid $\{p,q\}$ with 3-D objects in dimension 4 by replacing p with p,r. One can also project this object to dimension 3. In this manner one obtains a projection of 4-cube (tesseract) $\{4,3,3\}$ for which 3 cubes $\{4,3\}$ meet at each vertex ($2^4 = 16$ of them) and which has 8 3-cubes as faces as a 3-D object.

   In the case of hyperbolic tessellations also strange looking Schläfli symbols $\{(p,q,r,s)\}$ are encountered: icosa-tetrahedral tessellation involving only Platonic solids has symbol $\{(3,3,5,3)\}$. My understanding is that this object corresponds to $\{3,3,5,3\}$ as an analogue of Platonic solid associate with 4-sphere in 5-D Euclidian space and that the fundamental region of this tessellation in H^3 is analogous to a 3-D projection of this object. At a given vertex 3 objects $\{3,3,5\}$ meet. For these objects 5 tetrahedrons meet at a given vertex.

2. Vertex figure is a further central notion. It represents a view of the fundamental region of tessellation from a given vertex. The vertices of the figure are connected to this vertex. It does not represent the entire fundamental region. For instance, for a cube (octahedron) it contains only the 3 (4) nearest vertices. For icosa-tetrahedral tessellation the vertex figure is icosidodecahedron (`rb.gy/3u4pq`). The interpretation of the vertex symbol of the hyperbolic icosa-tetrahedral honeycomb (`htrb.gy/3u4pq`) is a considerable challenge.

3. One cannot avoid Coxeter groups and Coxeter symbols (`rb.gy/48qhg`) in the context of tessellations. They code the structure of the symmetry group of say Platonic solid (tessellation of S^2). This symmetry group is generated by reflections with respect to some set of lines, usually going through origin. For regular polygons and Platonic solids is its discrete subgroup of rotation group.

   The Coxeter group is characterized by the number of reflection hyperplanes H_i and the reflections satisfying $r_i^2 = 1$. The products $r_{ij} = r_i r_j$ define cyclic subgroups of order c_{ij} satisfying $r_{ij}^{c_{ij}} = 1$. Coxeter group is characterized by a diagram in which vertices are labelled by i. The orders of the cyclic subgroups satisfy $c_{ij} \geq 3$. For c_{ij} the generators r_i and r_{ij} commute. For $c_{ij} = 2$ the vertices are not connected, for $c_{ij} = 3$ there is a line and for $c_{ij} > 3$ the number c_{ij} is assigned with the line. For instance, hyperbolic tessellations are characterized by 4 reflection hyperplanes.

   For instance, for p-polygon the Coxeter group has 2 generators and the cyclic group has order p. For Platonic solids the Coxter group has 3 generators and the orders of cyclic subgroups are 3, 4, or 5. For icosa-tetrahedral tessellation the order is 4.

6.2.2 The most interesting honeycombs in hyperbolic 3-space

H^3 allows an infinite number of tessellations. There are 9 types of honeycombs. This makes 76 uniform hyperbolic honeycombs involving only a single polyhedron (hrb.gy/rs9h5).

4 of these honeycomes are *regular*, which means that they have identical regular faces (Platonic solids) and the same numbers of faces around vertices. The following list gives the regular uniform honeycombs and their Schläfli symbols $\{p,q,r\}$ telling that each edge has around it regular polygon $\{p,q\}$ for which each vertex is surrounded by q faces with p vertices.

1. H1: 2 regular forms with Schläfli symbol {5,3,4} (dodecahedron) and {4,3,5} (cube).
2. H2: 1 regular form with Schläfli symbol {3,5,3}(icosahedron)
3. H5: 1 regular form with Schläfli symbol {5,3,5} (dodecahedron).

There is a large number of uniform honeycombs involving several cell types. There exists however a "multicellular" honeycomb, which is completely unique in the sense that for it all cells are Platonic solids. This icosa-tetrahedral (or more officially, tetrahedral-icosahedral) honeycomb has tetrahedrons, octahedrons, and icosahedrons as its cells. All faces are triangles. The icosa-tetrahedral honeycomb is of special interest since it might make possible the proposed icosa-tetrahedral realization of the genetic code (rb.gy/h8xx0).

From the Wikipedia article about icosa-tetrahedral honeycomb (htrb.gy/3u4pq) one learns the following.

1. The Schläfli symbol of icosa-tetrahedral honeycomb is $\{(3,3,5,3)\}$. This combinatorial symbol allows several geometric representations. The inner brackets would refer to the interpretation as an analogue of the Platonic solid assignable to a 4-sphere of Euclidian 5-space. At each vertex 3 objects of type $\{3,3,5\}$ would meet. At the vertex of $\{(3,3,5)\}$ in turn 5 tetrahedrons meet.
2. Icosa-tetrahedral honeycomb involves tetrahedron $\{(3,3\}$, octahedron $\{(3,4)\}$, an icosahedron $\{(3,5)\}$ as cells. That there are no other honeycombs involving several Platonic solids and only them as cells makes this particular honeycomb especially interesting. Octahedron with Schläfli symbol $\{3,4\}$ can be also regarded as a rectified tetrahedron havig Schläfli symbol $r\{3,3\}$.
3. The vertex figure of icosa-tetrahedral honeycomb (htrb.gy/3u4pq), representing the vertices a lines connecting them is icosidodecahedron (rb.gy/q5w62), which is a "fusion" of icosahedron and dodecahedron having 30 vertices with 2 pentagons and 2 triangles meeting at each, and 60 identical edges, each separating a triangle from pentagon. From a given vertex VF=60 vertices connected to this vertex by an edge can be seen. In the case of cube, octahedron, and dodecahedron the total number of vertices in the polyhedron is 2(VF+1). It is true also now, one would have 122 vertices in the basic structural unit. The total number of vertices for the disjoint polyhedra is 6+4+12= 22 and since vertices are shared, the number of polyhedra in the basic unit must be rather large.
4. The numbers called "cells by location" could correspond to numbers 30, 20, and 12 for octahedrons, tetrahedrons and icosahedrons respectively inside the fundamental region of the tessellation defining the honeycomb. That the number of icosahedrons is smallest, looks natural. These numbers are quite large. The counts around each vertex are given by (3.3.3.3), (3.3.3), *resp.* (3.3.3.3) for octahedra, tetrahedra, *resp.* icosahedra and tell the numbers of vertices of the faces meeting at a given vertex.
5. What looks intriguing is that the numbers 30, 20, and 12 for octahedrons (O), tetrahedrons (T) and icosahedrons (I) correspond to the numbers of vertices, faces, and edges for I. As if the fundamental region would be obtained by taking an icosahedron and replacing its 30 vertices with O, its 20 faces with T and its 12 edges with I, that is by using the rules *vertex*

$\rightarrow$ *octahedron*; *edge* $\rightarrow$ *I*, *face* $\rightarrow$ *T*. These 3-D objects would be fitted together along their triangular faces.

Do the statements about the geometry and homology of I translate to the statements about the geometry and homology of the fundamental region? This would mean the following replacements:

(a) "2 faces meet at edge" $\rightarrow$ "2 T:s share face with an I".

(b) "5 faces meet at vertex" $\rightarrow$ "5 T:s share face with an O".

(c) "Edge has 2 vertices as ends" $\rightarrow$ "I shares a face with 2 different O:s".

(d) "Face has 3 vertices $\rightarrow$ "T shares a face with 3 different O:s".

(e) "Face has three edges" $\rightarrow$ "T has a common face with 3 I:s".

6.2.3 An attempt to understand the hyperbolic honeycombs

The following general observations might help to gain some understanding of the honeycombs.

The tessellations of E^3 and H^3 are in many respects analogous to Platonic solids as 2-D objects. The non-compactness implies that there is an infinite number of cells for tessellations. It is important to notice that the radial coordinate r for H^3 corresponds very closely to the hyperbolic angle and its values are quantized for the vertices of tessellation just like the values of spherical coordinates are quantized for Platonic solids. The tessellations for E^3 are scale covariant. For a fixed radius of H^3 characterized by Lorentz invariance cosmic time this is not the case. One can however scale the value of a. What distinguishes between regular tessellations in E^3 and H^3 is that the metric of H^3 is non-flat and has negative curvature. H^3 is homogeneous space meaning that all points are metrically equivalent (this is the counterpart of cosmological principle in cosmology). Since both spaces have rotations as symmetries, this does not affect basic Platonic solids as 2-D structures assignable with 2-sphere if the edges are identified as geodesic lines of S^2. Quite generally, isometries characterize the tessellations, whose fundamental region corresponds to coset space of H^3/Γ by a discrete group of the Lorentz group acting as isometries of H^3. The modifications induced by the replacement $E^3 \rightarrow H^3$ relate to the 3-D aspects of the tessellation. This is because the metric is non-flat in the radial direction. The negative curvature implies that the geodesic lines diverge. One can use a counterpart of the standard spherical coordinates and in these coordinates the solid angles assignable to the vertices of Platonic solid are smaller than in E^3. Also the hyperbolic planes H^2 emerging from edges of the tessellation of H^3 diverge in normal direction the angles involved are smaller.

It is useful to start from the description of the Platonic solids. They are characterized combinatorially by integers and geometrically by various kinds of angles. Denote by p the number of vertices/edges of the face and by q the number of faces meeting at vertex.

3. Important constraints come from the topology and combinatorics. Basic equations for the numbers V ,E, and F for the number of vertices, edges and faces are purely topological equations $VE + F = 2$, and the equation $pF = 2E = qV$. Manipulation of these equations gives $1/r + 1/p = 1/2 + 1/E$ implying $1/r + 1/p > 1/2$. Since p and q must be at least 3, the only possibilities for $\{p, q\}$ are $\{3, 3\}$, $\{4, 3\}$, $\{3, 4\}$, $\{5, 3\}$, and $\{3, 5\}$.

2. The angular positions of the vertices at S^2 are basic angle variables. In H^3 hyperbolic angle assignable to the radial coordinate is an additional variable of this kind analogous to the position of the unit cell in the E^3 tessellation. The cosmological interpretation is in terms of redshift.

3. There is the Euclidian angle ϕ associated with the vertex of the face given by π/p. Here there is no difference between E^3 and H^3.

4. The angle deficit δ associated with the faces meeting at a given vertex due to the fact that the faces are not in plane in which case the total angle would be 2π. δ is largest for tetrahedron with 3 faces meeting at vertex and therefore with the sharpest vertex and smallest for icosahedron with 5 triangles meeting at vertex. This notion is essentially 3-dimensional, being defined using radial geodesics, so that the δ is not the same in H^3. In H^3 δ is expected to be larger than in E^3.

5. There is also the dihedral angle θ associated with the faces as planes of E^3 meeting at the edges of the Platonic solid. θ is smallest for a tetrahedron with 4 edges and largest for a dodecahedron with 20 edges so that the dodecahedron is not far from the flat plane and this angle is not far from π. The H^3 counterpart of θ is associated faces identified as hyperbolic planes H^2 and is therefore different.

6. There is also the vertex solid angle Ω associated with each vertex of the Platonic solid $\{p, q\}$ given by $\Omega = q\theta - (q-2)\pi$. For tessellations in E^3 the sum of these angles is 4π. In H^3 its Euclidian counterpart is larger than 4π.

7. The face solid angle is the solid angle associated with the face when seen from the center of the Platonic solid. The sum of the face solid angles is 4π. For Platonic solid with n vertices, one has $\Omega = 4\pi/n$. The divergence of the geodesics of H^3 implies that this angle is smaller in H^3: there is more volume in H^3 than in E^3.

E^3 allows only single regular tessellation having cube as a unit cell. H^3 allows cubic and icosahedral tessellations plus two tessellations having a dodecahedron as a unit cell. Why does E^3 not allow icosahedral and dodecahedral tessellations and how the curvature of H^3 makes them possible? Why is the purely Platonic tetra-icosahedral tessellation possible in H^3?

The first guess is that these tessellations are almost but not quite possible in E^3 by looking at the Euclidian constraints on various angles. In particular, the sum of dihedral angles θ between faces should be 2π in E^3, the sum of the vertex solid angles Ω at the vertex should be 4π. Note that the scaling of the radial coordinate r decreases the dihedral angles θ and solid angles Ω. This flexibility is expected to make possible so many tessellations and honeycombs in H^3. The larger the deviation of the almost allowed tessellation, the larger the size of the fundamental region for fixed a.

Consider now the constraints on the basic parameters of the Platonic solids (`rb.gy/1cuav`) in E^3 while keeping their H^3 counterparts in mind.

1. The values of didedral angle for tetrahedron, cube, octahedron, dodecahedron, and icosahedron are

$$[\theta(T), \theta(C), \theta(O), \theta(D), \theta(I)] \approx [70.3^\circ,\ 90^\circ, 109.47^\circ,\ 116.57^\circ, 138.19^\circ] \ .$$

   Note that $r = 5$ tetrahedra meeting at a single edge in E^3 would almost fill the space around the edge. In E^3 $r = 4$ cubes can meet at the edge. In H^3 r should be larger. This is indeed the case for the cubic honeycomb $\{4, 3, 5\}$ having $r = 5$. For $r = 3$ icosahedrons the sum dihedral angles exceeds 2π which conforms with the that $\{3, 5, 3\}$ defines an icosahedral tessellation in H^3. For the $r = 4$ dodecahedra meeting at the edge the total dihedral angle is larger than 360°: $r = 4$ is therefore a natural candidate in H^3. There are indeed regular dodecahedral honeycombs with Schläfli symbol $\{5, 3, r\}$, $r = 4$ and $r = 5$. Therefore it seems that the intuitive picture is correct.

2. The values of the vertex solid angle Ω for cube, dodecahedron, and icosahedron are given by the formula $\Omega = q\theta - (q-2)\pi$ giving

$$[\Omega(C), \Omega(D), \Omega(I)] \approx [1.57080, 2.96174, 2.63455].$$

   The sum of these angles should be 4π for a tessellation in E^3. In E^3 This is true only for 8 cubes per vertex $(\Omega = \pi/2)$ so that the cubic honeycomb is the only Platonic honeycomb

in E^3. The minimal number of cubes per vertex is 9 in H^3. It is convenient to write the values of the vertex solid angles for D and I as

$$[\Omega(D), \Omega(I)] = [0.108174,\ 0.209651] \times 4\pi \ .$$

The number of D:s *resp.* I:s must be at least 10 *resp.* 5 for dodecahedral *resp.* icosahedral honeycombs in H^3.

3. The basic geometric scales of the Platonic solids are circumradius R, surface area A and volume V. The circumradius is given by $R = (a/2)\tan(\pi/q)\tan(\theta/2)$, where a denotes the edge length. The surface area A of the Platonic solid $\{p, q\}$ equals the area of face multiplied by the number F of faces: $A = (a/2)^2 Fpcot(\pi/p)$. The volume V of the Platonic time is F times the volume of the pyramid whose height is the length a of the face: that is $V = FaA/3$.

   Choosing $a/2$ as the length unit, the circumradii R , total face areas A an the volumes V of the Platonic solids are given by

$$[R(T), R(C), R(O), R(D), R(I)] = [\sqrt{3}/2, \sqrt{3}, \sqrt{2}, \sqrt{3}\phi, \sqrt{3-\phi}\phi] \ ,$$

$$[A(T), A(C), A(O), A(D), A(I)] = [4\sqrt{3}, 24, 2\sqrt{3}, 12\sqrt{25+10\sqrt{5}}, 20\sqrt{3}] \ ,$$

and

$$[V(T), V(C), V(O), V(D), V(I)] \approx [\sqrt{8}/3, 8,\ \sqrt{128}/3,\ 20\phi^3/(3-\phi), 20\phi^2/3]$$
$$\approx [.942809, 8, 3.771236, 61.304952, 17.453560] \ .$$

What can one say about icosa-tetrahedral tessellation?

1. Consider first the dihedral angles θ. The values of dihedral angles associated T, O, and I in H^3 are reduced from that in E^3 so that their sum in E^2 scene must be larger than 2π. Therefore at least one of these cells must appear twice in H^3. It could be T but also O can be considered. For $2T + O + I$ and $T + 2O + I$ the sum would be 388.26° *resp.* 427.43° in E^3. $2T + O + I$ *resp.* $T + 2O + I$could correspond to 4 cells ordered cyclically as ITOT resp. IOTO.

2. The values of the vertex solid angle Ω for tetrahedron, octahedron, and icosahedron are given by $[\Omega(T), \Omega(O), \Omega(I)] = [0.043870, 0.108174, 0.209651]4\pi$ If the numbers of T, O and I are $[n(T), n(O), n(I)]$, one must have $[n(T)\Omega(T), +n(O)\Omega(O) + n(I)\Omega(I) > 4\pi$ in H^3.

   If the number of the cells for the fundamental domain are really $[N(T), N(O), N(I)] = [30, 20, 12]$, the first guess is that $[n(T), n(O), n(I)] \propto [N(T), N(O), N(I)$ is approximately true. For $[n(T), n(O), n(I)] = [2, 3, 1]n(I)$, one obtains $\Omega = n(T)\Omega(T) + n(O)\Omega(O) + n(I)\Omega(I) = n(I) \times .629 \times 4\pi$. This would suggest $n(I) = 2$ giving $[n(T), n(O), n(I)] = [4, 6, 2]$

6.3 New results about the relation of the icosa-tetrahedral tessellation to the dark genetic code

How could the icosa-tetrahedral tessellation relate to the proposed dark realizations of the genetic code [L107, L122]?

6.3.1 About the problems of the earlier view of the dark realizations of the genetic code

Consider first the problems of the earlier views of the realization of the dark genetic codes in terms of dark proton triplets at monopole flux tubes parallel to the ordinary DNA and to the realization in terms of dark photon triplets.

1. The TGD based inspired model of the dark photon genetic code [L11] [L78, L107] assumes that the dark realization of genetic code involves 3 icosahedral Hamiltonian cycles giving rise to 20+20+20 dark DNA codons and the unique tetrahedral Hamiltonian cycle giving the remaining 4 codons.

   The obvious problem of icosa-tetrahedral picture is that one must assume that icosahedron and tetrahedron are disjoint. If they have a common face, the number of faces reduces to 63 and one DNA codon is missing. This raises the question whether icosahedron and tetrahedron could be disjoint pieces of a larger structure.

2. Icosahedron and tetrahedron should have a physical realization: what could it be? How the Hamiltonian cycles are realized physically? The cycles are defined only modulo the isometry group I of icosahedron having 60 elements and Z_n $n = 6, 4$ or 2 leaves the cycle and the orbits of this group (amino-acids) invariant. The Hamiltonian cycle has $\#(I/Z_n)$ isometric copies (the numbers of copies are 10, 15, and 32). Does this have a physical significance? How are the 12 frequencies associated with the edges of the cycle realized physically? What is the physical interpretation of octave equivalence: does it have something to do with 2-adicity?

3. In the dark proton realization a given codon would correspond to a selected triangular face of I or T carrying dark protons at the vertices of this face. The original view was that dark 3-proton states would correspond to 64 codons. The problem was that one obtains only 8 states for dark proton triplets from spin and antisymmetrization in spin degrees of freedom would not allow any states unless the spatial wave function is totally antisymmetric and spins are in the same direction.

   In the original proposal also neutrons were assumed so that the codon corresponds to a sequence of 3 nucleons with both spins. 3 nucleons would give rise to 64 states as required. Dark protons can also be effectively neutrons as far as charge is considered. This might be possible if the bonds connecting the dark protons can be both neutral and negatively charged. Weak interactions are as strong as electromagnetic interactions in a given biological scale (such as DNA scale) if the dark Compton length proportional to h_{eff} is larger than this scale and the weak transitions change the dark protons to effective dark neutrons.

   This option leads to a problem with the fact that DNA nucleotides have negative unit charge. One should have protons to neutralize this charge and stabilize DNA. Also variants of the proposal in which there are flux tube connections between dark protons having 2 different neutral states analogous to neutral pion and neutral ρ meson.

   The simplest proposal, which is consistent with the idea that genetic codons correspond to cyclotron transitions of dark proton triplets assignable to the triangular faces of an icosahedron or tetrahedron is as follows. Besides 2 spin states, dark protons can also have 2 states with spin ± 1 corresponding to the analog of rotation in the discrete space defined by the vertices of the triangle. This would give $2^3 \times 2^3 = 64$ states.

The realizations of the genetic code in terms of dark photon triplets and dark proton triplets should correspond to each other. This requires that dark proton triplet realization should naturally correspond to the icosa-tetrahedral realization.

1. The codons identified as dark proton triplets assignable to one of the 20 triangular faces of icosahedron and tetrahedron have in quantum situations a wave function in the discrete space of the faces, which is in general delocalized. Could these wave functions in the set of faces give rise to states in 1-1 correspondence with the icosahedral and tetrahedral codons? There would be 20 wave functions for an icosahedron and 4 wave functions for a tetrahedron. The number of icosahedral states must be tripled to 60 corresponding to the 3 basic types of icosahedral Hamiltonian cycles with symmetries Z_n, $n = 6, 4, 2$.

The 3 dark protons also have spin degrees of freedom. The dark proton triplet in the ground state(s) would be naturally spontaneously magnetized so that all spins are in the same direction. Also the states in which some dark protons are excited are allowed by Fermi statistics and are needed since these excitations could correspond to the spatial wave functions in face degrees of freedom.

2. Dark photon triplets are needed for communications. The vision is that they correspond to the representation of codons as frequency triplets represented by the realization of icosahedral and tetrahedral Hamiltonian cycles as frequency triplets. The assumption has been that the 3 frequencies of dark 3-photon are associated with the cyclotron (or Larmor transitions if only spin is dynamical) of dark protons of a dark proton triplet.

   Dark photon communications between identical codons would take place by 3-resonance. The de-excitation of the first codon would lead to the excitation of an identical codon: one would have a kind of flip-flop. Also dark genes as sequences of N dark codons could act as a single quantum coherent unit and 3-N resonances between identical dark genes would become possible. The mechanism is very similar to that used in the computer language LISP. The modulation of the frequency scale by modulating the thickness of the monopole flux tubes would make possible coding of the signal and it would be transformed to a sequence of resonance pulses at the receiving end.

   Dark photon triplet states could correspond to wave functions in the space of icosahedral and tetrahedral faces.

3. Cyclotron transitions would be needed in order to generate dark photon triplets. This would require excitations of the dark protons of the spontaneously magnetized ground state(s). If only spin matters, the cyclotron transitions reduce to Larmor transitions. The correspondence with the icosahedral Hamiltonian cycles in terms of dark photon triplets would suggest that these excitations correspond to icosahedral genetic codons as wave functions in the set of faces. The cyclotron transition would provide the energy needed to excite the wave function in the set of faces. 64 transitions would be needed. It is important to notice that cyclotron transitions rather than cyclotron states of dark protons would correspond to codons of icosa-tetrahedral representation represented as wave functions in the set of facs.

   There are however only 8 states per face if only Larmor transitions are allowed. This is much less than the number 20 20+20+4=64 for icosahedral and tetrahedral Hamiltonian cycles. An additional two-valued degree of freedom is needed. The simplest possibility is the assignment to each dark proton an analog of angular momentum eigenstate with spin ± 1 corresponding to a discrete rotation around the triangle. This would give $8 \times 8 = 64$ states per face. Could the excitations of these states correspond to 20+20+20 icosahedral states plus 4 tetrahedral states?

4. Hitherto the considerations have been implicitly classical in that a localization in the set of faces has been assumed. Quantum theory allows us to give up this assumption. Icosahedral realization suggests that dark proton triplet has a icosahedral wave function delocalized to the set of 20 faces with symmetry fixed by the Hamiltonian cycle to Z_n, $n = 6, 4$ or 2, and that the excitation of the dark proton triplet in the face degrees of freedom provides the energy changing the wave function in the set of faces. The same would apply to the tetrahedron with symmetry Z_4 allowing 4 wave functions.

   The orbital and angular momentum degrees of freedom would be coupled. The transition from the ground state for dark proton triplet would excite wave function in the set of faces. This could imply the desired correspondence between the dark proton representations and dark photon realizations of the code.

5. There is a further problem. Spontaneously magnetized states of 3 dark protons would define ground states of codons. The ground state proton triplet cannot have lower energy states and cannot emit dark photon triplets and are therefore "mute" and unable to communicate, presumably necessary for processes like transcription and translation. Note that ground states are however not deaf.

The proposed general view is attractive but the details remain to be understood and problems solved. Here the notion of icosa-tetrahedral tessellation could help. The proposal of [L122] was that the icosa-tetrahedral honeycomb at the light-cone proper time $a = constant$ surfaces identifiable as hyperbolic 3-space H^3 allows to realize the dark genetic code.

The icosa-tetrahedral honeycomb is the unique honeycomb, which involves only Platonic solids. This inspires the question whether genetic code could be universal and realized in all scales by induction, which means that the tessellation of H^3 induces tessellation of 3-surface $X^3 \subset H^3$ by restriction. Also the induction to $H^3(a)$ projection of X^4 makes sense.

The TGD view of holography indeed predicts the special role of hyperbolic 3-spaces. The space-time surfaces in $H = M^4 \times CP_2$ are analogs of Bohr orbits, which go through $H^3(a_n) \subset M^4 \subset H$, where a_n corresponds to a root of the polynomial with integer coefficients determining to a higher degree a given region of the space-time surface by $M^8 - H$ duality [L101, L102].

In the sequel the detailed realization of the genetic code in terms of the icosahedral honeycomb will be discussed with an emphasis on the problems noticed above.

6.3.2 The realization of the code in terms of icosa-tetrahedral tessellation

The fundamental region of the icosa-tetrahedral tessellation contains 30 octahedrons, 20 tetrahedrons, and 12 icosahedrons and the cautiously proposed interpretation is that the cells meeting at each *edge* of the tessellation have either the cyclic structure TOTI or OTOI, and each vertex involve 3 O:s, 2 T:s and 1 I. Could one interpret this in terms of the dark icosahedral realization of the genetic code?

Ideas related to the detailed realization of the genetic code

The detailed realization of the dark genetic code is far from completely understood and one might hope that icosa-tetrahedral realization could bring in the constraints allowing us to fill in the details. It is useful to proceed by considering basic requirements on the realization of the dark code.

1. There are 3 O:s per single I in vertex if 10 instead of 12 icosahedral cells are included. The reasons for this become clear from the proposed relation between DNA double strand and fundamental cell of icosahedral honeycomb. What could the role of O:S be?

   Imagine that it is possible to arrange the polyhedrons for a given I to cycles as -I-O-T-O-T-O-: here cyclicity is assumed. The two tetrahedrons and I would be disjoint. This would solve the problem due to the common face of T and I (only 63 DNA codons) but give 60+4+4 faces and 68 dark DNA codons. There is however the problem posed by the mute codons. Could the presence of mute DNA codons reduce the number of DNA codons from 68 to 64. This would imply that their transcription allows only 64 dark mRNA codons. Could mute mRNA codons reduce the effective number of mRNA codons to 61 for the standard code (stop codons would be mute)? What about its variants with a smaller number of stop codons?

2. Bioharmony involves 3 icosahedral Hamiltonian cycles. All the combinations of the 3 -cycles with symmetries Z_6, Z_4 and Z_2 predict the same code. These bioharmonies are interpreted as correlates for emotional states appearing already at the basic bio-molecular level. The motivation comes from the fact that the icosa-tetrahedral harmony emerges as a geometric model for the music harmony and music indeed both creates and expresses emotions.

   Could icosahedral honeycomb allow us to understand the realization of these 3 icosahedral Hamiltonian cycles in terms of cyclotron frequency triplets? One must have closed magnetic monopole loops in order to have cyclotron transitions. Could these loops form triangles of form I-T-O. This would be 6 different triangles and 3 different positions of I for given T. This kind of loop would be assigned with each vertex of the face. Could the magnetic field strengths depend on the loop and for a given T give rise cyclotron frequency triplets characterizing a given icosahedral Hamiltonian cycle.

3. One can criticize the assumption that there is only a single codon per single I and T. I:s could in principle carry several codons. This however gives a restriction that the codons inside given I and T are different and restricts the representative power of the code if it involves more than 2 strands. This restriction is however automatically satisfied for the base-paired codon and anticodon in the DNA double strand!

Dark photon realization of the icosahedral part of the code

Consider first the realization of the icosahedral part of the code in terms of dark photons.

1. The 3 icosahedral Hamiltonian cycles have symmetries. The 20 codons with Z_6 symmetry correspond to 3 6-plets and 1 doublet of Z_6 and for unbroken symmetry the codons inside these multiplets code for the same amino acid. This means 3+1= 4 amino acids. Z_4 symmetry has 5 4-plets and in absence of symmetry breaking this corresponds to 5 amino-acids. Z_2 symmetry as 10 2-plets, and also this symmetry is also almost exact and corresponds to the almost exact symmetry with respect to the third letter of the codon analogous to isospin symmetry.

2. Icosahedral part of the icosa-tetrahedral realization involves 3 icosahedral Hamiltonian cycles characterized by different symmetries. For Z_6 symmetry, there are 6+6+6+2=20 codons codons. These sets of codons can be regarded as orbits of Z_6 and correspond to amino-acids. This if the Z_6 symmetry is not broken. This means 3+1 amino acids in absence of symmetry breaking.

   Z_4 symmetry has 5 4-plets and in absence of symmetry breaking this corresponds to 5 amino-acids coded by 4 codons each. Z_2 symmetry has 10 2-plets and this symmetry is also almost exact. This symmetry corresponds to the almost exact symmetry with respect to the third letter of the codon.

3. Dark photon codons are represented as cyclotron frequency triplets of dark photons created in 3-cyclotron transitions for dark proton triplets involving simultaneous emission of 3 dark photons made possible by quantum coherence. In the case of genes with N codons one has 3N-cyclotron transition and 3N dark proton-state represents a gene as a quantum coherent unit.

Dark proton realization of the icosahedral part of the code

Consider next the dark proton realization of the icosahedral part of the code.

1. The basic problem of the dark proton realization of the code is that there are only 8 dark proton spin states. If one assumes that each dark proton can have spin ± 1 this problem the number of dark proton states is 4 and one obtains 64 states.

   If one allows the states with vanishing spin so that one would have 3 orbital states per dark proton, the number of cyclotron transitions per dark proton is 4. Since lowest energy states are mute and transitions define codons, this could be the correct identification.

2. Icosa-tetrahedral realization should give 20+20+20+4 =64 dark proton triplets assignable to the faces of I and T. Suppose that the cells can be thought of as forming a cycle O-I-O-T-O-T with O and T ends connected. The two T:s have no common faces with O and without additional conditions give rise to 4+4 additional codons giving 68 codons. How can one reduce the number of dark DNA codons to 64?

3. Dark proton codons have a ground state, or possibly several of them, which by definition cannot decay to lower energy states by emission of dark photon cyclotron triplet. Ground state codon is mute since it cannot produce dark photon triplets as 3-chords.

   The natural first guess is that the ground states correspond to the 6 combinations 3 icosahedral Hamiltonian cycles and 2 tetrahedral cycles assignable to $2\times$ T. The 3 stop codons are transcribed but not translated so that the interpretation of 3 DNA stop codons as icosahedral ground state dark codons unable to send 3-photon signals is not correct. For mRNA this

interpretation could make sense if the mRNA images of DNA stop codons represent ground state codons.

4. Cyclotron excitations of ground state codons are induced by dark photon triplets. Conversely cyclotron de-excitatons generate dark proton triplets except for the ground state codons with minimum total energy. Suppose that there are 6 ground state codons as combinations of 3 dark codon ground states assignable to the 3 icosahedral Hamiltonian cycles and 2 dark proton ground states assignable to tetrahedral cycles of the two T:s. This would give 8 mute states. The total number of dark DNA codons is 60+8=68. Note that the mute states are not deaf: they can receive messages.

   One would obtain only 60 DNA codons, which can be transcribed to mRNA codons if the transcription involving dark photon codons. How could one get 64 as an effective number of DNA codons?

   One can imagine transitions between otherwise mute codons, which generate dark photon triplets coupling to mRNA associated with DNA. Let A, B and C the ground state codons with minimal total dark cyclotron energies in an increasing order for the 3 icosahedral Hamiltonian cycles. If for a given T (two options) the cyclotron transitions are possible only between codons C and B and B and A one obtains 2 DNA-mRNA pairings for both T:s. One would have 60+2+2=64 mRNAs pairing with DNA and effectively 64 DNA codons.

   Note that the transcription produces only 64 dark mRNA codons from 68 dark DNA codons.

   For 64 mRNA codons it could happen that there are no transitions between the 3 icosahedral codons for both choices of T so that there are 6 mute mRNA codons. If there are transitions C $\rightarrow$ B and B $\rightarrow$ A, the number of mute icosahedral codons is 4. If there are no transitions between tetrahedral ground state codons, one has effectively 60 mRNA codons since the translation stops due to the absene of dark 3-photon signals to tRNA. If there is a transition between the 2 ground state nRNA codons associated with the two T:s, one obtains 61 effective mRNA codons of the standard realization of the code. The transitions between tetrahedral codons can increase the effective number of mRNA codons.

5. What about tRNA appearing as a pair of amino-acid and single RNA codon. Could the RNA of tRNA and amino-acids correspond to the unique icosahedral honeycomb of H^3 and to icosahedral Hamiltonian cycles so that the number of dark codons in absence of tetrahedral degeneracy would reduce to 32, which is the minimal number of ordinary tRNA codons, which is increased by the non-uniqueness of the ordinary tRNA itself? Note that mute tRNA codons are not deaf: they can receive messages but cannot send them. Obviously, tRNA and amino-acids would correspond to the lowest evolutionary level.

The tentative conclusion would be that in the TGD framework DNA-mRNA transcription is not 1-to-1: information is lost and could say that RNA represents a lower level of evolutionary hierarchy. This would conform with the RNA world vision. The numbers of dark proton DNA and mRNA codons are 68 and 64 respectively. The unavoidable existence of mute codons gives effective DNA codon number 64 as the number of mRNA codons. 3 icosahedral codons can be mute and one obtains 3 stop codons unable to communicate with tRNA. The number of mute codons can also be smaller.

The dark DNA and RNA codons are dynamical and are not fixed to be the same as ordinary codons. This is required only during the communications with ordinary DNA possibly taking place by dark photons transforming to ordinary photons and inducing resonant transitions of ordinary DNA and other basic biomolecules. This strongly suggests that dark DNA and RNA act as kinds of R&D laboratories making it possible to test variants of the genes. Actually their ground states would correspond to 3 icosahedral representations and 2 tetrahedral representations and would correspond to aminoacids via transcription and translation.

Needless to say, this picture is highly speculative and one can probably imagine variants for it. The basic idea is however clear: icosa-tetrahedral tessellation could explain the details of the standard genetic code and its modifications.

Realization of the flux tube structures associated with dark codons

The following represents an attempt to make the above picture more concrete.

1. The selection of 1 O from 3 O:s could mean a selection of an icosahedral Hamiltonian cycle with symmetry group Z_6, Z_4, or Z_2. This gives for icosahedral realization 20+20+20 =60 icosahedral codons. Tetrahedral Hamiltonian cycles associated with the two T:s should give the remaining 4 codons. One can however imagine several ways for how this could occur.

2. The selection of O should correspond to a choice of the icosahedral cycle. What does this mean geometrically? To each dark proton of the codon, one must assign a closed monopole flux tube. The strength of the magnetic field of the flux tube fixes the cyclotron frequency scale for each flux tube. The 20 dark-photon chords defining a given icosahedral bioharmony differ for different choices of O and T. The frequencies are fixed if the Hamiltonian cycle corresponds to a quint cycle such that the frequencies associated with the neighboring vertices of the Hamiltonian cycle differ by a scaling 3/2. This requires that the magnetic field strengths along the cycle differ by scaling 3/2.

3. How to concretely realize the correlation of the bioharmony with the choice of O and T for a given I? Suppose that for a given I, the closed flux tube connects I and the selected O and T. There would be a closed I-O-T flux tube for each vertex of the face defining the codon. This kind of flux tube would define an analog of a string of a musical instrument.

   These closed flux tubes would be hyperbolic analogies of closed circuits formed by Euclidian nearest neighbour lattice bonds. If makes sense to assign to each I a cycle O-I-O-T-O-T, with O and T at ends being connected, the cycle I-O-T would go through the either T, and this implies that tetrahedral codons correspond to the other face of T. One would obtain 64 dark proton codons with 3 mute dark proton codons identifiable as stop codons. In the transcription the signal as a dark photon triplet would not reach the dark RNA codon and the transcription would stop. Could this mean that dark RNA codon attaches first to dark DNA codon and the transcription of DNA to ordinary RNA occurs after that in the usual way.

4. The proposed transitions between ground state codons for icosahedral Hamiltonian cycles modify the cycle geometrically since the O in cycle I-O-T changes. If the transitions for given T are only of C$\rightarrow$ B and $B \rightarrow A$ with energies in increasing order, one can imagine that the O is replaced by a neighboring O in the transition in the O-I-O-T-O-T.

   Several questions remain to be answered.

1. The symmetry breaking for the icosahedral codons with Z_n, $m = 6, 4, 2$ should be understood. This symmetry breaking can be assumed to occur at the level of dark mRNA and modify the frequency triplets from those for completely symmetric mRNA codons. The replacement $T \rightarrow U$ might relate to the symmetry breaking.

   UUG, CUG, and the very common AUG appear as start codons. They correspond to symmetry breaking for 6-plet (Z_6) coding for leu and 4-plet (Z_4) coding for ile. All symmetry breakings occur for start codons UUG, CUG, and for codons UAA and UAG and UGA and UGG closely related to stop codons.

2. Can one understand the reduction of the number of mRNA stop codons to 2 or 1 occurring for some variants of the code? In these situations, the stop codon of mRNA can code for an exotic amino acid pyrrolysine and selenocysteine. Could the transition between stop codon of dark mRNA icosahedral Hamiltonian cycle to a stop codon of another Hamiltonian cycle take place such that the dark photon triplet generated couples to tRNA involving the exotic amino acid. Situation would be almost like in the case of DNA where only two ground state codons stop the transcription.

3. What can one say about the strength of the magnetic fields assignable with the monopole flux tubes? Nanometer length scale 1 nm, naturally assignable to the DNA double strand, corresponds from the formula $l_B = 26nm/\sqrt{B/Tesla}$ to 12.2 GHz. What is interesting is

that the gravitational Compton frequency for Earth is 67 GHz and defines a lower bound for the gravitational quantum coherence time. If the strengths of the magnetic fields span 7 octaves, the thickness of the flux tube would vary by a factor 10 in the range about .1 nm - 1 nm.

4. Note that the 12-note scale can be realized using powers $(3/2)^k$, $k = 1, ..., 12$, of the fundamental and by using octave equivalence to reduce the note to the basic octave. Since the monopole flux is quantized, the realization of the scale requires variation of flux tube thickness inducing variation of magnetic field strength and therefore of that cyclotron frequency scale.

   There is nothing cherished in the rational quint cycle as the basis of the 12-note scale. For instance, the well-tempered scale actually replaces the Pythagorean scale with an algebraic scale coming in powers of $2^{1/12}$.

6.3.3 Description of the entire DNA double strand in terms of icosa-tetrahedral tessellation

The most ambitious model would describe the entire DNA double strand and relate the model bioharmony to the properties of the icosa-tetrahedral tessellation. There are however many questions remaining.

1. Single DNA and RNA strand would correspond to a "half realization" for which the T and I cells would contain only single codon. The splitting of DNA could have a geometric interpretation as an effective replication of the induced tessellation to two tessellations to RNA type tessellations.

2. There are 20 amino-acids and an icosahedron involves 20 faces. Is this a mere accident? Could icosahedral honeycomb describe amino-acid sequences geometrically. tRNA appears as a single unit. tRNA-amino-acid pairing would involve pairing of two icosahedral tessellations as also the pairing of RNA and tRNA in the translation. tRNA would naturally correspond to a single cell of icosahedral tessellation. This would also explain why the number of tRNA molecules is considerably smaller than RNA codons.

3. Does RNA correspond to icosahedral or icosa-tetrahedral tessellation? Tetrahedral Hamiltonian cycles are needed, in particular the dark proton triplets associated with the tetrahedral faces. Therefore icosa-tetrahedral tessellation is the natural option also for RNA.

4. It is thought that DNA and RNA nucleotides float freely in the cellular water and DNA and RNA codons are built from them in replication/transcription. This is probably the case at the biochemical level, whose dynamics is controlled by dark level (I have however considered the possibility that freely floating nucleotides could actually form loosely bound codons).

   At the ark level both replication and transcription would involve replication of the induced icosa-tetrahedral tessellation: a similar process occurs for clay crystals, and is suggested to be a precursor of DNA replication. This process is a holistic quantum process occurring in a single quantum jump. This would explain the incredible accuracy of these processes, which is extremely difficult to understand in the chemical approach.

   The replication would determine the outcome, be it a pair of DNA double strands or of DNA and RNA. After this the chemical processes leading to the formation of chemical codons from nucleotides and their pairing with dark codons of the induced icosa-tetrahedral tessellation would take place.

DNA has a helical structure. Helical tessellations are known to exist (`rb.gy/5ova6`). If icosa-tetrahedral tessellation is induced, the helical structure would most naturally reflect the dynamics of the corresponding space-time surface. This suggests that only a sequence of I:s is selected from the set of 12 I:s in a given fundamental region of the icosa-tetrahedral tessellation.

To see whether this hypothesis can make sense one must use geometrical facts about DNA double helix, which has A-, B-, and Z forms `rb.gy/4kcrm`).

1. B-form is believed to dominate in cells. From the table of the Wikipedia article one learns that for the B-form the rise per base pair (bp) is 3.32 $\AA$, that full turn corresponds to 10.5 bps, and that the pitch of the helix per turn 33.2 $\AA$, which corresponds to 10 bps per turn. The pitch/turn should be equal to $10.5 \times 3.32 = 34.52$ $\AA$. There is obviously a mistake in the table.

2. The solution of the puzzle is that straight DNA in solution has 10.5 bps/turn and 10 bps/turn in solid state (`rb.gy/wqjbh`). If DNA double helix corresponds to solid state then 10 codons correspond to 3 full turns. Therefore my earlier assumption 10 bps/turn in the double helix is correct. 10 codons would correspond 3 full turns and to the length 99.6 $\AA \simeq 10$ nm, which in TGD framework corresponds to the p-adic length scale $L(151)$.

Double DNA strands cannot pair with all 12 I:s associated with the dark DNA. The length $L(151)$ should correspond to 10 I:s taking 80 per cent of the icosahedral volume. Is helical winding enough to achieve this?

1. The total volume of the fundamental region is $V = 20V(T) + 30V(O) + 12V(I) = 341.44$ using $2a$ as length unit. Using the estimate $V_{real} = L(151)^3 = 10^6$ $\AA^3$, one obtains $a = L(151)/2V^{1/3} \simeq 0.07 \times L(151)$. The volume fraction of single icosahedron would be $17.45/V \simeq .05$ and 10 I:s would take 1/2 of the volume.

2. The circumradius of single icosahedron would be $R = \sqrt{3-\phi}\phi a/2 \simeq .1 \times L(151) = 1$ nm. This conforms with the assumption that there are 10 codons per length $L(151)$! The diameter of the B-type DNA strand is 20 $\AA$ is also consistent with the value of the circumradius. Maybe the proposed picture works!

3. Notice that if an icosahedral cell corresponds to 2 tetrahedral cells and 3 tetrahedral cells, then 10 codons is the maximum for the realizable DNA codon.

What can one say about the straight form of DNA?

1. For 10.5 bps/turn for a straight DNA in solution, the smallest portion of strand, which corresponds to integer numbers of turns and of codons is 6 full turns. This corresponds to 63 bps and 21 codons.

2. With an inspiration coming from the notion of Combinatorial Hierarchy [A30, A40] defined in terms of Mersenne primes $M_n = 2^n - 1$ defined by the recursive formula $M(k) = M_{M(k-1)} = 2^{M(k-1)} - 1$, I proposed decades ago that ordinary genetic code could correspond to Mersenne prime $M_7 = 2^7 - 1$ [K39] [L29]. The basic idea is that a system with $2^7 - 1$ states corresponds to a Boolean logic with 7 bits but with one state missing: this state would correspond to empty set in the set theoretic realization or fermionic vacuum state in the realization as a basis for fermionic Fock states. Only 6 full bits can be realized and the number of realizable statements is 64, the number of genetic codons.

3. Memetic code corresponds to the Mersenne prime $M_{127} = M_{M_7} - 1 = 2^{127} - 1$. Now the number of codons would be $2^{126} = 2^{6\times 21}$ and is realizable as sequences of 21 DNA codons! Note that higher Mersenne numbers in the hierarchy were proposed by Hilbert to correspond to Mersenne primes but for obvious reasons this has not been proven.

4. Could 6 full turns of straight DNA define a memetic codon? During the transcription and replication, DNA double strand opens and becomes straight. Could memetic code be established during the transcription and replication periods? A further intriguing observation is that the cell membrane involves proteins consisting of 21 amino-acids.

6.3.4 Some questions

Many questions remain to be answered.

1. Hamiltonian cycles are fixed only modulo the 60-element isometry group I of icosahedron. Subgroups Z_n, $n = 6, 4$ or 2 as invariance groups of their orbits defining amino-acids coded by DNA codons assigned to them. Therefore the space I/Z_n corresponds to the space of orbits of Hamiltonian cycles having 10, 15, *resp.* 32 elements for $n = 6, 4$, *resp.* 2 . Suppose that the Hamiltonian cycles for various icosahedrons of the fundamental region proposed to be associated with the sequence of 10 DNA codons differ by a non-trivial isometry assignable to I/Z_n. Does this have physical implications or is it mere gauge degeneracy?

2. The wave functions defining quantal variants of the genetic codons can be assumed to be products of wave functions for the position of the face and 3-proton states assignable to a given face should form an orthonormal set. The face wave functions associated with tetrahedra are trivially orthogonal with those of second tetrahedron and icosahedron. For a fixed choice of the icosahedral or tetrahedral Hamiltonian cycle orthogonality can be realized for the wave functions associated with the position of the face.

   If the icosahedral face wave functions correspond to different Hamiltonian cycles then orthogonality of protonic states for a given face can guarantee the orthogonality. This is possible if the number of protonic states is larger than the number of icosahedral wave functions. This requires 20+20+20+20 protonic states so that four protonic 4 states are left if their number is 64.

3. Why Hamiltonian cycle and quint cycle? Without Hamiltonian cycles the number of frequencies defining 3-chords would be 30 and is reduced to 12 for Hamiltonian cycles. Hamiltonian cycles assigned to the genetic code define an additional symmetry as shifts along the cycle, which are represented as 3/2 scalings modulo octave equivalence. The quint cycle defines the 12 frequencies for a given magnetic field strength and the chords of different cycles consist of different combinations of frequencies.

   What does the Hamiltonian cycle as a 1-D closed path correspond physically?

The proposal that the fundamental region of the icosa-tetrahedral honeycomb could have interpretation as a kind of super-icosahedron raises several interesting questions.

1. Assume that the sequence of 10 DNA (2 codons missing) to the super-icosahedron having icosahedrons as 12 super-edges, tetrahedrons as 20 super-faces, and 30 octahedrons as super-vertices. Combinatorial equivalence suggests that one cdefine icosahedral Hamiltonian cycles as sequences of 12 icosahedrons serving as superedges. Could one define higher level icosahedral genetic codes in terms of icosahedral Hamiltonian cycles. The orthogonality of the face wave functions for the different Hamiltonian cycles would require the assignment of the analogs of dark proton triplets to the super-faces.

2. What could the notion of a super-Hamiltonian cycle as a sequence of 12 dark DNAs mean? The proposed interpretation is that the collection of tetrahedral and 3 icosahedral Hamilton's cycles defines a correlate of a mood, emotional state. It is difficult to say whether the mood is the same for all cells of the entire organism, for the genome of a single cell, for the genes, for the sequences of 10 DNAs, or for codons.

   Super-Hamiltonian cycle associated with the super-icosahedron would have as its edges icosahedrons with the associated 12 dark DNA codon. If the 12 icosahedrons can correspond to different Hamiltonian cycles, one would have a correlate for a sequence of moods. Hamiltonian cycle property allows only 60 sequences of this kind. Without this restriction one would have N^{12} mood sequences, where N is the number of Hamiltonian cycles.

3. One can of course ask whether super-octahedron and super-tetrahedron could make sense and whether they could combine to form a super-icosa-tetrahedron. Does one have any tessellation for which fundamental region would correspond to super-tetrahedron with tetrahedron as interior, 4 octahedrons as 4 super-vertices and 4 icosahedrons as super-edges. There is no mention of this kind of tessellation but it is known that hyperbolic tessellations constructible using the standard methods do exist.

One could even ask whether there could exist a fractal hierarchy of these super-structures constructible from the super-Platonic solids of the previous level and whether it could be realized as a hierarchy associated with dark DNA. This would mean a hierarchy of increasingly refined emotions emerging as the length of genes and DNA increases.

6.4 Further progress in the understanding of the icosa tetrahedral realization of the genetic code

TGD leads to two models of the genetic code. The first model emerges from a model of music harmony based on the combination icosahedral and tetrahedral geometries [L11] [L107]. The second model relies on the representation of the genetic codons as entangled triplets of dark protons at the monopoles flux tubes defining the dark variant of DNA accompanying the ordinary DNA [L78].

It took quite a long time to understand why both icosahedra and tetrahedra are needed and how the two models are related. The solution of the puzzle came from a universal model of the genetic code based on a completely unique tessellation of 3-D hyperbolic space H^3 realized as the light-cone proper time constant hyperboloid of the Minkowski space. This icosa tetrahedral tessellation (ITT) (known also as tetrahedral-icosahedral tessellation) makes sense in all scales and I have proposed its realization at the level of DNA in [**?**]essellationH3. The model involves several intuitive elements and the best way to proceed is to try to improve the existing understanding and to identify the possible weaknesses of the model.

I am not a professional hyperbolic crystallographer and my view of ITT (see this) relies on guesswork guided by physical and biological intuition based on what I call icosa tetrahedral model for the genetic code. In this article I represent some results based on using standard results from Platonic solids to deduce the numbers of tetrahedrons, octahedrons and icosahedrons emanating from a given vertex of the tessellation. The study of the vertex figure of ITT leads to a rather plausible guess for a manner to obtain ITT as a "blow-up" of icosahedral tessellation (IT).

The improved understanding of the icosa tetrahedral tessellation allows to answer some long standing questions related to the detailed realization of the genetic code. It however turns out that the notion of the super-icosahedron discussed in [L146] is not consistent with the improved view. However the 3-D generalization of the vertex figure of the ITT as its inverse image under projection permutes the numbers for the Platonic solids appearing in the super-icosahedron.

This section provides an answer to the question how many icosahedrons, octahedrons and tetrahedrons meet at the vertex of ITT: the answer comes by studying the vertex figure of ITT: these numbers are 12, 30, and 20. The study of the vertex figure of ITT suggests that the ITT can be constructed as a "blow-up" of the icosahedral tessellation (IT) by replacing icosahedral vertices with tetrahedra and dodecahedral vertices by pentagons and adding between icosahedral tetrahedra and dodecahedra octahedra as analogs of edges. Icosahedral and dodecahedral bioharmonies correspond to 12-note *resp.* assignable to Western *resp.* Eastern music. One can ask whether octahedral 4-codons should also be allowed.

The picture provided by RID is consistent with the earlier notion of "super-icosahedron". The model of the genetic code generalizes: besides the icosahedral Hamilton cycles (HCs) and codons for the three icosahedral codes and the tetrahedral HC and corresponding codons, also a unique dodecahedral HC and associated 5-codons plus pentahedral HC and codons are in principle possible. The fundamental region deduced from RID corresponds to a sequence of 10 or 12 DNA codons as proposed already earlier on the basis "super-icosahedron model".

The model allows us to understand the symmetry breaking of genetic codons. In particular, tetrahedral codons correspond to 3 stop codons and the codon coding for trp. A given codon corresponds either to I/T or D/pentahedron. The fundamental region represents a sequence of 10 or 12 DNAs so that all codons of the Hamiltonian cycle are used and the HC corresponds to a section of DNA. Fundamental region represents both DNA strands.

6.4.1 More precise views about some aspects of the icosa tetrahedral realization of the genetic code

The improved understanding of the icosa tetrahedral tessellation allows to answer some long standing questions related to the detailed realization of the genetic code.

6.4.2 What does the fundamental domain of ITT look like?

One basic question is how many tetrahedra (T), icosahedra (I) and octahedra (O) emerge from a given vertex of ITT.

The first guess was wrong as always

The wrong guess was that one can answer this question just from the knowledge of the solid angles associated with vertices of these Platonic solids. The solid angles are naturally defined as ratios of spherical areas to the radial distance squared and at the limit of very small hyperbolic radial distance approaching Euclidean distance, the total solid angle at this limit is 4π as in the Euclidean case.

However, the metric in the radial direction is non-Euclidean for the negatively curved hyperbolic 3-space H^3 so that the edges from the vertex diverge whereas in Euclidean spherical geometry they converge. Note that H^3 has 3-D rotation group as isometries so that the notion of Platonic solid applies also in H^3.

The lines emanating from the vertex are shared by neighboring T, O, and I emanating from the vertex. Two neighboring lines are associated with a triangular face shared by two Platonic solids involved.

The basic condition for the numbers $n(i)$ of the Platonic solids involved is $\sum_{i\in\{T,O,I\}} n_i\Omega_i = 4\pi$. Consider first the *Euclidean* case. One can find the general formulas for the solid angles from Wikipedia (see this).

1. Platonic solids are classified by 2 integers $\{q,p\}$ stating that q $p-$polygons meet at a given vertex. In the recent case one has only 3-polygons, that is triangles, for all Platonic solids involved. One has

$$[q(T),q(O),q(I)] = [3,4,5] \quad , \quad [p(T),p(O),p(I)] = [3,3,3] \quad .$$

2. Dihedral angle angle is the interior angle between the faces of the Platonic solid and satisfies the general formula

$$\theta(q,p) = 2asin(\frac{cos(\pi/q)}{sin(\pi/p)}) \quad .$$

In the *Euclidean* case the solid angle at the vertex is given as

$$\Omega(q,p) = q\theta(q,p) - (q-2)\pi \quad .$$

3. Suppose that all vertices are identical as the fact that there is only a single vertex figure. The vertex of vertex figure, call it V, involves $n(T) \equiv n(3)$ tetrahedrons, $n(O) \equiv n(4)$ octahedrons and $n(I) \equiv n(5)$ icosahedrons. The sum of the solid angles equals to 4π, which gives

$$\sum_{q\in\{3,4,5\}} n(q)[q\theta(q,3) - (q-2)\pi] = 4\pi \quad .$$

This gives

$$\sum_{q\in\{3,4,5\}} n(q)\ qasin(\frac{cos(\pi/q)}{sin(\pi/p)}) - (n(3)+2n(4)+3n(5))\pi = 4\pi \quad .$$

4. In the Euclidean case, one can guess the solution to the condition by starting from the icosa tetrahedral model [L78, L107] for the genetic code, which is a fusion of 3 icosahedral codes associated with Hamiltonian cycles (HCs) with symmetry groups Z_6, Z_4, Z_2 and of a single tetrahedral code defined by the unique tetrahedral HC. In the proposed model based on ITTs [L122, L146], the octahedron is passive and does not contribute to the code. A reasonable guess based on this model is $n(I) = 3$ and $n(T) = 1$.

The normalized vertex solid angles are

$$\frac{[\Omega(3),\Omega(4),\Omega(5)]}{4\pi} = [0.043871, 0.1082, 0.2097] \ .$$

The consistency condition is

$$\frac{n(T)\Omega(T) + n(O)\Omega(O) + n(I)\Omega(I)}{4\pi} = 1 \ .$$

This leaves only the guess $[n(T), n(O), n(I)] = [1, 3, 3]$ under consideration giving for the sum the value 0.9974 in the accuracy used partially determined by the approximation $\pi \simeq 3.1415926535897$.

The vertex figure for ITT contains the needed information

The vertex figure V codes the information about the fundamental domain as one can easily see in the case of say cube. Consider now the vertex figure V for ITT.

1. The vertex figure is obtained by cutting a 3-sphere around a vertex is a 2-D object to which the vertices as edges and faces of the fundamental region of the solid are projected. For ITT, the vertex figure is rhombicosidodecahedron (RID) (see this). This is an Archimedean solid, one of thirteen convex isogonal nonprismatic solids constructed of two or more types of regular polygon faces.

   RID has *20 disjoint triangular* faces (as also I has), *30 square* faces, which share their corners with other square faces, *12 disjoint pentagonal* faces (as D has), 60 vertices, and 120 edges. The numbers of faces are much larger than in the Euclidean case.

   The 20 triangular faces correspond naturally to intersections of 20 T:s with the sphere, the 30 square faces to the intersections with 30 octahedra, and 12 pentagons to the intersections with 12 icosahedra. From V one finds squares and common edges with triangles and pentagons.

2. The illustrations of RID (see this) gives a 2-D analog for what it means that the tessellation has different 3-D Platonic solids as building bricks. Interestingly, the faces of RID are faces of the duals of the Platonic solids T, O and and I. In RID the triangles are disjoint and share sides with squares.

   Since RID and ITT are combinatorially closely related, this suggests that the disjoint triangles of RID correspond disjoint T:s of ITT and the squares of RID having sharing only corners correspond to O:s of ITT sharing only edges whereas D:s would correspond to I:s.

Could an analog for the construction of RID allow to deform the hyperbolic icosahedral tessellation (IT) to ITT?

1. The construction would rely on the correspondence *triangle - self dual T, pentagon - I as dual of D, square - O as dual of cube*. One could generalize the correspondence to *triangle→ T , pentagon → I, and square → O.*

   The recipe would be as follows. Start from the hyperbolic icosahedral tessellation (IT) $\{(3,5,3\}$ with 3 I:s $\{5,3\}$ meeting at each edge. One could blow-up the icosahedral vertices to T:s and glue to the faces of a given T 4 O:s. O:s would also share faces with other T:s and I:s but not with O:s if there is a combinatorial analogy with RID.

2. The inspection of the RID shows that T:s and I:s do not have common faces and meet only at V. O:s share faces with I:s and T:s. Besides the vertex figure there are also T:s,I:s, and O:s emerging from the origin. They have triangular 3 ,4, 5 triangular faces respectively and they contribute to the genetic code. Second important point is that RID contains only one half of the vertex figure. The natural interpretation would be that these halves correspond to DNA strands. This however requires that the fundamental domain is realized at the magnetic body.

3. The maximally symmetric solution to the condition $\sum_{i\in\{T,O,I\}} n_i\Omega_i = 4\pi$ would be

$$\Omega_i = \frac{4\pi}{(n(T)+n(O)+n(I))} = \frac{4\pi}{62} \quad .$$

6.4.3 Some progress in the detailed realization of the genetic code

ITT emerged as a mathematization of the icosa tetrahedral realization of the genetic code and it is interesting to see whether the new results allow us to gain some understanding about the issues related to the detailed realizations.

In the original vision [L11], it was unclear whether there are 3 different I:s or only a single I realizing one of the 3 HCs at time. Also the relationship between T and I was unclear. The proposal was that there is a single I and T that shares a common face with it. The idea about a common face was however somewhat fuzzy and I have discussed several ways to understand the details of the genetic code, in particular those assignable to stop codons.

Also the selection of a single active triangle as a representation of the codon was adhoc. The natural idea is that the Hamiltonian cycle selects all codons so that the fundamental region represents a portion of DNA: in fact 10 codons.

The revised view of the genetic code

The number 12 of pentagons is the number of the faces of D, the number of squares is the number of O:s and the number of edges of I, and the number 20 T:s is the number of faces of I. This conforms with the idea of blow-up in which vertices of I are replaced with T:s.

The structure of RID suggests a rather dramatic revision of the view about how the genetic code is realized at the level of ITT assignable to the magnetic body of DNA double strand. The interpretation that O:s serve in the role of edges is attractive and suggests that there are no codons associated with them. The role of the possible O codons as edges means that they are determined by I and D codons and that the Hamiltonian cycle for the squares is not a useful concept. Furthermore, there is no analog of edge between O codons which intersect at their corners.

This leads to the following picture.

1. Codons are associated with RID, that is with both the intersections of T:s, O:s, and I:s with the S^2 and also with the triangles emanating from the vertex V to RID. One can interpret the 20 triangles and 12 pentagons and 30 squares as potential genetic codons.

2. The notion of Hamiltonian cycle generalizes for the blow-ups and the edges of the cycle connects the blow-up vertices: 20 triangles for the blow-up of D and 12 pentagons for the blow-up of D. There are also tetrahedral with 1+3 vertices and codons with 1+5 vertices. For I:s having triangles as vertices there is a larger number of Hamiltonian cycles. For D:s having pentagons as vertices there is only one Hamiltonian cycle. Hamiltonian cycles represent a piece of DNA strand.

   Octave Equivalence implies that the frequency scaling in transition between two neighboring vertices for $2^{1/V}$, where the number of vertices is $V = 12$ *resp.* $V = 20$ for the I *resp.* D, type Hamilatonian cycle D type Hamiltonian cycle is $2^{1/20}$. This corresponds to the micro scales used in Eastern music. For the tetrahedral cycle it is $2^{1/4}$: this corresponds to the chord $C, E, G\sharp$. For its analog for D, the scaling is $2^{1/6}$.

3. RID and its mirror image needed to obtain the fundamental domain represent the 20 DNA icosahedral codons or 12 dodecahedral codons.

In [L146], I proposed a heuristic model for the 10-codon piece of DNA sequence a candidate for the fundamental region of IIT. The idea was that it corresponds to what I called super-icosahedron (SI) having icosahedrons as 12 super-edges, tetrahedrons as 20 super-faces, and 30

octahedrons as super-vertices. What is worrying is that 2 DNAs would be missing so that there would be 10 Is.

The guess was essentially correct: the RID has 20 regular disjoint triangular faces (as also I has), 30 square faces, which share their corners with other square faces, 12 regular disjoint pentagonal faces (as D has) plus 60 vertices, and 120 edges. The triplet (20 triangles, 30 squares, 12 pentagons) contains the same numbers as appear in SI. The correct identification of SI could indeed be as the fundamental domain of ITT if one glues to RIDs together (consider cube as an simple example). ITT could be seen as a 3-D combinatorial lift of RID obtained by the inverse of the projection to the sphere defining the vertex figure (triangle $\to$ T, square $\to$ O, pentagon $\to$ I): this is supported by the view what vertex figure means. Could the sequence of 12 DNAs correspond to (20 T:s, 30 O:s, 12 I:s) as the 3-D inverse image of the RID?

Solutions of some problems provided by the new view

The model of genetic code has suffered from some cronic problems.

1. If each vertex of IT is replaced with T in the blow-up identified as ITT, a single icosahedral triangle of IT would be replaced with 3 T:s. A natural identification is in terms of a genetic codon with 3 letters, one T per letter.

2. The icosahedral realization leads the following problem. The icosahedral HC with Z_6 symmetry corresponds to 3 Z_6 orbits with 6 triangles and one orbit with 2 triangles (6+6+6+2=20). This corresponds to 5 amino acids (AAs) identified as orbits of Z_6. The HC with Z_4 symmetry contains 5 orbits with 4 triangles ($5 \times 4 = 20$) and gives 5 AAs. The HC with Z_2 symmetry gives 10 orbits and therefore 10 AAs. One has 19 AAs altogether. One AA is missing.

3. Tetrahedral cycle involves 4 triangles and Z_3 symmetry is natural. The triangle opposite to V would give a codon coding for single AAs and the remaining triangles related by Z_3 symmetry corresponding to 3 ordinary DNA codons. The frequencies of these dark codons differ only by order and this suggests that they code for a single AA (vertex of T and the vertices opposite to it). The triplet could correspond to stop codons coding for no physical AA. The singlet codon could correspond to the missing AA, most naturally trip. Another less plausible option corresponds to (ile,ile,ile,met). One cannot interpret this multiplet as a symmetry broken quadruplet since there are 5 quartets. The interpretation as a symmetry breaking of (met,met) (ile, met) however works.

4. There are also problems related to the chemical realization of the dark code. There are several slightly different chemical realizations of the code, which are not complete and violate the symmetries, which are exact for the dark realization. Also the number of stop codons van vary.

Representation of codons as 3-chords

There are also questions related to the HC and its realization and also the realization of the codons as cyclotron frequency triplets.

1. Icosahedral HC corresponds to a sequence of 12 vertices to which one can assign T:s. The basic idea of bioharmony is that one assigns to each vertex a note of 12-note scale and the notes associated with the triangular faces define the 20 chords of the harmony for a given T as dark counterparts of DNA codons.

   The 12 edges connecting the faces in the simplest model corresponds to a scaling of frequency by 3/2 or by $2^{7/12}$ corresponding to Pythagorean and well-tempered scales (HC as quint cycle module octave equivalence). Various HCs correspond to different realizations of the genetic code in terms of 3-chords realized as cyclotron frequency triplets assignable to the triangular faces of I and interpreted as different harmonies as representations of moods: this aspect is absent in the standard view.

2. How the cyclotron frequencies are assigned with the vertices of I. One could consider the situation also from the point of view of IIT as a blow-up of IT. Each vertex of I has T as a blow-up. One should assign a cyclotron frequency with this particular vertex of T.

3. Could one assign the frequency triplets with the 3 T:s associated with the blow-ups of the triangular face of I? A given cyclotron frequency is most naturally associated with the vertex which it shares with an active I. This seems necessary since the letters of the codon defined by the 3 T:s should be independent. Octave equivalence allows only one frequency triplet unless the order of frequencies $C, E, G\sharp$ matters. At the level of DNA it matters but at the level of AAs it does not. The T triplets could correspond to different DNA codons coding for the same AA.

4. The situation is very similar for the start codon and stop codons. The start codon of the gene coding for the met is very special. Could one assign the start codon to the triangle opposite to the active vertex of T, so that it would effectively reduce to a doublet and the three codons coding for ile to the other faces of T?

What DNA codons do the T codons correspond to? One can consider two options for which T codons would code for DNA triplet and singlet and there would be no symmetry at the level of T.

1. At the level of the ordinary DNA, T codons could correspond to 3 stop codons and a codon coding trp or to 3 ile codons and met. There would be symmetry breaking for the I quartet giving rise to (ile,ile,ile, met) but this is not possible since there are 5 AAs coded by 4 DNAs. Therefore this option fails.

2. For the second option dark T codons correspond to DNA codons coding for (ile,ile,ile,met). One doublet would code for (stop,stp) and a second doublet would break Z_2 symmetry and code for (stop,trp). This option might also allow us to understand the small deviations from the standard genetic code for which stop codons occasionally code for a real AA.

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Part II

SOME APPLICATIONS

Chapter 7

Homonymy of the Genetic Code from TGD Point of View

7.1 Introduction

This article was motivated by the article of Peter Gariaev [K85] about the linguistic notions of synonymy and homonymy applied to genetic code (for other works of Gariaev and collaborators on the linguistic aspects of DNA see [I54, I52]). In another article by Peter Gariaev and Ekaterina Leonova-Gariaeva to be published in Open Journal of Genetics the notion of syhomy fusing these concepts is introduced. Homonymy is visible in mRNa-tRNA pairing and induced by the 1-to-many pairing of the third mRNA nucleotide with tRNA nucleotide. The homonymy in mRNA-AA (AA for amino-acid) pairing is also present albeit rare and might be explainable in terms of context dependence of this pairing.

The article summarizes much what is known about the theoretically poorly understood role of the third nucleotide of mRNA in the translation of mRNA to AAs. That many tRNAs correspond to same mRNA - synonymy - is not surprising since the number of tRNAs is smaller than that of mRNAs. There is however also homonymy present - the third nucleotide of mRNA can correspond to several tRNAs. If the AAs associated with homonymous tRNAs are same, the is no homonymy in mRNA-AA pairing. This is not quite always the case but the deviations are surprisingly small.

The article emphasizes the fact that the codons for the standard code can be divided to two classes. For 32 codons the first two letters fix AA completely. For the remaining 32 codons there is almost unbroken symmetry in that U and C *resp.* A and G code for the same AA. This symmetry is broken only for the three 4-columns of the code table containing Stop codon or Start codon coding also for met: this symmetry breaking is unavoidable given that the number of both start and Stop codons is odd. This symmetry breaking is minimal and applies only to A-G whereas T-C symmetry is exact. For the deviations of the code from the standard code the deviation as a rule breaks A-G or T-C symmetry or re-establishes it.

The notion of homonymy is extremely interesting from TGD point of view. TGD leads to two basic proposals predicting the numbers of DNA codons coding for given AA rather successfully.

1. The first proposal [L27] relies on TGD view about dark matter as $h_{eff}/h = n$ phases of ordinary matter [K33, **?**, K61] [L51, L50] motivated by adelic physics extending physics to include also the correlates of cognition [L51] [L50]. The empirical motivation comes from several sources, in particular from the findings of Pollack [L15] discussed in [L15]. One can understand the formation of negatively charged regions - exclusion zones (EZs) - as being due to the transformation of part of protons to dark protons residing at magnetic flux tubes.

   Dark genetic code would be realized in ters of dark proton sequences - to be denoted by DDNA, DmRNA, DtRNA, and DAA - would provide dark analogs of DNA, mRNA, tRNA, and AA. Biochemistry would emerge as a shadow of the much simpler dynamics of dark matter at flux tubes and genetic code would be induced by dark code code. The dark code would be sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA$\rightarrow$ DAA of many-to-1 maps free of

homonymies.

2. Second model of genetic code emerged accidentally from a geometric model of music harmony [L11] (see `http://tinyurl.com/yad4tqwl`) involving icosahedral (12 vertices-12-note scale and 20 faces-number of AAs) and tetrahedral geometries leading to the proposal that DNA codons and possibly also AAs correspond to 3-chords defining the harmony and obtained as unions of 20+20+20 3-chords associated with icosahedral 20-chord harmonies with symmetries Z_6, Z_4, Z_2 plus tetrahedral 4-chord harmony. There is large number of these harmonies bringing in additional degrees of freedom.

   Remark: This model has obviously analogies with the notion of wave genome introduced by Peter Gariaev [I40, I41, I55].

   Since music both expresses and creates emotions the proposal is that these harmonies assigning additional hidden degrees of freedom to the magnetic bodies of DDNA, DRNA, etc... serve as correlates of emotions also at the molecular level. This emotional context could also give rise to context dependence of the code if several harmonies are realizable chemically. Taking seriously TGD inspired theory of consciousness [L53] and model of emotions [L64] (see `http://tinyurl.com/ydhxen4g`), one might say that the details of the code might depend slightly on the "emotional" state of DNA, RNA, and possibly other molecules.

In the sequel I will consider the following proposal for the various pairings of dark DNA and ordinary DNA visualizable as a 2×4-matrix with two rows representing DDNA, DmRNA, DtRNA, DAA *resp.* DNA, mRNA, tRNA, AA.

1. The proposal is that genetic code at dark level extends to a sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA $\rightarrow$ DAA of horizontal pairings analogous to projections is the fundamental one, and realized via dark photon triplet resonance expect for the coupling to DAA for which coupling is based on the sum $f_{XYZ} = f_1 + f_2 + f_3$ of 3-chord frequencies. One might perhaps say that AA sequence defines melody and mRNA sequence the accompaniment. The frequencies f_{XYZ} for codons coding same AA would be same modulo octave multiple. There is context dependence and homonymies already in DmRNA-DtRNA pairing and due the fact that DtRNA corresponds to a 2-harmony as sub-harmony of 3-harmony and can be chosen in 3 different way. Also this choice - perhaps by state function reduction - could correlate with emotional state.

2. There are also vertical mappings DDNA $\rightarrow$ DNA, DmRNA $\rightarrow$ mRNA, DtRNA $\rightarrow$ tRNA and DAA $\rightarrow$ AA. These pairings would induce the horizontal pairings DNA $\rightarrow$ mRNA $\rightarrow$ tRNA $\rightarrow$ AA at the chemical level. The homonymy at mRNA-tRNA level would have no effects on DNA-AA pairing.

3. Apart from mRNA-AA pairing all these pairings would be realized dynamically in terms of 3-chords (f_1, f_2, f_3) and giving rise to a resonant coupling between members of the pair connected by magnetic flux tubes to single dynamical unit carrying the dark photon triplets at the frequencies characterized by the 3-chord. The model for musical harmony [L11] leading also to a realization of genetic code suggests the existence of a large number of harmonies.

   It is not however obvious whether these harmonies can be realized bio-chemically since the 3-chords must be resonance 3-chords for bio-molecules. For DNA-AA and mRNA-AA correspondence the constraints are the slightest ones since they couple to $f_{XYZ} = f_1 + f_2 + f_3$: AAs could have emerged in rather early stages of the prebiotic evolution. One cannot even exclude the possibility f_{XYZ} are same for different harmonies. Slight chemical modifications of DNA and mRNA and AA analogous to wobbling for tRNA might allow to realize the slightly different collections of 3-chords defining the harmonies.

4. The model leads to an explanation for the homonymy of mRNA $\rightarrow$ tRNA pairing as being induced by the mRNA-tRNA homonymy realized already at dark level. The rather rare homonymies in DNA-AA pairing can be understood as accidental degeneracies. AA couples resonantly to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of frequencies associated with codon XYZ, and one can have $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$ modulo octave multiple for two codons. DAA coded by DDNA codes for AA and tRNA serves only in the role of transferring DAA-AA pairs and attaching

them to DmRNA-mRNA pairs: the mRNA-AA pairing would be determined completely by dark molecules. It is actually advantageous to have tRNA homonymy since it can happen that the concentration of particular certain kind of tRNA is low.

5. What distinguishes between DNA and RNA and between codons and anti-codons is not obvious in the harmonic model. The most plausible identification for the map mapping codons to anti-codons is reflection symmetry of the icosahedron permuting opposite faces. An internal reflection changing the orientation of the scale could map DNA to RNA: this makes sense if the chords can be regarded as arpeggios.

6. The vision of biological evolution as chemical evolution in which dark variants of genetic code gradually find biological representations suggests a concrete model for RNA era. At that era AAs would have catalyzed mRNA replication possibly as non-faithful process. This era might have preceded tRNA era with mRNA replaced with tRNA analog corresponding to the fusion of two 20-chord representations. The era before this could have been era with single 20-chord representation and corresponding tRNAs and amino-acids.

7.2 Some background

In the following I will discuss briefly the basic facts about genetic code at Wikipedia level with emphasis on the poorly understood aspects of the code.

7.2.1 Variations of the genetic code

There exists also as many as 31 genetic codes (see `http://tinyurl.com/ydeeyhjl`) and an interesting question is whether this relates to the context dependence. Mitochondrial codes differs from the nuclear code and there are several of them. The codes for viruses, prokaryotes, mitochondria and chloroplasts deviate from the standard code. As a rule, the non-standard codes break U-C or A-G symmetries for the third code letter. Some examples are in order (see `http://tinyurl.com/puw82x8`).

1. UUU can code Leu instead of Phe and CUG can code Ser rather than Leu. In bacteria the GUG and UUG coding for Val and Leu normally can serve as Start codons.

2. UGA can code to Trp rather than Stop: in this case the broken symmetry is restored since also UGG codes for Trp.

3. There is variation even in human mitochondrial code (see `http://tinyurl.com/puw82x8`). In 2016, researchers studying the translation of malate dehydrogenase found that in about 4 per cent of the mRNAs encoding this enzyme the UAG Stop codon is naturally used to encode the AAs Trp and Arg. This phenomenon is known as Stop codon readthrough (see `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5133446/`).

4. There is also a variant of genetic code in which there are 21st and 22nd AAs Sec and Pyl coded by Stop codons. UGA can code for Sec and Stop in the same organism. UAG can code for Pyl instead of Stop and introduces additional breaking of A-G symmetry for the third letter (UAA to Stop and UAG to Pyl).

7.2.2 Wobble base pairing

Wobble base pairing (see `http://tinyurl.com/y73se8vs`) emerges from the observation that the number of tRNAs pairing with mRNAs is smaller than 45 and considerably smaller than that of mRNAs. The needed minimum number of tRNAs is 32. Therefore the RNA-tRNA pairing cannot be 1-1 and some mRNA codons must correspond to several tRNA codons.

Remark: One could ask whether mRNAs code for tRNAs just like DNAs code for AAs. Homonymy for mRNA-tRNA pairing implies that the pairing can be many-to-1 only in given context.

1. According to the standard code, the first two bases of mRNA codon corresponds to two last bases of tRNA anti-codon and obey standard code. Wobble base pairing hypothesis applies to the pairing of the 3rd mRNA base to the 1st base in tRNA anticodon. At the level of chemistry the hypothesis is that the position of the first tRNA anticodon base pairing with the third mRNA base is variable and allows it to pair with several bases appearing as 3rd base in mRNA. This homonymy would be due to "wobbling" of the position of the first tRNA anticodon.

2. In the original model for wobble base pairing tRNA bases contain besides standard A, C, G, U also inosine I as a modification of G obtained by dropping NH_2 from the 6-cycle of G. It has turned out that there are actually variants of C and 5 variants of U (see `http://tinyurl.com/y73se8vs`). The large amount of homonymy for tRNAs forces to ask whether chemistry alone really dictates the genetic code.

3. The first tRNA letter is assumed to be spatially wobbling so that the association of tRNA with RNA is not unique and mRNA-tRNA pairing involves both synonymy and homonymy as the two tables for the pairing of the 1st 5' anticodon base of tRNA and 3rd 3' codon base of mRNA show. In the second column bold letters for mRN bases allow to read the standard pairing with tRNA codons in the first column and non-bold letters allow to deduce the non-standard behavior.

4. The first table (see `http://tinyurl.com/y73se8vs`) represents the original Watson-Crick proposal.

   (a) The pairings of the 3rd letter of mRNA codon to the 1st letter of tRNA anti-codon are following.

   - U $\rightarrow$ G.
   - G $\rightarrow$ U
   - {A, C or U} $\rightarrow$ I.

   The 2nd and 3rd tRNA letters A and C are paired with the 1st and 2nd mRNA letters in the canonical manner. There are only 3 tRNA letters, which implies that the number of tRNAs is smaller than maximal.

   (b) There is single 1-to-many pairing: U$\rightarrow$ {G, I} giving rise to 2-fold homonymy.

5. Revised pairing rules (see `http://tinyurl.com/y73se8vs`) are more complex since the number of tRNA bases is larger (U has 5 variants and C has 2 variants). All mRNA letters have 1-to-many pairing. Even if one counts the variants of U as single U there is 4-fold homonymy for U and homonymies for other codons. For A one has 9-fold homonymy.

These variations do not induce variation in DNA $\rightarrow$ AA pairing if the AA associated with the homonyms of tRNA are identical. This seems to be the case almost always since the variation of the genetic code is surprisingly small. This raises the question whether there is some mechanism eliminating to high degree the expected effects of homonymy in mRNA$\rightarrow$ tRNA pairing.

7.3 Two TGD based realizations of genetic code

During years I have considered several visions about genetic code. Two of them have allowed to build concrete contacts with the empirical reality. They are realized in terms of dark protons sequences [L27] and in terms of 3-chords of bio-harmony [L11].

7.3.1 Dark realization of genetic code

The first TGD view about this is based on the dark realization of the genetic code [L27] (see `http://tinyurl.com/jgfjlbe`). This relies on general vision that dark matter and magnetic flux tubes - magnetic body (MB) - controls the biochemistry and that biochemical realization need not be complete.

1. TGD proposal is that dark proton sequences - dark nuclei - at magnetic flux tubes parallel to DNA strands provide the fundamental realization of the genetic code. Dark proton triplets would represent the analogs of DNA, mRNA, tRNA, and AAs. There would be 64 DDNAs, 64 DmRNAs, 40 DtRNAs and 20 DAAs. Dark codon cannot be separated to a product of letters but is an entangled state of 3 dark protons. There is a linguistic analogy: in primitive languages entire words are holistic basic units having no decomposition to letters.

2. DDNA, dmRNA, dtRNA, and DAA would control their biochemical variants and would be associated flux tubes carrying dark proton sequences. Dark code would dictate what happens at the chemical level. Chemistry would be a shadow of dark dynamics. Transcription and translation would take place at dark level.

   One can argue that this assumption is too strong. It requires that also the Stop codon codes for DAA and this in turn requires at the level of chemistry to an analog of tRNA attaching to the Stop codon. For standard realization of the genetic code there are indeed 2 release factors RF1, RF2 which are proteins not involving RNA (see `http://tinyurl.com/ydcgnlb3`) attaching to Stop codons and stopping the translation. RF1 recognizes UAA and UAG. RF2 recognizes UAA and UGA.

   There is also release factor RF3 binding to GTP (not appearing in RNA) and leading to a dissociation of RF1/RF2 after peptide release. Therefore RF3 does not play a role of tRNA. Note that both release factors recognize UAA so that the map from RNA codon to release factor is 1-to-2.

   The 1-to-many character of mRNA-AA association requires hidden degrees of freedom for DDNA affecting the genetic code by changing DAA $\rightarrow$ ordinary AA pairingat the level of chemistry.

3. If there is **no** homonymy at the dark level, one would have the following picture to start with.

   Remark: One could of course ask whether the dark variants of the 3 codes unique - are there several dialects possible already at this level. The degeneracies of dark codons coding for dark codon at lower levels down the ladder DNA-mRNA-tRNAA-As are unique but how many codes satisfying this condition are possible? In the sequence dark code is however assumed to be universal.

   (a) Dark genetic code decomposes to a sequence of three many-to-one codes without context dependence/homonymy: DDNA $\rightarrow$ DmRNA, which is 1-to-1, DmRNA $\rightarrow$ DtRNA, which is 64-to-40 and DtRNA $\rightarrow$ AA, which is 40$\rightarrow$ 20.

   (b) Chemical representation of dark variants of biomolecules is induced by the dark-chemical pairing, which can be context dependent to some degree. This in turn would induce context dependence of mRNA-tRNA pairing and possibly tRNAA-A pairing and as a consequence also that of mRNAA-A pairing. It is important to notice that the DX-X pairing involves transformation of dark photons to ordinary photons. The proposal is that the ordinary photons are bio-photons with much higher frequencies. The transition reducing the value of $h_{eff}/h = n$ would allow energy preserving transformation of extremely low frequency photons with large n and to bio-photons inducing molecular transitions.

   Remark: mRNA-AA correspondence is basically induced by DAA $\rightarrow$ AA correspondence.

(c) One could say that there are several dialects each free of homonymies in their own context. Even the genes or the two strands of DNA might speak different dialects. What could be the quantum physics behind these dialects? At which level one can find the contexts causing the dialects? In TGD framework magnetic body (MB) carrying dark matter suggest itself.

One can ask whether DDNA and DRNA, and maybe DtRNA and DAA could have a context defined by internal degrees of freedom, which varies in the situation when same DNA/RNA codes for 2 different AAs or AA and stopping sign. Magnetic body (MB) would naturally give rise to these new integral degrees of freedom.

7.3.2 The notion of magnetic body carrying dark matter and resonance as a mechanism of pairing

Pairing is the basic mechanism of molecular biology appearing in DNA replication, translation, and transcription. Pairing could be based on resonance coupling by dark photons propagating along magnetic flux tubes connecting the pairing systems.

The pairing between DDNA and DmRNA and DDNA and ordinary DNA would rely on resonance. More generally both dark and ordinary variants of the basic biomolecules would be characterized by collections of frequencies and if the frequencies are same the objects pair with each other. The 3-letter structure of the genetic codon suggests that resonance coupling occurs simultaneously for 3 frequencies defining the 3-chord. The pairing objects able to pair must be characterized by same the 3-chord.

1. DDNA, mRNA, tRNA, and AAs would pair horizontally. These horizontal pairings together with vertical pairings of dark molecules to their ordinary counterparts (DDNA →DNA, DmRNA → mRNA- DtRNA → tRNA, DAA → AA would induce the horizontal pairings of DNA, mRNA, tRNA, and AAs.

2. All these pairings would rely on resonant coupling and the structure of codons suggests that 3-chords of frequencies are involved.

3. The first idea was that there is no context dependence at the level of horizontal pairings. It turned out that there are naturally 3 different DmRNA-DtRNA pairings for a given harmony for mRNA. This induces context dependence at the level of chemistry and would due to variation of the collection of 3-chords characterizing DtRNA.

7.3.3 The geometric model for music harmony and genetic code

For some years ago I developed a model of music harmony [L11] (see `http://tinyurl.com/yad4tqwl`), which should define map of dark codons to 3-chords represented as dark photon triplets and defining allowed 3-chords of music harmony (music of light and perhaps also of sound). The Appendix provides the tables describing the details of the harmonies.

1. The model of music harmony is separate from the model of genetic code based on dark proton triplets and one of the challenges has been to demonstrate that they are equivalent. The model relies on the geometries of icosahedron and tetrahedron and representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 AAs.

   Single step of Hamiltonian cycle connecting vertices of a face of icosahedron (triangle) is assume to correspond to a scaling of the frequency by factor 3/2. This leads to a problem since 12 scalings of this kind does not quite given 7 octaves which reduced octave equivalence to the basic octave would give 12-note scale. The solution is to add single notice slightly differing from 7 octaves and represented as vertex P of a tetrahedron glued to icosahedron along face. The Hamilton cycles are deformed so that they begin and end from this vertex. This also gives the missing 4 DNA codons realized as 3-chords and also defines unique ground note for the scales.

2. It turns out that has three basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6, Z_4 or Z_2. For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle.

   Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA.

   4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint. The model predicts a highly unique and realistic model for numbers of DNA codons coding for a given AA. The model in its original form predicts two codes and also explains the fact that there are two additional AAs Pyl and Sec that appear as end-products.

3. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA. Since music expresses emotions and produces them, the proposal is that these harmonies correspond to different molecular emotional states. The fundamental realization could be in terms of dark photon triplets replacing phonon triplets for ordinary music. Geometrically the two codes can be described as attachment of tetrahedron to icosahedron along face or as union of the two. Icosahedron corresponds to 60 DNAs and tetrahedron to 4 DNAs.

   During writing of this article I learned that the number of harmonies could be different, probably larger. There is however the question of the chemical realizability of the harmony: it is not at all clear whether there exist biomolecules to which the 3-chords of several harmonies could couple resonantly.

4. As I developed the model of bio-harmony [L11] (see `http://tinyurl.com/yad4tqwl`) it did not occur to me that also the tRNA part of the dark code should have counterpart in the icosahedral model. AAs correspond to single 20-codon code, DNA and RNA to union of 3 20-codon codes with symmetries Z_6, Z_4 or Z_2: here Z_2 would correspond to $Z_{2,rot}$ or $Z_{2,refl}$ and this would give to two two different codes.

   Could tRNA correspond to a union of 2 20-codon codes? Combining only 2 20-codon codes with 40 codons and tetrahedral code with 4 codons would give maximally 44-letter code and the upper bound for tRNAs is according to Wikipedia 45! Dark proton model predicts 40 DtRNAs suggesting that only the 40 isosahedral codons contribute to DtRNA code. The additional tRNAs could result from homonymy. The code sequences could be seen as a hierarchical sequence $3 \to 2 \to 1$ in this framework.

   An important implication is that there are many realizations of DtRNA and tRNA harmony: (Z_6, Z_4), (Z_6, Z_2), (Z_4, Z_2) and Z_2 could be either $Z_{2,rot}$ or $Z_{2,refl}$. This could explain the homonymy of mRNA-tRNA pairing via difference in the chords in turn affecting biochemical counterparts. Note however that the chords for tRNA must be a subset of chords for mRNA so that RNA harmony determines tRNA harmony apart from the three choices (Z_6, Z_4), (Z_6, Z_2) or (Z_4, Z_2) giving rise to 3 different contexts. If DAAs code by 3-chords the AAs then this choice does not affect AAs.

What conditions pairings pose on the frequency triplets?

The realization of DDNA-DtRNA and DDNA-DAA pairings in terms of frequencies must involve a loss of information since the correspondence is many-to-one.

1. For DNA-mRNA pairing information is not lost and the pairing must be of form $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$. Note that the frequencies cannot be associated with the letters. It is however possible to consider the assignment of (f_1, f_2) to the first letter pair XY as a whole and f_3 to the third letter Z.

2. For DDNA-DAA and DmRNA-DAA pairing the natural hypothesis is $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$. AA couples to the sum of the frequencies of the triplet. The simplest possibility is that the $f_1 + f_2 + f_3$ is same for all codons codin for given AA. One might say that AA sequence defines melody and mRNA sequence the accompaniment.If the sums for codons coding given AA are different they must couple resonantly to it. If there are several harmonies the sum must same for all realizable 3-harmonies or all chords of 3-chord harmonies coding for same AA couple to it resonantly. Since one has linear 1-D structures one might ask whether frequency differences coming as multiples of lattice frequencies are allowed. Second natural possibility is octave equivalence. mRNA-AA pairing would take place directly rather than with the mediation of of tRNA.

3. In the case of DmRNA-DtRNA pairing one one does not lose so much information since the number of dark DNAs is 40 (as also the 3-chords if tetrahedron does not contribute). One must remember that tRNAs are pairs of RNA like codons - call them RNA_t, and AAs. Therefore there pairing involves also the pairing mRNA-AA give by $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$ and guaranteeing that the code is realized by this pairing alone irrespective of mRNA-RNA_t pairing. At chemical level the first to mRNA codons pair with tRNA anticodons according to the standard rules. Could RNA_t have completely passive role in carrying the AA? This cannot be the case since the last two letters of RNA_t couple in standard manner to the first two letters of mRNA.

   Remark: tRNA is analogous to melody + accompaniment using one of the 3 possible 2-harmonies for a given 3-harmony.

   Suppose that mRNA-RNA_t pairing corresponds to 3 possible choices of 2-harmonies as sub-harmonies of 3-harmony. This would suggest these different sub-harmonies define maps $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$ such that RNA_t pairs only with two sub-harmonies. For each choice RNA_t would correspond effectively to 40 sub-codons of the entire code (forgetting the tetrahedral part giving 4 additional codons). The three different realizations of the projection would give rise to the homonymy. Also the AA-trNA coupling would come out correctly.

DAAs would be different in the sense that they couple only to the sum of the frequencies. This is in accordance with bio-harmony in which AAs correspond to orbits of 3-chords for DNA under isometries rather than single 20-chord harmony. The coupling to the sum of frequencies is in accordance with the quantal interpretation as 3-dark-photon state whose energy is $E = h_{eff}(f_1 + f_2 + f_3)$ and couples to AA chemically via the transition to ordinary photons with the same energy.

This leaves some questions.

1. Could one consider the possibility that the chords of one of the 20-chord harmonies corresponds to AAs? There would be 3 basic types of AAs. This does not look plausible and the association of AAs with the orbits of 20-note chords is more natural and fits nicely with $f = f_{XYZ}$ picture.

2. It would be nice to assign notes to the individual letters of codons. This is not possible since codons with 2 or 3 identical letters would reduce to 2-chords or 1-chords. It is also impossible to assign frequencies with letters at dark level since letter decomposition does not exist. Thus the 3-chord has resonant interaction with the entire codon.

3. The symmetries of the genetic code however suggest that it might make sense to treat the first two letters XY of the codon as a single unit and the third letter as separate single unit. Could one assign to XY a 2-chord not reducible to frequencies for the letters X and Y, and to letter Z its own frequency. The frequencies of A, G, T, C as third letter must be different. Four 32 codons of standard code the AA would not be sensitive to the frequency of Z: this is possible if these frequencies are resonance frequencies of the same AA. For the remaining 32 codons the AA would not distinguish between frequencies of T and C *resp.* A and G so that the two frequencies would be both resonance frequencies of the corresponding AA.

Probabilistic estimates for single 20-chord harmony

One can make first some naïve probabilistic estimates about single 20-chord harmony.

1. Given 20-chord harmony makes $20/220 = 1/11 \simeq 9$ per cent about al possible 3-chords. Three 20 chord harmonies would make $3 \times 9 = 27$ per cent about all possible 3-chords if there are no common chords so that the optimistic expectation might make sense. Of course, one cannot exclude the possibility that there are also triplets of 20-codon codes which gives smaller number of codons.

2. The total number of chords with different notes is $12 \times 11 \times /3! = 220$. Bio-harmony has 64 chords corresponding to faces of icosahedron: this is about 64/220 making 29 per cent of all possible 3-chords with different notes. Given bio-harmony thus throws out roughly 2/3 of all possible codons. This should be easy to test. For instance, does given gene correspond to a fixed bioharmony? Or does even entire genome do so. If bio-harmony is realized for non-nuclear genomes, it must satisfy rather strong constraints.

3. Given 20-chord harmony corresponds to 12 edges. Each edge is shared by two adjacent triangles. If all 20 triangles would contain just single face, there would be 24 triangles altogether. Therefore there must be triangles containing two subsequent edges of the cycle. Each triangle of this kind reduces the number of 24 neighbours by 2 units. Hence it seems that one must have at least 2 triangles with 2 edges at the cycle (two quints in the 3-chord).

   If there are more than 2 triangles of this kind, there must be triangles having no edges along the path. Each vertex of icosahedron is shared by 5 triangles and there are 5 edges starting from it.

4. The notion of Hamilton cycle generalizes to any graph and magnetic flux tube networks define such graphs as tensor networks. Why only icosahedron? Could one consider the possibility that any tensor network is characterized by harmonies characterize by Hamiltonian cycles and that one could assign some kind of codes with the combinations of these cycles? In the general case symmetries would be absent so that the notion of code in the proposed sense would fail: one could not identified codons as points at orbits of symmetry group. Rather, one can imagine that the notion of code could be defined quite generally in terms of orbits as AAs and points at them as DNAs coding them. For regular polygons in any dimension the symmetries are present and one could define the notion of code and also fuse the codes.

   For arbitrary tensor network the faces need not be symmetry related and one can also have faces that can be interpreted as higher-dimensional polytopes.

   One can also ask whether the icosahedron is realized physically. Icosahedral geometry is indeed very common in biology. Could the fusion of icosahedral and tetrahedral geometries have some concrete realization at molecular level?

Is the maximal number of codons for the fusion of 3 20-codon codes possible?

It has not earlier occurred to me to wonder whether the chords associated with the 3-different icosahedral harmonies giving 20 codons each correspond to 20+20+20=60 different chords as assumed. Could there be common 3-chords? This question could be answered by studying the Hamiltonian cycles at icosahedron.

Remark: Perhaps more important constraint than absence of common chords is the chemical realizability of the codes. If same mRNAs and DNAs realized different bio-harmonies then they must be able to respond resonantly to several 3-chords.

One can make naïve probability estimates for a pair of codes to allow the maximal number of 60 codons. It seems natural to assume that the isometries of icosahedron (or their subgroup) can be applied separately and only the isometries acting on both in similar manner are symmetries. The situation would be the same as in the case of many-particle system: only the translations acting on all particles simultaneously remain symmetries and relative translations cease to be symmetries.

With this assumption the icosahedral group gives a large number of code pairs. For the fusion of 3 20-codon codes giving DNA/RNA the number is even higher. By choosing suitably the relative isometries it might be possible to obtain the maximal number of 60 different codons

for the icosahedral genetic code. On the other hand, by a suitably choice of relative isometries one might have undesired common 3-chords. In any case, the earlier estimate 256 for the number of bio-harmonies [L11] suggested to correlate with "emotional" states of the basic biomolecules is expected to change.

Before going to estimates one must consider some delicacies related to the notion of 12-note scale as Hamiltonian cycle.

1. One can regard the cycles as purely geometric objects without orientation or assign to them orientation. For two different orientations the scales would run in opposite directions as scalings by 3/2 along single edge of the cycle. If two codes have common edge, the scaling must be same along it. If the orientation of the second cycle is changed, the common edge ceases to be common.

2. The basic note of the 12-note scale at cycle can be chosen arbitrarily: this corresponds to the choice of the key in music (one could of course argue that the key does not make sense in 12-note scale if one has tempered scale with notes comes as powers of $2^{1/2}$ scaling of ground note rather than Pythagorean scale with rational ratios of notes).

   The fusion of tetrahedron to icosahedron selects one particular triangular face and brings in one additional vertex outside the icosahedron, call it P. It would be natural to assign the ground note as P. The isometries not affecting P would correspond to those of icosahedron leaving the common face invariant and isometries of tetrahedron leaving P un-affected and continuable to icosahedral isometries. One would have subgroup of icosahedral group as allowed isometries acting on the cycles to be fused.

3. If one assigns note sequences to the cycle by quint rule, cycles C_1 and C_2 can have common triangle in geometric sense but if the distances of the vertices A, B, C of the triangles from P measured as the number of edges of cycle portion connecting them are not same along C_1 and C_2, the triangles correspond to different chords and are thus orthogonal in the proposed description as many-fermion states.

4. To sum up, the states associated with triangles would be characterize by the position of triangle (20 values), by the notes of the triangle characterized by the distances from P, and the number 0, 1, 2 of the edges belonging to the cycle and should make easier to find ortogonal basis.

Again one can make probabilistic estimates: cycles are treated as purely geometric entities without orientation and without assignment of notes to the triangles.

1. Given cycles C_1 and C_2 what is the probability that they have at least one common edge as purely geometric entities without the sequence of notes? There are 30 edges so that given edge is shared with probability 1/30. If the edges of cycles were chosen randomly (certainly not true), the probability of having a common edge for two cycles would be $P(1) = 12/30$. The assumption of note sequence reduces this probability dramatically.

2. By the above estimate each cycle contains at least two triangles with 2 edges at the cycle with minimal angle between them. One can call these these edge pairs V-corners. Assume that for cycle C_1 one has V-corner ABC at vertex A, call it $V_{1,A}$. What is the probability that one one of the V-corners of C_2 is located at A coincides with ABC. The probability of V-corner of C_2 to locate at A is 1/12 and the probability that the edge of C_2 from B is BC is is 1/4 so that the probability of having common V-corner is 1/48. If C_2 contains n V-edges the probability is naïvely $n/48$.

   This estimate takes into account only geometry. The situation changes if one assumes that the cycles are oriented. In this case one can have common V-corner if the local orientations of C_1 and C_2 are opposite at the V-corner. If one assumes that the external vertex P of the tetrahedron defines the ground note then the number of edges connecting P to A defining distance $d(P, A)$ must be same for C_1 and C_2.

3. Given C_1 and C_2 (and vertices A with same distance $d(P, A)$) it might be possible to perform suitable isometry for C_2 that there is common V-corner. Therefore not all possible

combinations of three code types allowing relative isometries need not maximal number of 3-chords.

Remark: An interesting question is whether these can be allowed meaning that some codons are missing in the chemical realization of the dark codons in terms of ordinary DNA codons. Also the 1-1 pairing between dark DNA and and dark RNA would not be 1-1 if mediated by 3-chord resonance and one would have homonymy. This suggests that only codes without common chords can be allowed.

4. What about chords having 1 edge at cycle for two cycles C_1 and C_2? Let the edge be AB. As found, the naïve probability for this is $P(1) = 12/30$. Both cycles must go through the third vertex C of the triangular face. The subsequent notes along cycle differ by a quint that is scaling of the frequency by factor 3/2. Notes are same if the numbers of the needed quints are same for C_1 and C_2 For C_1 the number $n_B > 1$ of quints is known. In the approximation that possible portions of C_1 represent n-step non-self-intersecting random walks from B to C, one must estimate the number of all non-self-intersecting n-step-paths from B to C and find what is the number of the paths leading to C. One can go from A to C with n_A steps and similar estimate applies.

5. The third possibility is that the one has 3 common vertices A, B, C forming a triangular face such that neither cycle contains any of its edges.

The cautious conclusion is that it is plausible that one can find 3 cycles having no common chords if one allows relative rotations of the cycles and that this condition is necessary for realizing the absence of homonymies at dark level. The automatic orthogonality of the Hamiltonian cycles cannot be excluded but would allow also codes with codons containing more than 3 letters so that one could have kind of super-DNA. Whether they can be realized chemically depends on whether there are biomolecules resonating with the the n frequency triplets involved. Octave equivalence for frequencies might give hopes about chemical realization of several harmonies. Therefore the evolution might be seen as gradual emergence of molecules able to pair with DDNA and one can even imagine artificial evolution by tailoring the frequencies involved (maybe cyclotron frequencies).

Could harmonies form a Hilbert space

The condition that there are no common 3-chords brings in mind orthogonality and suggests that harmonies as Hamiltonian cycles could be defined as quantum states in suitable Hilbert space.

1. One could define inner product for Hamiltonian cycles as the number of common chords suitably normalized so that the norm of cycle of cycle equals to one. The number of common chords in the norm squared is 20 in the icosahedral case and 24 for the fusion of icosahedral and tetrahedral codes. Could Hilbert space picture for cycles make sense? The fusion of 2 (tRNA) or 3 (DNA) codes does not however naturally correspond to quantum superposition but rather tensor product.

2. Could one think that each cycle correspond to a 20-fermion product state with 3-chord characterizing the state of given triangle created by fermionic oscillator operator so that product P of 20 fermionic oscillators assignable to the triangles would create the harmony? The fusion of cycles C_1 and C_2 would be obtained by product P_1P_2. By fermionic statistics the resut would be zero if there are common cycles.

These considerations are purely formal and have no implications for what follows.

7.3.4 How the symmetries of the model of harmony could relate to those of the genetic code?

Genetic code has surprisingly strong symmetries. I have discussed a possible interpretation of these symmetries using analogies with particle physics and considered also a mechanism explaining their emergence earlier [K4, **?**]. The proposal was that 3-letter code emerged as a fusion of 2-letter code with 16 codons and 1-letter coded with 4 codons. In the recent framework, a more natural option

is that the third codon of 3-letter code was originally passive and became active via symmetry breaking distinguishing first between UC and AG pairs and later between U and C *resp.* A and G. Note that for the standard code the breaking is minimal and caused by odd number of Start and Stop codons.

1. For vertebrate code one half of codons has very high symmetry in the sense that the two first letters dictate the AA for 32 cases. Exception is UUU, which codes for Phe or Leu for some modifications of the standard code. UUU $\rightarrow$ Leu means breaking of maximal symmetry.

2. There is also a second symmetry, which I have referred to as isospin symmetry. It is only slightly broken. For general codons XYU and XYC code for same AA as also XYA and ad XYG. For the standard code this symmetry is broken only in columns containing initiation codon or stop. The Start codon AUG codes also for met. UGA and UGG code for Stop and Trp. For the remaining codons one has slightly broken "isospin symmetry". The breaking of isospin symmetry is minimal for vertebrate code. The modifications of the code tend to break the isospin symmetry and even the maximal symmetry of 32 codons. This must be important.

If the model of genetic code based on music harmony [L11] is correct, the symmetries for the model of music harmony must relate to those of genetic code.

1. How the symmetries of the genetic code relate to the symmetries of icosahedron (60-element group) and tetrahedron (permutation group S_4 with 24 elements) in the model of bio-harmony? Icosahedral symmetry group has 60 elements and has sub-groups $Z_2, Z_4, Z_5, Z_6 = Z_2Z_3$. Note that there are two Z_2:s having rotation by π and reflection as generators.

   The gluing of tetrahedron to icosahedral along single face reduces its group of symmetries to S_3 leaving the point P not belonging to icosahedron invariant. S_3 has as subgroups reflection group $Z_{2,refl}$ and Z_4 consisting of rotations.

2. What is the counterpart for maximal symmetry in icosahedral and tetrahedral groups? Do the 3-chords for codon XYZ decompose to two-chord characterizing XY and a note characteriing Z= A,U,C,G, which can depend on XY. The symmetry relating UC pair and AC pair could correspond to $Z_{2,refl}$ reflection symmetry, which is shared by icosahedral and tetrahedral groups. For 32 icosahedral codons the action of $Z_{2,refl} \times Z_{2,rot}$ would be trivial so that AA would not depend on the third letter at all. For most of the remaining codons the action of the symmetry group on icosahedral codons would reduce to $Z_{2,rot}$ permuting the third letters U and C *resp.* A and G. At the level of frequencies the sums of frequencies for codons coding for the same AA sould be same modulo octave equivalence.

   The addition of tetrahedron brings in 4 tetrahedral codons with one of them shared with icosahedron. Icosahedral $Z_{2,rot}$ does not make sense for these codons. Intriguingly, there are 4 codons in vertebrate code which break isospin symmetry AUA and AUG coding for I and Met/start and UGA and UGG coding for Stop and Trp. If these codons correspond to the tetrahedral codons which cannot have $Z_{2,rot}$ as isospin symmetry, the breaking of $Z_{2,rot}$ would follow from the breaking of symmetry induced by the attachment of tetrahedron to icosahedron.

7.3.5 What distinguishes between codons and anti-codons and between DNA and RNA?

The icosahedral model should provide answer to several questions not considered yet.

1. The model for the genetic code in terms of dark proton sequences both DNA and RNA are predicted. This should be the case also in the icosahedral model. The 3-chords for DNA and RNA should be the same but there should be some inherent distinction between the two realizations.

2. Besides the active DNA strand there is also the inactive DNA strand (no transcription to mRNA) consisting of anti-codons. What does anti-strand correspond in the representation

consisting of 3-chords? The chords assignable to the anti-strand should exist but there should be some difference between chords and anti-chords. Why this strand is inactive? mRNA is produced only via the pairing of RNA codons with active DNA strand. Could RNA_t as part of tRNA and counterpart of anti-RNA be unable to form stable strands in the recent biological environment and could lonely RNA_t codons fail to exist stably so that the transcription of DNA anti-strand to RNA_t strands would be impossible.

3. What does anti-DNA anti-RNA and anti-tRNA mean at the level of dark proton sequences?

I have approached these problems from particle physics point of view by using analogies and they might be helpful in the attempts to answer these questions [K34, K35]. There are two mirror symmetries in the icosahedral harmony: 3-D reflection with respect to origin and change of the direction of the 12-note scale. Could these reflection symmetries help to understand the situation?

1. The symmetry mapping letters to antiletters (T $\leftrightarrow$ A, G $\leftrightarrow$ C) is mirror symmetry like charge-parity symmetry CP of particle physics equivalent with time reversal T by CPT theorem. CP is mysteriously broken: we have matter but where is the antimatter?

   The biological analogy with matter-antimatter asymmetry is that strand is active but anti-strand is passive - no transcription to mRNA. This would be the case if anti-RNA does snot exist as stable sequences. This would also explain why RNA does not replicate and does not form stable double helices.

2. Codons and conjugate letters for DNA are related by the CP like transformation (T $\leftrightarrow$ A, G $\leftrightarrow$ C). There should exist an icosahedral symmetry realizing this symmetry. Icosahedron allows also 3-D reflection through the origin as a symmetry (see `http://tinyurl.com/y8capjz7`). It permutes the opposite faces of icosahedron and extends the icosahedral rotation group with 60 elements to a group with 120 elements. The extended symmetry should preserve the set of 3-chords: they should be identical for DNA codon and anticodon.

   Harmony and anti-harmony for DNA would differ in that the attached tetrahedron would be at opposite face for the anti-codon representation since the reflection maps the tetrahedron to the opposite face. Could one see this as an analog of matter antimatter asymmetry? For double DNA strand anti-codons would correspond to icosahedron with tetrahedron attached to the opposite face. This symmetry should map the codons to their anticodons and there should be no fixed codon - this is indeed the case since there are no fixed faces.

   Icosahedral reflection should however leave the chords invariant apart from transponation by some power of 3/2 in order to leave the harmony invariant: codons and anticodons would be in different key in order to resonate. Icosahedral reflection would be an additional symmetry of the Hamiltonian cycles. The tetrahedron attached to the opposite face in reflection would be shifted back in transponation.

mRNA should have icosahedral realization with same 3-chords as DNA. What distinguishes mRNA from DNA at icosahedral level?

Could only mRNA exists as stable sequences and anti-mRNA fails to exist in this manner? This would be analog of CP breaking and the codons RNA_t in tRNA would correspond to anti-RNA_t existing only as single codon attached to AA. Could also the 4 tetrahedral anticodons for RNA_t (anti-tRNA) fail to exist (this would give 40 tRNA codons as also dark proton model predicts). Otherwise one would have 44 RNA_t codons.

DNA and mRNA differ only in single aspect: the letter T is replaced with letter U. How the replacement of U $\rightarrow$ T (and the replacement of riboses with de-oxy-riboses) is visible in the icosahedral harmony if the set of chords remains the same - perhaps modulo transponation by some number of quints?

Could the order of notes along the Hamiltonian cycle distinguish between DNA and RNA? The chords would remain the same but the order of notes in the chord would change.

1. If the reversed scale proceeded downwards in quarts (quint backwards, say C-G to C-G), the 3-chords would be same for the scales and the two scales are identical. Could one imagine that 3-chords are "played" as arpeggios! The order of arpeggio (upwards downwards in scale) would be opposite for up-chord and down-chord. RNA_t would define down-chords for mRNA up-chords but they would not form stable sequences and 4 anti-chords might be even missing.

2. If it proceeds in quints, the chords for the harmonies would not be same in general (for instance C-G upwards quint is replaced with C-F downwards quint). The scalings $(3/2)^k$ are replaced by scalings $(3/2)^{12-k}$ and the cycle becomes mirror image retaining its shape so that it is still a cycle and since the shape is preserved the symmetries are preserved too. Chords are in reflected positions and related by the map $(k_1, k_2, k_3) \to (12 - k_1, 12 - k_2, 12 - k_3)$. The chords are obviously different so that DNA and mRNA cannot differ in this manner.

   The scale and its quint-reversed counterpart differ much like major and quint scales as one easily finds (consider only the upwards scale Cmajor scale $CDEFG...$ in C major and the downwards Cminor scale $CB\flat A\flat G...$). They could therefore correspond to two different moods rather than mRNA-RNA.

3. TGD and TGD inspired theory of consciousness bringing observer part of physical system relies on zero energy ontology (ZEO). In ZEO the scale and its quint reversal could correspond to two different arrows of time for zero energy states. As self dies in state function reduction to the opposite boundary of causal diamond (CD), it is predicted to reincarnate with reversed arrow of time [L53]. Death is a sad event: could it be that the death of subself representing mental image is experienced by self as sad event and that in bio-harmony time reversal would change joy to sadness?

This relates in an interesting manner to the earlier speculations in TGD inspired view about pre-biotic life.

1. The proposal made in [K34, K35] is that during RNA era preceding DNA era RNA replicated and AAs associated with pre-tRNA served as catalyst and later stole the stage so that RNA replication became translation. The greatest betrayal in the history of life! At this moment also DNA had to emerge. Otherwise RNA and life would have disappeared.

   Amusingly, also in cosmology CP symmetry was broken, when antimatter and matter annihilated and what remained was matter (there was slight imbalance originally).

2. Could one think that before the breaking of the analog of CP symmetry the tetrahedral part of the code was not present and the number of mRNA codons was 60. mRNA and anti-mRNA realized as mRNA_t had common chords related by icosahedral reflection symmetry. Also the 1st letter of mRNA_t was just like the other letters.

   In the transition A and C as 1st letters disappeared and were replaced with G,U and I (in Watson-Crick scenario). The 4 tetrahedral codons containing Start and Stop codons emerged in the transition.

   In the symmetry breaking DNA with opposite direction of the scale (the reversed scale proceeded downwards as quarts rather than quints) and arpeggios emerged. Perhaps this required the replacement of U with T and perhaps also of riboses with de-oxy-riboses.

3. Did the 4 additional tetrahedral codons responsible for the breaking of the analog of isospin symmetry (A $\leftrightarrow$ G and T $\leftrightarrow$ C) associated with the stop and Start codons emerge in this event so that 60-codon realization of the code was replaced with 64 codon realization. If Start and Stop emerged in this event the entire mRNA strand replicated before it.

4. Was the letter mRNA letter U replaced with DNA letter T in this transition. Did this make possible the existence DNA as double strands stable in the presence of nuclear or cell membrane but not stable as single strand. Did the 4 additional tetrahedral codons responsible for the breaking of the analog of isospin symmetry (A $\leftrightarrow$ G and T $\leftrightarrow$ C) associated with the stop and Start codons emerge in this transition. Before the transition the entire mRNA strand would have been able to replicate. mRNA-AA pairing was present and AA would have catalysed the replication.

5. Was the homonymy present in mRNA replication before the transition. The updated scenerio for mRNA-tRNA correspondence allows the replication albeit not in 1-1 manner (see `http://tinyurl.com/y73se8vs`). Was the letter I present at that period: was it part of both mRNA and rNA_t or of only RNA_t giving therefore rise to a leakage?

If RNA era in the proposed sense was realized, what happened before it?

1. One imagine that before RNA era the RNA_t - not necessary identical with its recent form - as a realization of 2-harmony (or perhaps of all 3 different types of 2-harmonies) with 40 codons was realized and was able to replicate with AAs serving as catalysts attached to RNA_t.

   Only the complementary RNA_t was able to appear as sequences: tetrahedral codons were absent. In the transition from 2-harmony to 3-harmony both DNA and full RNA emerged. Replication of RNA_t transformed to translation of AAs. This vision would be more in spirit with the idea about the gradual emergence of biological representations of the dark variants of biomolecules.

2. One could go even further and ask whether this period was preceded by a period during which pre-tRNA identifiable as single 20-codon representation choosable in 3 ways. Pre-tRNA $\leftrightarrow$ AA correspondence would have been 1-1. AAs would have decomposed to three types corresponding to these 3 choices. For instance for the code with Z_6 symmetry only 4 AAs would have been present. For the details of harmonies see the Appendix of [L11] (see `http://tinyurl.com/yad4tqwl`).

7.4 Context dependence from TGD point of view

The original idea was that context dependence and homonymy are absent at the level of dark variants of various codons and AAs and would result from the pairing with chemical counterparts of dark codons. More precisely: the horizontal dark DX-DY pairings would be context independent and would not depend on emotional state whereas the vertical DX-X pairings are induced by DX-DY pairings and induce X-Y pairings. This is obviously something new from the point of biology as chemistry paradigm.

It however turned out that the context dependence appears very naturally at the dark level. DtRNA bio-harmony allows naturally 3 different representations as 2-harmonies realized as sub-harmonies of 3-harmony associated with DNA and mRNA. One would have 3 basic context already at this level.

One can imagine at least 3-sources of context dependence and expression of emotions by gene expression.

1. Several bio-harmonies are possible and DX and X would couple by different resonant 3-chords for each harmony. It is of course possible that very few of these bioharmonies - perhaps only one - are realized at the level of DNA and mRNA. This would explain the uniqueness of DNA and mRNA codons in biological sense.

   If several bioharmonies are realized for DNA then both mRNA, RNA_t and AA must have resonance couplings to all these bioharmonies. For AA this is satisfied if $f_{XYZ} = f_1 + f_2 + f_3$ is same (perhaps modulo octave equivalence) for all harmonies involved or if AA has all all the frequencies f_{XYZ} as resonance frequencies. For mRNA $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$ pairing would require even larger spectrum of resonant 3-chords at the level of chemistry. Hence it is quite possible that only single 3-harmony is realized for DDNA, DmRNA, and DAA. If several harmonies are present, the evolution would have gradually invented the biomolecules having the needed spectrum and would still be in progress.

2. The situation with DtRNA is different. The DmRNA-DtRNA pairings would involve 3 different unions of 2 20-chord harmonies. This choice implies context dependence already at dark DNA level and could be the fundamental reason for mRNA-tRNA homonymy. What is however important that the decomposing of tRNA to (RNA_t,AA) pairs guarantees automatically genetic code via $f_{XYZ} = f_1 + f_2 + f_3$ coupling. AA dictates the pairing unlike usually thought.

3. If the frequencies are cyclotron frequencies determined by the magnetic fields at flux tubes, the variation of magnetic field strength due to the variation of flux tube thickness changes the frequency scale. This could be also seen as emotional expression (in analogy with membrane

potential in biology inducing variation of Josephson frequencies and varying the degree of alertness in neurons).

The gradual variation of magnetic fields strengths during evolution could explain the slight differences in the genetic code. Evolution would be clearly in question in the sense that the symmetries of the code are maximal for the nuclear code. It will be found that also this mechanism is needed in order to understand all deviations of the code.

7.4.1 Context dependence as "emotional expression" at molecular level?

Using the attribute "emotional" certainly raises eyebrows and I will drop even the quotation marks in the following. Reader can freely add them.

Basic guide lines

Consider first the basicguidelines.

1. One plausible possibility is that genetic code as DNA-AA pairing is unique in given context - whatever it is physically - but there exist what one might call dialects just like slight modifications of vertebrate genetic code. There is homonymy, which however disappears when context is taken into account: same mRNA can correspond to two AAs or AA and stop. The homonymy is associated with mRNA-tRNA pairing for the third mRNA letter which is many-to-one and 1-to-many. Which the actual choice depends on context as in ordinary language.

2. Wobble base pairing is the model explaining both the many-to-1 and 1-to-many pairings. An interesting finding is that for 32 codons the pairing does not depend on third letter at all. I have proposed long time ago a model in which 2-letter code emerged first and then fused with 1-letter code to give 3-letter code. A more plausible interpretation is as activation of the 3rd letter in 3-letter code. The wobble base pairing and homonymy would have emerged in this fusion of codes.

3. From the tables of Wikipedia at article (see `http://tinyurl.com/y73se8vs`) for standard code one can read when the pairing of the third letter is many-to-one and 1-to-many. If it is 1-to-many and unless the resulting tRNA anticodons correspond to the same AA, the outcome can be several AAs.

   This does not lead to 1-to-many mRNA $\rightarrow$ AA if the RNAs associated with tRNAs in mRNA $\rightarrow$ tRNA pairing couple with the same AA. The pairing between mRNA and AAs is 1-to-many rather rarely and could be accidental. It seems that there is a principle taking care that the deviations from the standard code get minimized.

4. The homonymy for mRNA-AA pairings is very rare. This suggests that it is accidental and disappeared during the evolution.

The origin of mRNA-tRNA homonymy and mRNA-AA homonymy

mRNA-tRNA homonymy is clearly exceptional and the proposal that tRNA bio-harmony corresponds to a fusion of 2 20-chord codes together with the fact that there are 3 basic types of these codes could explain this.

1. Suppose that DtRNA harmony corresponds to a sub-harmony of full bio-harmony for DDNA and DRNA as a fusion of two sub-cycles from the union of 3 cycles defining DDNA and DRNA harmony. One can make this choice in 3 ways corresponding to the choices (Z_6, Z_4), (Z_6, Z_2) and Z_4, Z_2. These 3 basic choices would naturally explain the DtRNA-tRNA homonymy without the dependence on emotional state. This would not however explain the deviations from the standard code.

   In the case DtRNA- tRNA pairing it is enough that tRNA couples resonantly only to the 3-chord representatives associated with one 2-harmony appearing as sub-harmony of 3-harmony

that is selected and defines the context. This obviously allows larger number of tRNAs satisfying the resonance conditions. This could relate to the homonymy.

The function of tRNA as an agent transferring DAA-AA pair and attaching it to DmRNA-mRNA pair. Hence tRNA homonymy is desirable - it can happen that the concentration of particular certain kind of tRNA is low so that second kind of tRNA coupling to same mRNA can handle the job.

2. tRNA homonyms for the first anticodon of tRNA would reflect the emotional state of DDNA/mRNA. Why only the third? This might relate to the idea about fusion of 2-letter codes and 1-letter codes. For 2-letter code there would be no "emotional expression" and no context dependence. The emergence or perhaps better, the activation of additional letter at the level of chemical expression, would have brought in the chemical emotional expression.

Consider now mRNA-AA homonymy. This homonymy is rather rare and could be accidental.

1. If AA couples to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of the frequencies characterizing the codon $X_1Y_1Z_1$, it can happen that one has $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$ modulo octave multiple so that besides codon $X_1Y_1Z_1$ also the wrong codon $X_2Y_2Z_2$ codes for the same AA. Of course, this condition might hold true only approximately. This could explain mRNA-AA homonymies as accidental.

2. There is however an objection against the proposal. If the frequencies f_{XYZ} are identical in octave equivalence for all codons coding for AA, the accidental degeneracy would suggests that the entire mRNA multiplet containing $X_2Y_2Z_2$ codes for AA. Typically however only one member of the mRA multiplet codes for wrong AA.

   Should one give up the idea that the members of mRNA multiplet satisfy $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$. If so, AA would have the frequencies f_{XYZ} of mRNA multiplet as distinct resonance frequencies. For instance, could one think that the A-G and T-C breakings at the level of frequencies are present although they are not large enough to make themselves visible in the mRNA-AA correspondence (say for the mRNA 4-plets coding for same AA). This is the case if AA has all these frequencies as resonance frequencies. Also the number of octaves distinguishing between $X_1Y_1Z_1$ and $X_2Y_2Z_2$ matters somewhat. In this case the accidental resonance condition for wrong AA could be satisfied for single member of mRNA multiplet only.

A concrete objection against the model

One can try to understand the possible dependence of code on the emotional state by looking the numbers of 3-harmonies obtained as fusion of Z_6, Z_4 and Z_2 symmetries. One can find explicit tables for the codes in the Appendix of [L11] (see `http://tinyurl.com/yad4tqwl`).

1. A crucially important thing to notice is that Z_6 harmony is unique. This harmony allows 3 6-plets for which 6 DNAs code for single AA. There is also one doublet. Therefore the codons associated 3 6-plets and doublet should always code the same AA unless the magnetic fields at flux tubes determining the cyclotron frequencies van vary. It is easy to verify that this prediction is correct for the nuclear code.

   For non-nuclear codes the situation is different. There are 3 6-plets and they code for Leu, Ser, and Arg. These 6-plets should be stable under the modifications of the standard code. This rule is however broken in at least two cases:

   (a) For CUG coding for Ser instead of Leu. Ser is coded usually by UCG. Both DAA and AA couple to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of the 3-chord frequencies. The simplest explanation already discussed is that DSer and DLeu have accidentally $f_{CUG} = f_{UCG}$ modulo octave multiple. T

   (b) UUG coding for Stop rather than Leu. Stop is coded usually by UGG. Accidental degeneracy would be the explanation also now. Stop identified as release factor FR1 or FR2 playing the role of AA and possibly having also dark AA counterpart would have $f_{UGG} = f_{UUG}$.

2. All deviations from the standard code could be determined solely by the accidental degeneracies for the frequencies f_{XYZ} associated with two codons coding for different AAs or AA and stop. For standard code they would have been eliminated almost completely by evolution: as noticed earlier, even in human mitochondrial code there is this kind of homonymy.

3. For 3-chords with Z_4 as isometry group one has 2 different harmonies, which means non-trivial conditions on DNA and mRNA since the 3-chords of all these harmonies must act as resonance chords. In principle homonymy becomes possible for DDNA $\rightarrow$ DNA and DmRNA $\rightarrow$ mRNA pairings but is not realized. Either coupling to both harmonies is possible or there are no DNAs or mRNAs coupling resonantly to all 3-chords of either harmonies so that only 1 harmony is realized completely. This is important if one requires uniqueness of the genetic code.

4. For 3-chords having Z_{rot} isometries there are 3 harmonies and for Z_{refl} 5 harmonies. This gives increasingly stronger conditions on resonant couplings. The uniqueness of the code suggests that only a subset of possible harmonies is possible. Also the probability of homonymy for DAA-AA pairing increases and might explain 21st and 22nd AAs Pyl and Sec coupling to non-standard representation. Deviations typically occur for the doublets as indeed found.

What is interesting that if one loosens the conditions and allows different couplings and allows several 3-harmonies, it is in principle possible to have larger number of DNA and mRNA codons than usually. Also analogs of AAs can be considered. Frequency coding relates interestingly to extended genetic codes with 4 or 5 codons (see `http://tinyurl.com/ycsfgu7n`) and nucleic acid analogues (see `http://tinyurl.com/y8tj8hsm`).

7.4.2 Is the notion of reading frame consistent with the proposed realizations of the genetic code?

Reading frame (see `http://tinyurl.com/yb6wr3d7`) represents also a context dependence of the code. Reading frame begins with the Start codon and new reading frame can begin at second or third letter of codon. There must be also Stop after $3 \times n$ letters also in the new reading frame.

Shifting of reading frame by 1 or 2 units can take place for viral, prokaryote, and mitochondrial genomes but for some reason not in nuclear genome. Shift makes sense if the first codon is Start codon. For human genome MT-AOT8 and MT-ATP6 are examples of reading frames for mitochondrial genes coding for different proteins. The interesting question is why the shift occurs only at the level of viruses, prokaryotes, and mitochondria and chloroplasts.

Does the notion of reading frame make sense for the two models of genetic code? Consider first the representation of 64 codons as 3-chords. If all 64 codons are are realized as chords, shift does not produce chords not belonging to the harmony. Since the notes of chords cannot correspond to the letters the shift is highly non-trivial since it is not only shifted decomposition of notes to triplets but change also the notes.

Is this possible at the level of DmRNA? At the dark level code words do not have decomposition to letters. Dark proton triplets should re-organize in a new manner into triplets. If the dark protons inside proton triplet are connected by colored bonds to form color singlet, the shift would produce colored 3-proton states unless also the color structure of the states is re-organized so that it is consistent with the shift at the level of codons. Kind of phase transition would take place and induce the change of the reading frame.

Chapter 8

The Realization of Genetic Code in Terms of Dark Nucleon and Dark Photon Triplets

8.1 Introduction

I have worked for more than 10 years with a proposal for a realization of the genetic code in terms of dark proton or nucleon triplets forming closed or open strings. I have considered several variants of the code but the details have remained poorly understood and I have spent a considerable time on wrong tracks. Also the contents of this chapter reflect this wandering.

It however seems that the dust is finally settling (I am writing this in the beginning of 2022). One can see the model as a generalization of the quark model of nucleon and Δ baryons obtained by replacing u and d quarks with dark nucleons. The color group solving the statistic problem for Δ baryon is in the receint case solved by Galois confinement involving Galois group Z_3 assignable to the codons.

8.1.1 Basic notions and ideas

The basic notions behind the models of genetic code and of biomolecules rely on the notion of dark matter as $h_{eff} = nh_0$ phases of ordinary matter predicted by number theoretic vision. $n = h_eff/h_0$ serves as a measure for algebraic complexity and as a kind of universal IQ.

Dark matter at the magnetic body (MB) has large h_{eff} so that it is quantum coherent in long scales and acts as a master controlling ordinary biomatter. The control dynamics at dark level is very simple as compared to the biochemical dynamics, which is a kind of shadow dynamics.

Galois confinement is an essential element of the picture. Physical states are singlets under the action of the Galois group associated with the real polynomial with rational coefficients permuting the roots of the polynomial defined a 4-surface in M^8_c and mapped by $M^8 - H$ duality to $M^4 \times CP_2$. Among other things, this implies that the quark momenta, which are algebraic integers in an extension of rationals defined by the polynomial, sum up to an ordinary integer when the momentum scale corresponds to the largest ramified prime assignable to the extension.

Galois confinement provides a universal mechanism for the formation of bound states. Dark codons as dark nucleon- and dark photon triplets are Galois confined states behaving like a single quantum unit. Dark 3N-nucleons and dark 3N-photons define dark genes.

8.1.2 Two models of the genetic code based on dark particles

Both models are based on Galois confinement providing a universal mechanism for the formation of bound states in TGD Universe.

Bioharmony model

The faces of icosahedron and tetrahedron (and octahedron) are triangles. They would correspond to 3-chords made of dark photons, which in turn represent genetic codons. m

Communications are by dark 3N-photons representing genes and are based cyclotron 3N-resonance. Information coded in the frequency modulation of cyclotron frequencies. The chords serve as address and the message is coded to the frequency modulation. The outcome is sequence of resonances giving rise to pulses. Nerve pulse patterns could emerge by this mechanism.

Biophotons are ordinary photons resulting from the decay of dark N-photons to ordinary photons.

Codons as dark 3-nucleons

This work led to a more detailed model of the realization of the genetic code in terms of dark nucleon triplets forming a linear structure as the dark counterpart of linear biomolecule pairing and parallel with it.

The nucleons are connected by pionic flux tubes carring charge $0, \pm 1$ to form a closed string-like entity carrying angular momentum 0,1, or 2. The dark variants DDNA, DRNA, DtRNA, DAA of DNA, RNA, tRNA, and and amino acids (AA) follow as a prediction. AAs correspond to non-rotating analogs of N (p,n) and Δ, DNA and RNA to rotating analog of Δ, and tRNA to rotating analog of N.

Also the pairings between dark information molecules can be understood to a high degree, and the chemical and functional differences between DNA and RNA could reflect the differences between DDNA and DRNA. The almost exact T-C and A-G symmetries of the third letter of the genetic codon could be seen as reflection of almost exact spin or isospin symmetry. The latter option was considerd in [K39] but this work strongly favors spin symmetry. One can understand the numbers of DDNAs coding for given DAA and also the the breaking of spin symmetry. The number of DtRNAs is the minimal 32 and this predicts 1-to-many character of DtRNA-tRNA pairing which would induce wobble base pairing.

8.1.3 The relationship between the two models of genetic code?

The precise relation between the two models of genetic code remained poorly understood for a long time. The connection came from the realization of bioharmony model as so-called icosa-tetrahedral tessellation of hyperbolic 3-space H^3, which corresponds to either mass shell in momentum space or light-cone proper time constant hyperboloid [L122]. H^3 allows an infinite number of tessellations as analogs of 3-D lattices in the Euclidean 3-space E^3.

1. Basic biomolecules would correspond to linear sub-lattice-like structures of the icosahedral tessellation formed from triplets of icosahedron, tetrahedron and octahedron. One can say that DDNA codon X is associated with icosahedron-pair and corresponds to a face. This face represents X in the bioharmony model and also the entangled dark nucleons at its vertices represent X.

2. The cyclotron frequencies for the nucleons of X correspond to the frequencies of a dark 3-photon emitted by the dark 3-nucleon. This picture generalizes to genes represented as dark 3N-codons and dark 3N photons emitted in their communications involving 3N-resonance and frequency modulation yielding a series of resonance peaks at the end of the receiver as an analog of nerve pulse pattern.

3. Hamiltonian cycle must be physically realized at the icosa-tetrahedron which would serve as the basic structure for all dark counterparts of the information molecules. The simplest option is that the Hamiltonian cycle corresponds to a closed flux tube going through all vertices of the tetra-icosahedron. If the cyclotron frequencies, that is magnetic field strengths, are scaled by factor 3/2 (and scaled down to the same octave by octave equivalence) at each step along the cycle, the model of bioharmony is realized in terms of cyclotron frequencies. The codon realized as 3 dark nucleons associated with corresponds to the codon realized as dark photon triplet.

4. This picture generalizes to DtRNAs and DAAs. DtRNAs would have as active faces those DtRNA codons, which pair with DmRNA codons. DAAs would have at active faces those DtRNA codons which pair with them. Common dark codon would make pairing by dark 3-photon resonance possible. DtRNA could attach to correct DmRNA during translation and for DAA to correct DtRNA. Ordinary biomolecules would be paired with their dark variants so that dark variants of basic processes would induce their biochemical variants as a kind of shadow dynamics. The pairing by 3N-resonance could be a completely general mechanism involved with biocatalysis.

A concrete realization of bioharmony [?]n terms of the dark nucleon model for codons emerges. The small symmetry breaking effects - the members of doublet that should code for the same amino acid (or act as stop codons), code for different amino acid (or amino acid and stop), are understood. A crucial piece of the puzzle is that one particular chord $CEG\sharp$ has identical intervals between the notes in even tempered scale. Also the failure of the Pythagorean quint cycle (notes are obtained by scaling the basic frequency by power powers of (3/2) and using octave equivalence) to close, which bothered Pythagoras, is in an essential role. Also the differences between vertebrate and bacterial codes are understood.

8.2 Dark nucleon realization of the genetic code and basic information molecules

In this section I will represent the arguments leading to the recent (2022) view about dark nucleon realization of the genetic code and dark counterparts of basic information molecules DNA, RNA, tRNA, and amino acids.

8.2.1 The basic vision and the first guess

The basic vision is that dark matter and magnetic body (MB) serves as a master controlling the dynamics of the ordinary biomatter so that its dynamics is shadow dynamics, and the huge complexity of living matter could reduce to relatively simple control dynamics at the level of MB.

Biomolecules are information molecules and dark matter has a higher "IQ" than ordinary matter measured as the dimension $n = h_{eff}/h_0$ of the extension of rationals associated with the space-time regions characterizing the system measuring also the scale of quantum coherence. Therefore the natural expectation is that basic information molecules have dark counterparts and genetic code is realized at a darl level so that the chemical realization would be a secondary realization.

1. I started with a proposal [L1, K87, L58, K95] that dark codons could correspond to dark nucleons, that is dark quark triplets, assignable to open or closed string like objects (flux tubes). This led to the proposal for the basic group theoretical decomposition DDNA and DRNA codons in terms of group representations of $SU(2)_I \times SU(2)_R$ as $(4_I \otimes 4_s \oplus 2_I \otimes 2_s) \otimes (5_s \oplus 3_s) = [(3/2,-3/2)_I + (1/2,-1/2)_I] \otimes (4_s \oplus 2 \otimes 2) \otimes (5_s \oplus 3_s) = 64_{DNA} \oplus 64_{RNA}$. In the quark model, this corresponds in fermionic degrees of freedom to nucleon N and Δ assuming color degrees of freedom to get statistics right. $5 \oplus 3$ could be assigned to 2 *rho*-meson-like bonds for an open string-like object.

2. The realization of $4 \times 4 \oplus 2 \oplus 2$ in terms of quark color triplets is not physically plausible and the challenge is to realize $4 \times 4 \oplus 2 \oplus 2$ and $5 \oplus 3$ physically in terms of more plausible dark states. The natural guess is that this realization involves dark protons and neutrons. u and d would be replaced with p and n.

3. Color would be absent and since the Δ is completely symmetric, antisymmetry required by Fermi statistics must be realized by bringing in some new degrees of freedom. Galois confinement is suggestive in the TGD framework [L122, L128, L127, L133, L134]. Z_3 is a natural guess for the Galois group in the case of codons and one has 3 states in geometric degrees of freedom and 3-nucleon state, which is Z_3 singlet would be antisymmetric.

Since the induced spinors do not have color as spin-like quantum numbers, one must leave open the possibility that even ordinary color confinement has this kind of description as a description at space-time level (as opposed to the descriptions at embedding space and "world of classical worlds" (WCW) level).

8.2.2 The charge DNA as a guideline

A strong constraint comes from the observation that DDNA and DRNA codons have charge -3.

1. If DDNA and DNA form parallel string-like structures, this strongly suggests that there is a neutralizing charge +3 associated with the dark codon paired with the ordinary codon. This charge could be assigned either to 3 protons or 3 nucleons if there is some additional charge allowing to take care that the total charge is 3 units in the case of DDNA and DRNA.

   If also the notions of DAA and DtRNA make sense, charge neutrality for them is a plausible option. Of course, the additional charges could be dynamical in the same way as the charges of corresponding bio-molecules.

2. The compensating charge could be assigned to meson-like states with charges $0, \pm 1$. They could be meson-like bonds connecting the dark nucleons to a string-like object. ρ mesons with spin 1 and charges $(0, \pm 1)$ and pions with spin 0 and charges $(0, \pm 1)$ are the natural candidates. For closed string-like objects one would have 3 bonds and for open string-like objects 2 bonds.

   For ρ mesons associated with two bonds one would have spin representations $3 \otimes 3 = 5 \oplus 3 \oplus 1$. One should somehow get rid of the spin singlet if one assumes the proposal considered above. Spin-statistics represents the second problem: Bose-Einstein statistics does not allow 3.

   For $3 \otimes 3 \otimes 3 = (7 \oplus 5 \oplus 3) \oplus (5 \oplus 3 \oplus 1) \oplus 3$ associated with closed string-like objects, the number of states is quite too high. The only completely symmetric representation is 7 whereas 1 is antisymmetric. Thus it seems that the ρ-meason option is not realistic so that only pionic realization remains.

   This leaves open only the possibility that $5 \oplus 3(\oplus 1)$ corresponds to the rotational degrees of freedom of a closed or open string-like object.

8.2.3 Dark nucleons or dark protons?

Are both dark p and n needed or are dark protons enough as mildly suggested by the model [L15] of Pollack effect [I53, L15, I89, I76]? Could one build the needed states using only dark protons and suitably chosen bonds?

1. Could number theoretic Galois degrees of freedom [L121, L110, L101, L102, L128, L133, L134] come to rescue? The analog of isospin could be assigned with Galois degrees of freedom. For 3-D algebraic extension of rationals replacing color, the extension increases the algebraic dimension of the 3-space consisting of rational points by factor $n = 3$ to nd, $d = 3$. The dimension of number theoretic spinors would be $2^{n(d-1)}/2 = 2^3$, which is much larger than the dimension $d = 2$ of isospin spinors in 3-D space. One could speak of Galois-spin or G-spin. Nucleon isospin is therefore a more reasonable candidate.

2. The objection against the dark nucleon-triplet picture is that, in the standard nuclear physics, neutrons are not thought to be important in living matter. Note however that the dark electroweak length scale scaled by h_{eff}/h_0 could be much longer than the ordinary weak scale, even of the order of cell length scale.

   Weak gauge bosons would be effectively massless below the dark weak scale and weak interactions associated with the dark pion-like bonds would be as strong as electromagnetic interactions. This could explain the mysterious large chirality breaking effects in living matter.

3. One can also ask whether the dark neutron is effectively a dark proton plus pionic bond so that dark protons would be the basic building bricks after all. One cannot exclude the possibility that this applies also to the neutrons of ordinary nuclei [K79, L1]. This does not however conform with charge +3 for DDNA codons . This would leave the option that the dark neutron is an ordinary proton plus dark π^- bond.

8.2.4 Dark variants of information molecules as analogs of nucleon and Δ obtained by replacing quarks with dark nucleons

Could the dark analogs of N and Δ with quarks replaced by nucleons give rise to the genetic code and dark analogs of the basic information molecules?

1. The analogs of N and Δ would give 2 spin doublets (counterparts of p and n as ppn and pnn) and 4 spin 4-plets as a counterpart of Δ (ppp,ppn,pnn,nnn): altogether 20 states, which brings into mind AAs. Note that pion bonds could modify the charges for ordinary nucleons.

2. The analogs of N and Δ can be tensored with $A = 5_s \oplus 3_s \oplus 1_s$ or $B = 5_s \oplus 3_s$. $\Delta \otimes B$ would give $[(3/2,-3/2)_I \oplus (1/2,-1/2)_I] \otimes (5_s \oplus 3_s)$: these two 64-plets could be identified as DDNA and DRNA.

   $N \otimes 1$ could give 20 AAs. For both options, $N \otimes B = (2_I \oplus 2_s) \otimes (5_s \oplus 3_s)$ would give 20+12=32 states, which is the minimal number of tRNA codons. The number of chemical tRNA codons is larger than 40 so that DtRNA-tRNA pairing would be 1-to-many. This could induce the wobble base pairing [I21].

3. DDNA and DRNA would correspond to the analogs of Δ nucleons with rotation. For instance, ppp and ppn as counterparts of Δ^{++} and Δ^+ could correspond to DDNA and pnn and nnn as counterparts of Δ^- and Δ^0 could correspond to DRNA. This implies charge asymmetry which should relate to the differences between DNA and RNA. DtRNA would correspond to N with rotation. DAA would correspond to Δ and N without rotation, which should relate to the different functions between AAs and molecules DNA, RNA, and tRNA.

   Remark: Note that pionic bonds would guarantee that the total charge of DDNA and DRNA codons is 3 units.

8.2.5 Angular momentum of the nuclear string as origin of $5 \oplus 3 \oplus 1$

One must understand the origin of $5 \oplus 3 \oplus 1$ or of $5 \oplus 3$. There are 3 scenarios to consider. Closed string scenario favors $5 \oplus 3$ but does not predict AAs. Open string scenario favors $5 \oplus 3 \oplus 1$ and allows the identification of dark counterparts of all basic biomolecules. If ρ mesons do *not* give rise to $5 \oplus 3 \oplus 1$, both closed and open strings can be considered.

1. What came first into mind was that the bonds between protons are analogous to ρ mesons. This would allow only an open string option. There is however a problem with statistics: 3 is antisymmetric (analogous to the cross product of 3-vectors).

   This suggests that the bonds are pionic and do not contribute to the spin but allow to obtain desired total charges for 3 proton states. Charge neutrality is attractive for AAs and would require maximum neutralizing charge -3 so that only the closed string option with ordinary nucleons plus dark pionic bonds remains. Even dynamical charges would be possible also at the level of dark bio-molecules and one can consider the possibility that the MB controls the charge state of the basic biomolecules.

2. Concerning the identification of $5 \oplus 3(\oplus 1)$, the rotational degrees of freedom of string seem to be the only reasonable option. 1 and 5 could correspond to spin 0 and spin 2 states of the Regge trajectory and 3 to spin 1 state of a possibly exchange degenerate trajectory. What is encouraging is that only the bosonic spins 0, 1, and 2 and fermionic spins 1/2 and 3/2, which are in a very special role physically would be needed.

To sum up, closed strings with dark nucleon triplets and stringy rotational degrees of freedom allow us to predict the dark counterparts of all basic information molecules as analogs of nucleon and Δ states with pionic bonds. The number of dark tRNA codons is predicted to be minimal and equal to 32, and the considerably larger number of the chemical tRNA codons implying that dark tRNA-tRNA pairing is 1-to-many. This would explain wobble base pairing.

8.2.6 Various pairings of the information molecules

The basic vision is that the dynamics of the MB induces the dynamics of the biological body and the observed chemical pairings are induced by dark pairings. One should therefore understand the DDNA-DRNA, DRNA-DtRNA, and DtRNA-DAA pairings.

1. DDNA-DRNA pairing is obtained trivially. DDNA-DAA pairing is induced by DRNA-DtrNA pairing and DtRNA-AA pairing.

2. The decomposition $2 \times (20 \oplus 12)$ for DRNA suggests a natural pairing with tRNA identified as $20 \oplus 12$. The spin contents of the codons are however different and the situation is more complex. This leads to a model for the breaking of the (A,G) symmetry of the third codon in RNA-AA pairing. The pairing of DtRNA with DAA requires pairing of $20 \oplus 12$ with 20. $20 \to 20$ is a natural pairing but how to realize $12 \to 20$?

3. Could icosa-tetrahedral realization of the genetic code in terms of dark photon triplets (bioharmony) [L11] [L107, L122] help here? In this realization the faces of icosahedron and tetrahedron identifiable as 3-chords correspond to codons and 3 isohedral Hamiltonian cycles providing a model for 12-note scale and the unique tetrahedral Hamiltonian cycle are needed for the realization of bioharmony as genetic code.

   Icosahedron has 20 faces and 12 vertices defining Hamiltonian cycles essential for the realization in terms of bioharmony. Hamiltonian cycles have Z_6, Z^4 or Z^2 as a symmetry group: Z_2 can correspond to reflection of rotation by π. Z_6 has 3 orbits with 6 faces and 1 orbit with 2 faces. Z_4 has 5 orbits with 4 faces. Z_2 has 10 orbits with 2 faces.

   Could the missing faces correspond to the missing orbits for one of these symmetry groups: a) to 6-orbit and 2-orbit for Z_6 or b) 2 4-orbits for Z_4 or c) 4 2-orbits for Z_2. Z_6 and Z_4 Hamiltonian cycles are unique and part of any realization. Option b) is more symmetric than option a) and is a more promising candidate.

Consider now the pairings of type DX-X.

1. All dark pairings as a bound state formation by Galois confinement [L133, L134] would involve formation of a composite $P_n \circ P_{n-1} \circ ... \circ P_1$ of the polynomials P_i determining at M^8 level the 4-surfaces of systems participating in the interaction. This implies that Galois groups extend to a larger group having the Galois groups of composites as normal subgroups.

2. The already mentioned charge asymmetry reflecting the violation of the weak isospin symmetry between DDNA and DRNA could explain why DNA *resp.* RNA involves deoxyribose *resp.* ribose molecule and the nucleotide T is replaced with U in RNA. The instability of RNA molecules and the rarity and short life-time of double RNA strands could derive from the properties of DRNA .

   The almost exact T-C and A-G symmetries of the third letter of genetic codon could also reflect almost exact isospin symmetry as proposed in [K39]. The number of DtRNAs is the minimal 32 and this predicts 1-to-many character of DtRNA-tRNA pairing which would induced wobble base pairing.

   Dark base pairing could involve an extension of Galois group Z_3 of codon to Z_6 of codon pair. This could make DDNA double strand stable and perhaps induce the stability of DNA double strand. DDNA double strand would permanently be in the bound state with Z_6 as the Galois group of the dark base pair. This would support the view that DDNA is above DRNA in the dark master-slave hierarchy.

Also the functional differences between DNA and RNA could relate to the differences of their dark counterparts. The DDNA double strand with larger h_{eff} would represent a higher evolutionary level than the DRNA strand.

3. The number of DtRNA molecules is 32, and minimal one, so that DtRNA-tRNA pairing is not unique. This explains the wobbling of RNA-tRNA pairing [I21]. Does the wobble phenomenon have some biological function or does it signal that dark tRNA-tRNA pairing has not yet evolved to its final form?

   That tRNA as such does not represent information storage but plays a role of servant in the translation process, supports the first view. The basic function of dark tRNA in the translation is unique but it is less risky to have several ways to perform this function: hence the large number of ordinary tRNAs.

8.2.7 A model for the symmetry breaking of the genetic code

The model predicts that the numbers of DRNA and DtRNAs are 64 and 32 respectively. This condition does not force DRNA-DtRNA correspondence to be 2-1 in a codon-wise way. This is however true in an excellent approximation as becomes clear by looking at the code table.

For the third letter, RNA-AA correspondence has an exact U-C symmetry and almost exact A-G symmetry. There are only 2 exceptions. TTX 4-plet decomposes to 3× ile + 1 met: (A,G) doublet for the third codon splits to (ile,met). The (A,G) doublet in TGX splits to (stop,trp). Both stop codons and met as a start codon are therefore very special.

In bacterial genetic codes also the (A,G) doublet in TGX, which usually corresponds to (stop,stop), corresponds sometimes to (stop,pyl) doublet so that CG symmetry is broken. Also the (A,G) doublet usually mapped to (stop,trp) can be mapped to (sec,trp). The interpretation would be that a stop codon is obtained if DtRNA corresponding to UAG or UGA does not pair at all with tRNA. If it pairs, UAG codes for pyl and UGA codes for sec.

One should understand this symmetry breaking.

1. Since iso-spin and spin are involved, either isospin or spin symmetry breaking is suggestive. In the nucleon sector the situation is completely symmetric between spin and isospin. In the string sector, the situation is different for DDNA, DRNA and DtRNA.

2. The earlier interpretation for (U,C) and (A,G) doublets was as isospin doublets and isospin symmetry breaking. The conjugations $G \leftrightarrow C$ and $U \leftrightarrow A$ were interpreted as an analog of particle-antiparticle conjugation.

   The following model leads to the proposal that dark (T,C) doublet corresponds to spin (rather than isospin-) doublet $2_s = (1/2, -1/2)$ and (A,G) doublet to pseudo-spin doublet $(3/2, -3/2)$. As if rotational symmetry would have reduced to axial symmetry (this would conform with the linear structure of DNA). Letter and its conjugate would correspond to different spin doublets. Interestingly, the repetive purine (A, and G) sequences for intronic portions of active DNA strandd would correspond to dark (3/2,-3/2) doublet for which the breaking of rotational symmetry is larger for the active strands in the transcribed portion of DNA.

   At the level of DNA, DRNA and DtRNA, the natural possibility is that (T,C) doublet corresponds to 2_s and (A,G) doublet to the spin symmetry violating $(3/2, -3/2)_s$. (T,C) and (A,G) could form an isospin doublet.

3. An important point to note is that (3× ile,met) and (stop,stop), (stop,trp) dot correspond to identical situations since 2 iles correspond to (T,C) for which there is no symmetry breaking. Actually one has 3 (A,G) symmetry breakings.

Consider now the identification of spin- and isospin contents of various dark information molecules.

1. Suppose that the spin symmetry is not broken at DDNA and DRNA level but isospin 4-plet $4_I = (3/2, 1/2, -1/2, -3/2)$ splits into pseudo-doublets $2_{I_1} = (1/2, -1/2)$ and $2_{I_2} =$

$(3/2,-3/2)$. If DDNA were maximally symmetric it would correspond to $2_{I_1}=(1/2,-1/2)$. Which option one chooses, does not matter in the sequel so that this option is selected.

This would give

$$DDNA = 2_{I_1}\otimes[4_s\otimes(5_s\oplus 3_s)] \ ,$$
$$DRNA = 2_{I_2}\otimes[4_s\otimes(5_s\oplus 3_s)] \ .$$

2. DtRNA and DAA correspond to

$$DtRNA = 2_I\otimes[2s\otimes(5_s\oplus 3_s)] \ ,$$
$$DAA = 4_I\otimes 4_s\oplus 2_I\otimes 2_s \ .$$

3. One would expect that the pairing minimizes the breaking of rotational symmetry meaning that spins are the same for paired dark molecules if possible and the spin difference is minimized otherwise. To get some idea about the symmetry breaking, one can decompose the tensor products for the spin representations

$$DRNA = 2_{I_2}\otimes(8_s\oplus 2\times 6_s\oplus 2\times 4_s\oplus 2\times 2_s) \ ,$$
$$DtRNA = 2_I\otimes(6_s\oplus 2\times 4_s\oplus 2_s) \ .$$

The representation contents are different and the number of spin states for DRNA is twice that for DtRNA so that the symmetry breaking relates to spin pairing rather than isospin pairing.

The first thing to notice is that $2\times 2_s$ for DRNA naturally projects to 2_s for DtRNA. Also $2\times 6_s$ projects to 6_s . Bothe decomposis however have $2\times 4_s$:s so that 8_s must pair with $2\times 4_s$. Symmetry breaking must localize to this pairing.

8_s is not present in DtRNA and forces a pairing between different spins. This should cause the violation of spin symmetry for dark (A,G) doublets in the sense that they couple to different DAAs, which in turn requires that they couple to different DtRNAs.

1. One can decompose 8_s as

$$8_s = (7/2,-7/2)_s\oplus(5/2,-5/2)_s\oplus 4_{s_1} \ .$$

8_s should correspond to $2\times 4_s$ in DtRNA. The pseudo 4-plet 4_{s_1} pairs with 4_s in a spin conserving manner.

2. What is left is $2_{I_2}\otimes[(7/2,-7/2)_s\oplus(5/2,-5/2)_s]$, which should pair $2_I\times 4_s$. This pairing cannot conserve spin and the 2-1 symmetry must be violated in the sense that the DRNAs paired with $(3/2)_s$ and $-(3/2)_s$ are different. One can ask whether the change of the magnitude of the spin component is minimal in the DRNA-DtRNA pairing.

3. At the level of DAA and DtRNA, ile could correspond to the first DtRNA doublet $((3/2)_I\otimes(1/2,-1/2)_s$ and $(3/2)_I\otimes(3/2)_s$ as a singlet and met to $(3/2)_I\otimes(-3/2)_s$ as a singlet. $(stop,stop)$ and $(stop,trp)$ could correspond to $(3/2)_I\otimes(3/2,-3/2)_s$ and $(-3/2)_I\otimes(3/2,-3/2)_s$. Spin symmetry breaking would therefore mean that different DRNAs pair with DtRNAs in the doublet $(3/2,-3/2)_s$.

How do DRNAs and DtRNAs correspond to each other in the (A,G) symmetry violating sector? In the absence of symmetry breaking DRNA-DtRNA pairing is 2-1 in a codon-wise way if DRNA with opposite values 3/2 and -3/2 of isospin pair with the same DtRNA. Symmetry breaking would mean that some DRNAs with spins 3/2 and -3/2 pair with different DtRNAs and therefore with different DAAs for some (A,G) doublets $(3/2,-3/2)_s$. For the (T,C) doublets $(1/2,-1/2)_s$ this would not occur.

1. There are 8 spin symmetry violating DRNAs and 8 DtRNAs corresponding to $UA(A,G)$ and $UG(A,G)$ and $UA(T,C)$ and $UA(A,G)$ (3× ile+ met). $UA(T,C)$ is strictly speaking not spin symmetry violating but ile corresponds to DRNA triplet instead of doublet. As if the DRNA doublet paired with 2 DtRNAs pairing with met would pair with DtRNAs coding for ile and met.

   There are 2 $[(7/2,-7/2)_s \oplus (5/2,-5/2)_s]$ multiplets at the DRNA side. At the DtRNA side one has pseudo doublets $(3/2,-3/2) \oplus 2_{s_1}$, $s_1 = (1/2,-1/2)$. There are two of these corresponding isospin doublet 2_{I_1}.

2. Since there are 3 UCAG 4-plets with symmetry breaking, the symmetry violation is not independent of the value of isospin for $(3/2,-3/2)_I$ for DRNA and $(1/2,-1/2)_I$ for DtRNA. Symmetry breaking for isospin should localize to the DRNA side. There are several options (3,0), (0,3), (2,1) (1,2) for the numbers of symmetry breakings for DRNA multiplets. One can restrict in the sequel to a single value of isospin, say 3/2.

3. One should find symmetry violating pairing between these 8 DRNAs and 8 DtRNAs. $[(7/2,-7/2)_s \oplus (5/2,-5/2)_s]$ should be mapped to $(3/2,-3/2)_s \oplus 2_{s_1}$. Assume that the spin difference between paired DRNA and DtRNA is as small as possible.

   (a) (T,C) doublet without symmetry breaking would correspond to the pairing

   $$(5/2,-5/2)_s \to (1/2,-1/2)_s \quad .$$

   (T,C) symmetry is not violated if the both doublets correspond to the same DAA and DtRNA.

   (b) (A,G) doublet could correspond to the pairing

   $$(7/2,-7/2)_s \to (3/2,-3/2)_s \quad .$$

   Now the members of the doublets would correspond to different DAA.

   (c) For instance, the DRNA corresponding to the second met in (met,met) in absence of symmetry breaking, would pair with DtRNA, which pairs with ile. The symmetry present at the DRNA level would be broken by the pairing.

   In the case of (stop,trp) doublet, the same would occur. This would also happen in the replacements (stop,stop) → (stop,pyl) and (stop,trp)→ (sec,trp). Now the DtRNA in question would not pair at all with tRNA and AA or it would be with exotic tRNA pairing with an exotic AA.

8.2.8 Chemical bonds as flux tube links and a realization of dark codons using only dark protons

In the proposed model of dark DNA, one must assume that the dark codon is formed by a triplet of dark nucleons (proton and neutron). In the TGD framework one could justify the presence of neutrons by the large value of Planck constant increasing the weak scale to at least atomic length scale so that weak bosons would behave like massless particles in atomic scales at the MB. Therefore the dark protons could transform to dark neutrons easily. Neutron would be connected to either neighbor by a meson-like flux tube bond which is positively charged so that each codon would have a charge of 3 units neutralized by an opposite charge of 3 phosphates.

The sign of the magnetic flux as bit?

The introduction of neutrons brings in an additional bit. Therefore one could use only dark protons, if one could bring in this additional bit in some way. An obvious candidate would be the direction of a monopole magnetic flux assignable to the letter of the codon as a closed flux tube with respect to reference direction defined by the DNA sequence. If the letters of codon are closed linked flux tubes containing dark protons forming dark DNA as a chain, this kind of option might work.

Consider first the topology of the monopole flux tubes.

1. Magnetic monopole flux tubes correspond to closed 3-surfaces in the TGD framework. They are closed because the boundary conditions do not allow boundaries with a monopole charge nor boundaries at all. In dimension 3, these flux tubes can become knotted and closed flux tubes can get linked.

2. If one has a braiding of N flux tubes, one can connect the ends of the N flux tubes. There are many ways to connect the ends, and one obtains at most N linked closed flux tubes, which are knots. The simplest option is that the ends of each braid strand are connected so that one has N linked flux tubes. This corresponds to the "upper" ends as a trivial permutation of the "lower" ends.

3. Any permutation in the permutation group S_N is possible. A given permutation can be expressed as a product of permutations such that each permutation leaves invariant a subset. Permutations are therefore characterized by a partition of N objects to subsets such that the given set consist of N_i objects with $\sum N_i = N$ and that these sets do not decompose to smaller subsets. The allowed permutations for N_i objects correspond to elements of the cyclic group Z_{N_i}. These cyclic permutations give rise to a single closed tube when the ends of the braid ends and permuted braid ends are connected. The number of closed flux tubes is therefore the number of summands in $\sum N_i = N$.

   These permutations are obtained by reconnections from the permutation corresponding to N closed loops so that there are two levels: the level of braiding and the level of reconnections behind the stages not visible in the properties of the braiding.

Linking is a metaphor for bonding. One speaks of the chain of generations, of a weak link in the chain, etc.

1. Chemical bonds are classified into ionic bonds, valence bonds involving delocalization of electrons, and hydrogen bonds involving delocalization of protons. Chemical bonds are not well-understood in the framework of standard chemistry. TGD suggests that they involve space-time topology: monopole flux tube pairs would be associated with the bonds and the splitting of the bond would correspond to a reconnection splitting the pair to two U-shaped flux tubes. Flux tubes and connecting molecules as nodes are proposed to form a network.

2. I have not considered in detail how the U-shaped flux tubes are associated with the nodes. Bonding=linking metaphor encourages a crazy question. The members of the flux tube pairs, which are proposed to connect molecules, which serve as nodes of a network . These flux tubes must close and could be linked with shorter closed flux tubes assignable to molecules.

3. Could this linking bind the molecules and atoms to a single topological structure. If so, both chemistry and topological quantum computation (TQC) in the TGD framework would involve linking, braiding, and reconnections as new topological elements. Biomatter at molecular level would consist of chains of closed flux tubes which can be also stretched and give rise to braids.

   Note that 2 U-shaped flux tubes can reconnect and this transition can lead to a pair of flux tubes or to a linked pair of U-shaped flux tubes so that 3 different states are possible.

4. I have proposed that the pairing of molecules by a pair of monopole flux tubes serves as a correlate for entanglement. If dark protons are associated with closed flux tubes, they must entangle. Could also the linking of the U-shaped flux tubes give rise to entanglement? Stable linking correlates the positions of the flux tubes but this need not mean entanglement since wave function can be a product of wave functions in cm coordinates and relative coordinates.

Linking as an additional topological element inspires some quantum chemical and -biological speculations.

1. Could the presence of valence-/hydrogen bonds involve a closed flux tube at which the electron (pair)/proton is delocalized and that this flux tube is linked with another such flux tube. This picture is consistent with the proposed role of quantum gravitation in metabolism [L135] and generation of the predecessor of the nervous system [L137] based on very long variants of

hydrogen bonds characterized by gravitational Planck constant. In this view, living matter would be an extremely highly organized structure whereas in the standard chemistry organism would be a soup of biomolecules.

2. What comes to mind as an example, is the secondary structure of proteins (`https://cutt.ly/sZ5rRiQ`) involving α- helices, β-strands and β-sheets. Tertiary structure refers to 3-D structure created by a single protein molecule. It can have several domains. There are also quaternary structures formed by several polypeptide chains. Proteins consist of relatively few substructures known as domains, motives and folds. Could these structures involve braided and linked flux tube structures with dynamical reconnections?

Dark codons as triplets of dark protons at linked closed flux tubes?

Consider now a possible model of dark DNA involving only dark protons.

1. One can imagine that dark protons are associated with closed flux tubes acting as hydrogen bonds, such that 3 closed flux tubes as letters are linked to form a dark codon. The dark codons could in turn be linked to form genes as sequences of codons. The direction of the magnetic flux can be opposite or parallel to that of the chain so that each closed flux tube represents a bit of topological information. The chains of links would define sequences of bits and even qubits. Could this define the predecessor of the genetic code for which letter represents a single bit?

2. If one has only dark protons, one obtains only 32 dark codons. An additional bit is required to get 64 codons. Could the direction of the closed flux tube in the chain provide the missing bit and thus represent strong isospin distinguishing between p and n?

   What implications could this identification have?

1. It is known that the genetic code has a slightly broken symmetry with respect to the last letter of the codon. For almost all RNA codons U and C resp. A and G define code for the same amino-acid. A possible interpretation of the symmetry is that this symmetry is that U-C pair and A-G pair correspond to the bit defined by magnetic flux so that the sign of magnetic flux would not matter much at the level of proteins. For this interpretation, the additional bit would not mean much at the level of proteins.

   Dark DNA and presumably also RNA codons are linked chains of 3 closed flux tubes serving as bits. Could this chain in the case of dark amino acids be replaced with a single closed flux tube obtained by two reconnections so that amino-acid becomes a basic unit?

2. Could the breaking of A-G symmetry (stop-trp pair and ile-met pair) have a topological meaning? Could the direction of the magnetic flux for the third flux tube of the dark codon coding for these pairs matter (this is not the only possibility that one can imagine)? Note that the 4 tetrahedral dark codons in the bioharmony model [L143, L107] correspond to stop-stop and stop-trp pairs.

3. What could topologically distinguish met as a starting codon and stop codons from the other codons? Could it be that met is not linked to the codons preceding it so that transcription would naturally start at it.

   Could stop codons be unlinked to the codons following them so that the transcription would naturally stop at them? Or could the stop codons correspond to a single closed flux tube so that no RNA codon could be assigned to them?

4. Genes contain intronic parts and the splicing of RNA eliminates these parts after the transcription. Could the topology of DNA and RNA isolate intronic portions from those to be translated. Could the intronic portions correspond to a single flux tube linked to the rest of the gene both at the level of DNA and RNA. If so, the information about the decomposition of intron to RNA codons would be missing and the assignment of tRNA codons to the intronic portion would not be possible.

8.2.9 Could dark genes be dynamical?

In [L139] it was found that the earlier 1-1 correspondence between dark codons and ordinary genetic codons is unnecessarily strict and a modification of the earlier picture of the relation between dark and chemical genetic code and of the function of dark genetic code was considered.

1. Dark DNA (DDNA) strand is dynamical and has the ordinary DNA strand associated with it and dark gene state can be in resonant interaction with ordinary gene only when it corresponds to the ordinary gene. This applies also to DRNA, DtRNA and DAA (AA is for amino acids).

   This would allow DDNA, DRNA, DtRNA and DAA to perform all kinds of information processing such as TQC by applying dark-dark resonance in quantum communications. The control of fundamental biomolecules by their dark counterparts by energy resonance would be only one particular function.

2. Most importantly, flux tubes magnetization direction could define qubit. If the additional qubit corresponds to nucleon isospin, it is not clear whether this is the case. One can also allow superpositions of the dark genes representing 6-qubit units. A generalization of quantum computation so that it would use 6-qubits units instead of a single qubit as a unit, is highly suggestive.

3. Genetic code code could be also interpreted as an error code in which dark proteins correspond to logical 6-qubits and the DNA codons coding for the protein correspond to the physical qubits associated with the logical qubit.

4. The teleportation mechanism discussed in [L139] could make possible remote replication and remote transcription of DNA by sending the information about the ordinary DNA strand to the corresponding dark DNA strand by energy resonance. After that, the information would be teleported to a DNA strand in a ferromagnetic ground state at the receiver. After this, ordinary replication or transcription, which would also use the resonance mechanism, would take place.

8.2.10 The newly discovered spatial grammar of DNA from the TGD perspective

The SciTechDaily article "Scientists Discover Spatial Grammar in DNA: Breakthrough Could Rewrite Genetics Textbooks" (see this) the discovery of the spatial dependence of the function of the transcription factors. There is a Nature article [I37] (see this) about the finding by Duttke et al with the title Position-dependent function of human sequence-specific transcription factors

The essential feature of spatial grammar is that transcription factors are effective only when they are attached to preferred positions of DNA. It has been thought that transcription factors can act as activators of repressors. The new finding is that most active transcription factors can also act as repressors. Moreover the removal of the activator need not lead to the loss of the activity. It was also found that the function of the activators is highly position dependent. In particular, the ambience, that is the spacing between transcription factors and their position relative to where a gene s transcription began, determined the level of gene activity.

This conforms with the TGD view of how genes and proteins, now transcription factors interact. The key ideas of the TGD view are as follows.

The TGD based view of space-time and quantum are essential for the TGD inspired quantum biology.

1. Ordinary DNA and also RNA, mRNA, tRNA, and proteins are accompanied by dark variants [L78, L27, L7, L143] with a non-standard value of effective Planck constant h_{eff}, which can be understood in the number theoretic view of TGD [L157, **?**]. The dark variants are realized as dark proton sequences at the monopole flux tubes parallel to the ordinary DNA, RNA, or amino-acid considered. Also tRNA has a dark variant.

   The monopole flux tubes carry sequences of dark codons realized as dark proton triplets associated with closed monopole flux tubes at a larger long monopole flux tube. Also neutrons

can be considered but whether they are needed is still unclear. In any case, in the case of DNA the codons would consist of dark protons.

2. The dark codons at the monopole flux tube would bind to form dark genes behaving as quantum coherent units. Both DNA, RNA and tRNA are obtained. One can form a representation of the genetic code based on the dark proton states and one also obtains a representation assignable to amino-acids. The dark protons can be characterized by cyclotron frequencies assignable to the magnetic fields at closed flux tubes at which they reside.

The icosa tetrahedral realization of the genetic code is essential [L11] [L107, L143, L122, L146].

1. Dark codon corresponds to a triplet of cyclotron frequencies and a given transition between different 3-proton states induces an emission of a dark photon triplet. Even more: entire dark genes with N codons can emit 3N-triplets of dark photons and in communications these can give rise to 3N-resonance so that only similar gene sequences can interact resonantly. Also partial resonance can be considered.

2. Icosa tetrahedral realization of the genetic code is in terms of cyclotron frequency triplets. This realization corresponds to a completely unique tessellation of the hyperbolic space H^3 (light-cone proper time= constant hyperboloid) involving not only single platonic solid but tetrahedrons, octahedrons and icosahedrons as building bricks of the fundamental domain. This would be a universal realization of the genetic code, which could appear in all scales, not only in biology.

   In this realization, 60 codons of the dark DNA correspond to 3 different Hamiltonian cycles of icosahedron and 4 codons to the unique Hamiltonian cycle of the tetrahedron. Each icosahedral cycle gives 20 codons identifiable as 20 triangles as faces of the icosahedron.

3. This view emerged from a geometric model for music harmonies. Musical 12-note scale is realized using a closed icosahedral Hamiltonian path going through all 12 icosahedral vertices. One can realize the notes of the cycle by assuming that for a given step of the path, the frequency is scaled by factor 3/2 and then scaled to the basic octave (octave equivalence). Since the music expresses and induces emotions, the interpretation is that various bioharmonics defined by different combinations of Hamiltonian cycles correspond to different emotional states at the molecular level [L64].

4. There are a large number of Hamiltonian cycles and therefore many realizations of the genetic codons in terms of frequency triplets associated with the faces of icosahedron and tetrahedron. These realizations are obtained as fusions of three Hamiltonian cycles with symmetry $Z_6(only\ one\ cycle), Z_4(2 cycles) and Z_{2R} or Z_{2,rot}(larger\ number\ of\ cycles) and would correspond to different molecular$

5. Icosahedron gives 20+20+20 codons for a given bioharmony and the number of DNAs coding a given amino acid are obtained correctly. The tetrahedral cycle gives the remaining 4 codons.

What about amino-acids?

1. In the icosa tetrahedral realization of the DNA and RNA codons, amino acids correspond to the orbits of a given triangle of the icosahedron under the action of the symmetries of the Hamiltonian cycle. This strongly suggests that the representation in terms of dark proton triplets makes sense also for the amino-acids.

2. The problem is that amino-acids do not have a constant charge density of -3e per amino-acid. Could ordinary protons associated with the amino-acids transform to dark protons only when this is needed?

   The dark protons of dark DNA and RNA are ordinary protons transferred to the monopole flux tubes. This charge separation means that the ordinary DNA becomes negatively charged. This is just the Pollack effect and requires metabolic energy feed as photons but also other energy sources are possible.

   Could most protons of the amino-acids be ordinary? This would save metabolic energy since the increase of h_{eff} requires energy and h_{eff} tends to decrease spontaneously. When protein is just a geometric building b
   acids be dark only when they are reactive, that is serve as a biocatalyst, in particular as a transcription factor? The activation

3. 3N-cyclotron transition to a smaller subset of 3N dark protons makes possible a communication mechanism by 3N-cyclotron resonance (see this). Pieces of dark DNA, RNA, trNA, and dark amino acids can communicate resonantly. This is like tuning the radio to a correct wavelength: now there would however be several wavelengths defined by the codon sequences or a sequence of amino-acids. This would also be the basic mechanism of biocatalysis.

4. 3N-frequency would serve as an address in these communications and the modulation of the cyclotron frequencies by varying the magnetic field strength, or equivalently the monopole flux true thickness, makes possible a coding of information to the frequency modulation. Therefore a given modulation generates a characteristic sequence of pulses analogous to nerve pulses: this mechanism would be involved also with communications of sensory data from the neuronal membrane to the magnetic body of the brain [K29, K69, K1, **?**] [L137, **?**, L153]. Fractally scaled variants of the same communications would occur also at the level of the ordinary cells [L155].

5. Also dark-ordinary communications are possible but require the transformation of dark 3-N photons from dark molecules to ordinary photons.

6. A natural proposal is that the cyclotron frequencies assignable to dark amino-acids are the same as those associated with DNA codons coding from them. This would mean that a given protein can attach by 3N-resonance to all DNA sequences for which the codons code for it. This correspondence is testable and would mean an enormous amount of information about how the biocatalysis for the basic information molecules works.

This framework would allow us to understand positional coding. Multi-resonance between a piece of dark DNA accompanying ordinary DNA and the dark transcription factor protein characterized by the same cyclotron frequencies makes it possible an optimal selection of the portion of DNA by 3N-cyclotron resonance. Partial 3N-resonance would lead to a reduced activity. The modulations of the cyclotron frequencies could also make possible information exchange during the transcription process and the biomolecules could interact like conscious intelligent agents.

8.3 Connection between dark nucleon code and bioharmony

The model of genetic code based on bioharmony has evolved through many sidetracks [L11] but the version discussed in [L78, L107, L122] is roughly consistent with the original model and also gives a connection with the model of dark nucleon code.

8.3.1 Bioharmony and resonance mechanism for dark photon communications

The faces of icosahedron and tetrahedron (and also octahedron appearing in the model of genetic code as icosa-tetrahedral tessellation of hyperbolic space H^3 [L122]) are triangles. The proposal is that they somehow correspond to 3-chords made of dark photons, which in turn represent genetic codons.

Communications by dark 3-photons represent codons. 3N-photons represent in turn genes. The communications rely on cyclotron 3N-resonance so that the vertices of the faces of icosa-tetrahedron must contain charged particles coupling to a magnetic field. The magnetic field strengths at flux tubes associated with charged particles would determine the cyclotron frequencies.

Information is encoded to the frequency modulation of cyclotron frequencies. The chords serve as addresses much like in computer language LISP. If the modulations of 3N frequencies are identical and in synchrony, the outcome of the receiver consisting of 3N charged particles is a sequence of 3N-resonances giving rise to an 3N-pulse sequence. Nerve pulse patterns could emerge by this mechanism.

One can also consider 3N-signals for which only $M < 3N$ modulations are identical and in synchrony. In this manner communications to subsets of the receiver are possible. For instance, some subset of codons of dark gene or dark protein can be selected as a receiver, possibly controlled. This selection could de-entangled the receiver to de-entangled coherent pieces.

There is a direct connection with empiria. Biophotons, whose origin remains poorly understood, can be identified as ordinary photons resulting from the decay of dark 3N-photons to ordinary photons.

The realization in terms of dark nucleons looks more plausible if also DtRNA and DAAs are realized in terms of icosa-tetrahedral picture. This is because the amino acids (AAs) are often neutral unlike DNA nucleotides, which are negatively charged. The dark charge assignable to the dark codon can be controlled by pion-like bonds with charges $0, \pm 1$ so that it can be 3 units for DDNA and vanish for AAs. A natural proposal is that the pionic charge of the codon compensates the charge of the AA and tRNA but the dark charge could be also dynamical and control the ionization of the biomolecule.

Large value of h_{eff} would make possible dark nuclear interactions in the scale of the dark codons (about codon size) allowing the transformation of dark protons to neutrons by dark variant of strong interactions (dark nuclear interactions are central in the TGD based model of "cold fusion" [L41, L105] having implications also for the stellar evolution [L90]). Dark codons would be analogous to dark nuclei tritium (pnn), ^{3}He (ppn), and also ppp and nnn not realized as ordinary nuclei).

There are pairings of type DX-DY. The pairings DDNA-DRNA, DRNA- DtRNA and DtRNA-DAA induce the biochemical dynamics of transcription and translation. There are also pairings DX-X involving the transformation of dark 3-photon to ordinary 3-photon and occurring via energy-resonance but involving downwards scaling of wave-length. DDNA-DNA and DRNA-RNA unique DtRNA-tRNA pairing is 1-to-many and relates to the wobble phenomenon. The pairings between dark nucleon variants of biomolecules and corresponding dark 3N-photons make possible biocommunications and control.

8.3.2 Details of the bioharmony model

Consider now a more detailed bioharmony model of the genetic code based on the geometries of icosahedron and tetrahedron.

1. Icosahedron has 12 vertices and 20 faces, which are triangles. The idea is that the 12 vertices correspond to the notes of 12-note scale. Tetrahedron has 4 vertices and 4 faces and is self-dual whereas the dual of icosahedron is dodecahedron having 20 faces and 12 faces.

2. 12-note scale can be represented as a Hamiltonian cycle at an icosahedron going once through all vertices. The frequencies at the neighboring points as edges of a face in cycle relate by a frequency scaling of 3/2: this gives rise to the Pythorean variant of quint cycle.

   Octave equivalence means the identification of frequencies differing by a multiple of octaves. Octave equivalence can be used to reduce all frequencies to a single octave. If the scaling is exactly 3/2 at all steps there is a slight-breaking of octave equivalence since $(3/2)^{12}$ does not quite correspond to an integer number (7) of octaves. Pythagoras was well aware of this.

   Given cycle assigns to faces 3-chords defining a harmony with 20 chords assignable to the faces of the icosahedron. For dodecahedron there is only single harmony with 12 chords and 20-note scale which could correspond to Eastern scales. For the tetrahedron the Hamiltonian cycle is unique.

3. Icosahedral Hamiltonian cycles can be classified by symmetries. The group Z_6, Z_4, or Z_2 (rotation by π or reflection) as a group of symmetries

The connection with the genetic code emerges in the following manner.

1. The natural idea is that the faces of the icosa-tetrahedron correspond to both 3-chords and genetic DNA/RNA codons. If the orbits of faces could correspond to AAs (AAs), the DNA codon would code for AA AA if the corresponding face is at the orbit corresponding to AA.

2. One wants 64 DNAs: Z_6,Z_4 ja Z_2 cycle give rise to 20+20+20 =60 DNa codons. Tetrahedron gives the remaining 4 codons.

3. Does one obtain a correct number of AAs? Do the numbers of faces at the orbits correspond to numbers of DNAs coding for the corresponding AA?

(a) Z_6 decomposes to 3 6-orbits and 1 2-orbit ()$3 \times 6 + 2 = 20$). There are 3 AAs coded by 6 DNAs. 2-orbit corresponds to AA coded by two DNAs.

(b) Z_4 decomposes to 5 4-orbits. There are 5 AAs coded by 4 codons.

(c) Z_2 corresponds to 10 2-orbits predicting 10 AAs coded by 2 codons.There would be 11 2-orbits altogether. There are 9 AAs coded by 2 codons.

Some kind of symmetry breaking is present as in the case of dark nucleon code. 2 AA doublets must split to singlets. If (ile,ile,ile,met) coded by UAX could correspond to (ile,ile) and (met,met) such that (met,met) is split to (ile,met). In absence of symmetry breaking one would have 11 doublets as predicted.

4. There are also 4 tetrahedral codons.

   There is (stop,stop) doublet (UAA, UAG) and (stop,trp) doublet (UGA,UGG). These doublets could correspond to the faces of the tetrahedron. Only one face would code for AA in the vertebrate code. Other faces would not have corresponding tRNA?

   For bacterial codes, the situation can be different. Pyl and sec appear as exotic AAs. Could (UAA,UAG) for code for (stop,pyl) and (UGA,UGG) for (sec,trp) instead of (stop,trp)? Orientation preserving rotations form a 12-element group having Z_2 and Z_3 as subgroups. For Z_2 the orbits consist of 2 vertices and for Z_3 of 3 vertices (face) and 1 vertex. Z_3 symmetry could correspond to trp as singlet and vertebrate stop codons as triplet. For bacterial pyl and sec Z_2 with symmetry breaking is suggestive.

8.3.3 Bioharmony, dark nucleon code, and icosa-tetrahedral code as a tessellation of H^3

Bioharmony model involves icosahedron and tetrahedron. This looks ugly unless there is some really deep reason for their emergence. One can also ask why not also octahedron having triangular faces.

Hyperbolic 3-space H^3 has interpretations as a mass shell of Minkowski space M^4 at the level of M^8 and as light-cone proper-time constant surface at the level of H. The 4-surface X^4 in M^8 contains mass shells of M^4 corresponding to the roots of the polynomial P defining X^4. Hence one expects that H^3 plays a key role in quantum TGD both discretized momentum as defining a cognitive representation with momenta, which are algebraic integers associated with extension of rationals defined by P. H^3 has infinite discrete subgroups of the Lorentz group analogous to discrete groups of translations in E^3 as isometries and H^3 allows an infinite number of tessellations (lattices). Perhaps the simplest tessellation is icosa-tetrahedral tessellation involving also octahedrons and thus all triangular Platonic solids. This tessellation could give rise to genetic code by induction of tessellation to 3-surfaces or lower-D objects such as linear biomolecules, and cell membranes [L122]. I do not however understand the mathematical details well enough but the following discussion is general.

Consider first the model for DDNA and DRNA allowing us to understand the connection between dark nucleon and dark photon realization of the genetic code physically.

1. The realization of DDNA/DRNA/DtRNA/DAA could correspond to a sequence of icosahedron-tetrahedron pairs at H^3 contained by the 4-surface $X^4 \subset M^8$ and its H images which is also H^3.

2. Each icosa-tetrahedron would contain a dark codon realized both as a face and dark nucleon triplet associated with it. The dark photon chord associated with the face must be the same as the codon defined by dark nucleon triplet. The dark nucleon triplets correspond to cyclotron frequency triplets, which in turn correspond to dark photon 3-chords associated with the Hamiltonian cycles.

3. The cyclotron frequencies are determined by magnetic fields at flux tubes so that Hamilton cycles must correspond to flux tube patterns. The simplest hypothesis is that the Hamilton cycle is a closed flux tube connecting all vertices of the icosahedron. Dark codon triplet

corresponds to a face. It does have 1 or 2 flux tube edges if the corresponding chord contains 1 or two quints and otherwise no flux tube edges. Therefore cyclotron frequencies cannot be always associated with the edges of the triangle.

The simplest option is that the Hamiltonian flux tube following the vertex at the cycle defines the cyclotron frequency associated with the vertex. The harmony depends on the orientation of the cycle and for 8-note scale roughly corresponds the transformation from major to minor. The variation of flux tube thickness implies frequency modulation crucial for communications.

The realization of the Hamilton cycle requires that the magnetic field strength along the cycle is scaled by factor 3/2 to give a Pythagorean quint cycle. For an evenly tempered quint scale the scaling is $2^{5/12}$.

4. An interesting question relates to the relation of DDNA strand and its conjugate. The change of the orientation of the Hamiltonian cycle changes the chord of the harmony. For the ordinary 8-note scale one can roughly say that major and minor chords are transformed to each other. The orientation reversal could correspond to time reversal. The fact that the orientations of two DNA strands are opposite suggests that DNA and conjugate DNA are related by the orientation reversal of the Hamiltonian cycle inducing the map $G \to C$, $U \to A$ a the level of DNA letters. The conjugation does not imply any obvious symmetry for the corresponding AAs as the inspection of the code table demonstrates.

How could the Hamiltonian cycle determine the DtRNA codons?

1. DRNA codons pair with 32 DtRNA codons and DtRNA codons pair with trNA codons in 1-to-many manner. Therefore DRNA-DtRNA pairing could be universal and 2-1, although not in a codon-wise manner. This pairing should be the same for both bioharmony and dark nucleont triplets.

2. The pairing by 3-resonances requires that DtRNA icosa-tetrahedron contains the DRNA codons, which pair with DtRNA codon. There would be 2 DRNA codons in DtRNA icosahedron for most DtrNA codons and 1 codon for DtRNA pairing with DAA corresponding to met and trp. The number 32 of DtRNA implies in the case of icosa-tetrahedral code that there are 10+10-10=30 icosahedral DtRNAs and only 2 tetrahedral DtRNAs so that two faces of tetrahedron cannot correspond to DtRNA codon so that corresponding DRNAs must serve as stop codons.

   One of the DtRNAs could correspond to trp. The second one would correspond to a stop codon in the vertebrate code: either the DtRNA codon is not present at all or or it does not pair with tRNA. TAG and TGA can code for pyl and sec in some bacterial versions of the code and in this case the corresponding dark DRNA codon would be represented at the DtRNA tetrahedron.

3. For bioharmony DDNA-DAA correspondence means that AAs correspond to orbits of the faces of icosahedron under the subgroup Z_6, Z_4, or Z_2 which could correspond to reflection or to a rotation by π.

   Since DRNA-DtRNA correspondence is 2-1 although not codon-wise, the natural first guess is that Z_2 orbits of the faces define the DRNA codons at the DtRNA icosahedron so that it would contain 2 codons for most DtRNAs. At the DtRNA tetrahedron the only option is Z_1 so there is a symmetry breaking.

   If Z_2 corresponds to a reflection, the orbit always contains 2 codons. If Z_2 corresponds to a rotation by π, it might happen that the face invariant under π rotation and the orbit would consist of a single point. Could this explain why one has (ile,ile,ile,met) instead of (ile,ile) and (met,met)? The rotation axis should go through the invariant face and since the face is a triangle, π rotations lead out of the icosahedron. Therefore the answer is negative.

Ile-met problem deserves a separate discussion.

1. The pairing of Z_2 related DDRNA faces with two different DtRNAs coding for ile and met rather than two mets means Z_2 symmetry breaking at the level of bioharmony. Could the fact that AUG acts as a start codon relate to this? Could it be that both AUG and AUA cannot act as start codons? It is difficult to invent any reason for this.

2. The symmetry breaking could occur in DtRNA-DAA pairing and replace Dmet with Dile. Is it possible that the 3-chords for coding for ile and second met are nearly identical so that the resonance mechanism selects ile instead of met? Could the situation be similar for the codons coding for (stop,stop) and (stop,trp) and cause the coding of pyl or sec in some situations? The scale for the quint cycle model with octave equivalence does not quite close. Could this have some role in the problem?

3. Since similar ambivalence occurs for stop codons assigned to the tetrahedral Hamiltonian cycle, one can look at the tetrahedral Hamiltonian cycle. In this case one has 3-quint cycle and a given edge of the cycle corresponds to a scaling by $(3/2)^3$ so that 4 steps gives $(3/2)^{12}$, which is slightly more than 7 octaves. For the quint scale in Pythagorean sense, one obtains 4 notes in the same octave.

   Exact octave equivalence corresponding to equally tempered scale in which half-note corresponds to frequency scaling $2^{1/12}$, implies that there is only one 3-chord $CEG\sharp$: this would explain why there are 3 stop codons in the vertebrate code!

   The original guiding idea in the attempts to understand the fusion of icosahedral and tetrahedral codes was that the tetrahedron is effectively glued to the icosahedron along one face. This is consistent with the icosahedral quint cycle only if the common face contains no edges of the icosahedral cycle but contains tetrahedral flux edges with $(3/2)^3$ scaling. This would give strong constraints on the common face.

   If bacterial codes correspond to Pythagorean scale, there would be two different 3-chords since $CEG\sharp$ and $EG\sharp C$ are not quite the same. The reason is that the frequency ratios of chords are powers of $3/2)^{12}$. This situation is completely exceptional.

   In the quint scale there are small differences between the 4 chords. Could this explain why only one of these 3-chords codes for AA (trp) in vertebrate code and pyl or sec is coded instead of stop in bacterial codes? Amusingly, the chord $CEG\sharp$ ends many finnish tangos and therefore acts like a stop codon!

   Could bacteria have a perfect pitch and live in a Pythagorean world? Could the transition to multicellulars mean the emergence of an algebraic extension of rationals containing $2^{1/12} \simeq 1.059$(, which is considerably larger than to $(3/2)^{12}/2^7 \simeq 1.0136$)! Could people with perfect pitch have in their dark genome parts using Pythagorean scale or can they tune the magnetic flux tube radii to realize Pythagorean scale?

4. Could the ile-met problem have a similar solution? The chords associated with ile and met would differ by ascaling with $(3/2)^3$ or $(3/2)^6$ using octave equivalence. These chords are not quite the same: could it happen that the 3-chord associated with the second met is nearer to that for ile? These 3-chords do not contain quint scaling and should correspond to the special chords for which no edge belongs to a Hamiltonian cycle.

   Also DtRNA-DAA pairing is based on the 3-resonance.

1. DAA icosahedron must contain the DtRNA codons pairing with DAA. This raises the question whether DDNAs could have a direct resonant coupling to DAAs. Could this pairing occur in DDNA-DAA occurring in transcription (`https://cutt.ly/QPP46St`) so that pieces of DDNA and DAA associated with an enzyme involved could pair with each other by 3N-resonance at DDA-DAA level? At the chemical level the base-AA interactions are extremely complex involving stereochemistry and formation of hydrogen bonds (`https://cutt.ly/RPP7plM`) so that the reduction of these interactions to 3N-resonance would mean a huge simplification.

2. Could this resonance pairing serve as a universal mechanism of bio-catalysis and take place for various enzymes and ribozymes? One example are promoters and enhancers involved with

the transcription. Enhancers and promoters induce a highly non-local process generating a chromosome loop in which two portions of DNA become parallel and near to each other and dark 3N-photons could explain the non-locality as an outcome of quantum coherence in long scales.

3. Why would DDNA-DAA pairing not occur? 3N-resonance relies on cyclotron frequencies and therefore on the magnetic field strength determined by the radii of the monopole flux tubes. One explanation would be that the frequency scales of DAA and DDNA are slightly different. Could the attachment of DRNA to translation machinery scale the magnetic field strengths of the flux tubes and their cyclotron frequencies so that only dRNA-DtRNA and DtRNA-DAA couplings are possible.

8.4 Pythagorean number mysticism, music harmony, and genetic code

The discussion with Marko Manninen renewed my interest in the ideas of Pythagoras related to mystics and mathematics and its role in music.

8.4.1 Rational Platonia

Pythagoras believed that rationals are all that is needed for a Universe and for him the discovery of $\sqrt{2}$ represented geometrically by the diagonal of a unit square was probably a shock.

It is interesting that in the TGD framework the rationals appear naturally. In its simplest form, Galois confinement [L133, L134] states that the total 4-momenta of physical states are Galois singlets invariant under Galois group permuting roots of a given polynomial (the notion generalizes if one considers functions in momentum space). This would allow only momenta with components, which are integers when a physical natural momentum unit is used. Platon would have been right in a certain sense!

However, Galois singlets would at fundamental level consist of quarks (in particular leptons and bosons would do so) having 4-momenta with components, which are algebraic integers in the extension of rationals defined by the polynomial defining the space-time region considered [L101, L102]. One could regard the algebraic integer valued momenta as virtual momenta characterizing the building bricks of physical states.

8.4.2 Special role of primes 2, 3 and 5

The number mysticism of Pythagoras involves the idea that the numbers 2 and 3 are very special. Using the language of modern number theory, one could say numbers 2 and 3 span a group with respect to multiplication consisting of numbers $2^m 3^n$, where m and n are integers. One could call this group $B(2,3)$. If m and n are restricted to non-negative integers, the inverses do not exist and only a semigroup is obtained. This object could be called $A(2,3)$.

If Pythagoras identified rational numbers as a kind of Platonia, this group might be said to define an important province of Platonia. A more general object would be ideal consisting of all integers proportional to, say, $6 = 2 \times 3$ closed with respect to multiplication by any integer.

It should be noticed that any set $(p_1, ..., p_n)$ of primes and even integers defines a group with respect to multiplication as the group $B(m_1, m_2, ..., m_n)$ of integers. Especially interesting example is the group $B(2,3,5)$ containing $B(2,3)$ and $B(3/2)$.

p-Adic length scale hypothesis states that powers of small primes near to prime define important p-adic length scales. Powers of 2 are of special importance in p-adic mass calculations [K55] but there exists also evidence for powers of 3 [I61, I62].

Decimal system is the decimal system used in everyday life and very often numerologists freely change the position of a decimal number and get results, which make sense only if the decimal system is in a special role. Could this be the case? If so, then the decimal system would not reflect only the fact that we have 10 fingers, and also the algebras $B(2,5)$ and $B(10)$ could be special.

There are some indications that this might be the case.

1. The faces of icosahedron *resp.* dodecahedron are triangles *resp.* pentagons so that numbers of 3 and 5 are natural.

2. DNA is a helical structure with a twist angle $2\pi/10$ between to codons so that 10 codons make a 6π twist and define length scale 10 nm which is the p-adic length scale associated with Gaussian Mersenne prime $M_{G,151} = (1+i)^{151} - 1$, one of the 4 Gaussian Mersennes defining p-adic length scales in the range 10 nm, 2.5 μm. These scales are a number theoretic miracle. Numbers 2,3, and 5 relate to the geometry of DNA.

8.4.3 Pythagorean scale

Pythagoras also studied music and introduced the notion of Pythagorean scale for which the frequencies of notes are in rational ratios. A standard manner to realized this scale is by quint cycle, which means that one forms the multiples $(3/2)^n f_0$ of fundamental frequency f_0 and identifies them by octave equivalence with a frequency in the basic octave $[f_0, 2f_0]$. The quint cycle appears very often in jazz.

For $n = 12$ the frequency obtained is almost a full number of octaves but quite not. This imperfectness of Platonia troubled Pythagoras a lot. In an equal tempered scale one introduces powers $2^{m/2n} f_0$ and avoids this problem. This means replacement of rationals by its algebraic extension generated by $2^{1/12}$.

Obviously, the Pythagorean scale is very natural in the framework of group $B(3/2)$. Pythagoras also had ideas about the relationship of music scale and Platonic solids.

8.4.4 Pythagorean scale and genetic code

In the TGD framework, the idea about a possible connection between music and Platonic solids inspired the proposal about realization of the 12-note scale as a Hamiltonian cycle at icosahedron. The Hamiltonian cycle is a closed curve connecting only neighboring points of the icosahedron and going through all its 12 vertices. There are quite a large number of icosahedral cycles and they assign to the 20 triangles of icosahedron 3-chords proposed to define icosahedral harmony with 20 chords. The non-chaotic icosahedral cycles have symmetry groups Z_6, Z_4, and Z_2, which can act as a rotation or reflection.

The big surprise was that the model of icosahedral harmony leads to a model of genetic code. The code would involve a fusion of 3 different icosahedral harmonies with symmetry groups Z_6, Z_4, and Z_2 giving 60 codons plus tetrahedral code giving 4 codons. The counterparts of amino-acids would correspond to the orbits of these symmetry groups: 3 orbits with 6 triangles and 1 with 2 triangles as orbits for Z_6, 4 orbits with 4 triangles for Z_4 and 10 orbits with 2 triangles for Z_2. The number of triangles at the orbit is the number of DNA codons. Tetrahedron would give the missing 4 codons and stop codons and one missing amino acid.

For a given choice of the 3 Hamiltonian cycles, the realization would be in terms of 3-chords of light defining harmony for a music of light (and possibly also sound). Since music expresses and generates emotions, the proposal was that this realization of the genetic code expresses emotions already at the molecular level and that emotional intelligence corresponds to this realization whereas bit intelligence would correspond to the interpretation of codons as 6-bit sequences.

It should be mentioned that Hamiltonian cycles are solutions to the travelling salesman problem at the icosahedron: cities would correspond to the vertices. In the case of dodecahedron, which is dual of icosahedron, there is only one Hamiltonian cycle so that the harmony is now unique. If this corresponds to harmony, the first guess is that there would be a 20-note scale and 12 5-chords.

8.4.5 What about dodecahedral harmony and analog of genetic code?

Could also dodecahedron define a bioharmony and an analog of genetic code?

1. The first guess is that dodecahedral harmony has 20 notes per octave and perhaps corresponds to the scale defined by micro-octaves used in Eastern music. There would be 12

5-chords and the harmony would be unique. There would exist only a single emotional mood, a kind of enlightened state.

2. Since the harmony is unique, and there are no other Platonic solids with pentagons as faces. The analog of genetic code should correspond to dodecahedral harmony. The 5-chords would define 12 analogs of DNA codons.

   The dodecahedral cycle Z_3 acts as a symmetry group (`https://jrh794.wordpress.com/2021/04/01/the-original-hamiltonian-cycle-continued/`). This means that there are 4 orbits of Z_3 with 3 codons at each and they would correspond to 4 different analogs of amino-acids.

3. Could one consider instead of an icosahedral quint cycle with scaling 3/2 replaced with scaling 5/2? The tempered system would use powers of $2^{1/20}$ to generate a 20-note scale. A single step along Hamilton's cycle connecting neighboring vertices of dodecahedron would correspond to a scaling $f \to 5/2f$ plus octave equivalence.

   By octave equivalence the scaling b y 5/2 would correspond to a transition from say C to a note between E_b and E. The microintervals between this note and either $E\flat$ or E appears in blues, jazz etc as a blue note. This interval is between minor and major.

4. One can test this. The cold shower is that $(5/2)^{20}$ is not near to a power of 2. However, one has $(5/2)^{19}/2^{25} = 1.084$ (for the quint cycle in the icosahedral case the deviation that Platon was worried of, is about 1 percent). As if one had a 19-note scale. A completely analogous situation is encountered with bio-harmony. The scales assigned to Z_6, Z_4, and Z_2 give rise to 19 amino-acids as orbits of these groups. One amino-acid is missing and the tetrahedral code gives this amino-acid plus 3 stop codons [L143].

   The icosa-dodecahedral duality suggests that the scale should consist of 19 notes only. Note however that for an equal tempered variant of the scale one does not have this problem.

5. Dodecahedral code predicts 4 analogs of amino acids. Could these "amino acids" correspond to the 4 DNA codons? 3 dodecahedral codons would be needed to code for a single genetic codon.

   Could he dodecahedral codons, which correspond to 5-chords, be realized as dark 5-photons and sequences of dark 5-protons. One should check whether the states of 5 dark protons could give rise to 12 dark dodecahedral codons and whether something analogous to 12 dark RNA codons, dark tRNA codons, and 4 dark amino acids could emerge.

   For the dodecahedral bioharmony, 5-chords would label the codons and they would serve as addresses based on communications relying on cyclotron resonance. Icosahedral harmony would control codons and dodecahedral harmony would code for their letters so that the codes would appear in different scales.

This speculation raises some questions. One can argue that in the transcription and replication the control of both codons and individual letters is important. This suggests that both realizations are needed for both DNA strands and correspond to different control scales. This would be true for the transcribed DNA, at least.

One can however consider alternatives. For instance, could the passive DNA strand correspond to a dodecahedral realization at the level of letters and the active strand to the icosahedral realization at the level of codons. Or could "junk" DNA and introns in promoter regions correspond to the dodecahedral realization with dark dodecahedral DNA controlling single letters.

Chapter 9

Horizontal Gene Transfer by Remote Replication?

9.1 Introduction

This article was inspired by a Quantamagazine article "DNA Jumps Between Animal Species. No One Knows How Often" (`https://cutt.ly/7UKasRp`), which described the findings of Laurie Graham and Pete Davies published in the article "Horizontal Gene Transfer in Vertebrates: A Fishy Tale" in Trends in Genetics [I25] (`https://cutt.ly/SUKamqP`).

1. Marine life around the Arctic and Antarctica has evolved many defense mechanisms against the lethal cold. One common adaptation is the ability to make anti-freezing proteins (AFPs) that prevent ice crystals from growing in blood, tissues and cells. This solution has emerged repeatedly and independently, not just in fish but in plants, fungi and bacteria. AFPs make possible survival at water temperature, which is by 1 degree C colder than the *unprotected* freezing point of fish blood and this offers an evolutionary advantage.

   Remark: TGD based general mechanisms possibly associated with heat and cold shock, involving zero energy ontology (ZEO) [L92] [K93] in an essential way, have been considered in the model for the effects of various shock proteins in [L162]. The key idea is that the macroscopic counterparts of ordinary state function reduction changing the direction of time change the arrow of time at the level of the magnetic body of the system so that, from the point of view of observer with the standard arrow of time, the system seems to extract energy from the environment instead of dissipating it.

2. Herrings and smelts are two groups of fish, which have learned to make AFP. The story began when Graham discovered that smelt had a protein gene very similar to one of the AFG genes of herring. The gene's introns, stretches of non-coding DNA involved also with TEs, which in general mutate rather fast, are more than 95 % identical. That both have exactly the same gene coding for AFP proteins, is surprising since their ancestors diverged more than 250 million years ago and the AFP gene is absent from all species relating to them. Somehow the AFP gene must have found its way to the genome of smelt.

3. Cross breeding of herring and smelt is not possible so that direct horizontal gene transfer (HGT) should have occurred. HGT is known to be possible between prokaryotes (mono-cellulars) and also between prokaryotes and eukaryotes (multi-cellulars). Herring and smelt are not rare exceptions: recent studies demonstrate that HGT occurs also in other fish, reptiles, birds and mammals.

4. However, the belief has been that HGT is not possible for eukaryotes (multicellulars) and there are several good arguments in favor of this belief. In the case of bacteria, it is enough for the gene to get through the cell membrane since there is no nucleus and HGT occurs quite generally. The DNA of eukaryotic cells is however isolated inside the nuclei and most of the time the DNA is tightly bound in chromosomes. Gene should also find its way to germ

cells in order to have a lasting effect. The transferred gene of the donor should also integrate to the genome of the host.

5. In 2019, the full genome of herring was published. It turned out that the genome contains several AFP genes with associated transposable elements (TEs). The herring genome contains several copies of these TEs but they are absent from other fish with a single exception: the genome of smelt contains only a single AFP gene and this gene with similar transposable elements occurs also in the genome of herring. Therefore there is little doubt that the HGT has taken place.

   Somehow HGT must be possible.

1. 94 % HGTs occur between fishes and only 3 per percent between birds and mammals. Therefore the water environment must be part of the explanation.

2. What comes first in mind is spawning. In a situation in which one has sperms and eggs in water, germ cells which are effectively monocellulars apart from the presence of cell nuclei. Most of the cells degrade and could produce fragments of DNA, say TE+AFP gene.

   If the spawning of two species occurs at the same time at the same location, HGT might have taken place from the sperm or egg cells of herring or of their degradation products to the sperm cells of smelt. These would have naturally found their way to the eggs of smelt. The amount of spawn in the sea water is so high that it changes the color of water white: this would increase the probability of HGT.

3. Maybe the AFP gene of herring has somehow attached to the DNA of the smelt sperm cells during spawning. Sperm mediated gene transfer is indeed a standard technique of genetic engineering. The challenge is to understand how the AFP genes were transported from herring cells to the smelt sperm cells. AFP gene is not able to make the travel between cells alone. In standard biology, some vector should have transported the gene between the two cells and one can make only guesses about the mechanism.

9.1.1 The notions of transposon and horizontal gene transfer

The notions of transposon or transposable element (TE) and horizontal gene transfer (HGT) will be needed in the sequel.

Transposons

Transposable elements or simply transposons (TEs) (`https://cutt.ly/HUZIItW`) were discovered by Barbara McClintock. TEs are jumping genes, which involve introns were once regarded as "junk". The basic operation is cut and paste operation.

TEs are now known to have several important functions: they make the genome dynamic and affect its identity and size, induce mutations or their reversals, and can also lead to a duplication of pieces of the genome. TEs are also involved with the control of gene expression and epigenesis (amusingly, they are still regarded as selfish genes!).

TEs are abundant in eukaryotic cells. TEs make approximately 64 % of the maize genome, 44 % of the human genome, and almost half of the mouse genome.

TEs serve as a kind of text editing tool. The TE (`https://cutt.ly/HUZIItW`) consists of inverted repeats (TEs in my terminology) at its beginning and end, and the structural genes between them.

There are at least two kinds of TEs: class I and class II. In the human genome 98 per cent of TEs class I and the rest are of type II.

1. Class I TEs or retrotransposons are first transcribed to RNA, and reverse transcriptase often encoded by the TE itself catalyzes the reverse transcription of RNA to DNA, which is then pasted to DNA sequence. The text processing analog is copy and paste.

   Retrotransposons are classified into 3 types:

- Retrotransposons with long terminal repeats (LTRs), which encode reverse transcriptase producing DNA from the RNA transcribed from TE, which is then glued to a DNA. Retrotransposons are similar to retroviruses.

- Retroposons, long interspersed nuclear elements (LINEs). Also they encode reverse transcriptase but lack LTRs and are transcribed by DNA polymerase II to RNA.

- Short interspersed nuclear elements (SINEs) do not encode reverse transcriptase and are transcribed by DNA polymerase II.

Also retroviruses can be regarded as TEs. They can transfer genes between eukaryotic target and host cell. The integrated gene in the host cell is called produces and this transfer can be seen as an eukaryotic analog of the transfer of bacterial TEs.

2. Class II TEs or DNA transposons encode for protein transposase, which they require for excision and insertion. No intermediate RNA is produced. The text processing analog is cut and paste.

   The figure `https://en.wikipedia.org/wiki/File:DNA_Transposon.png` of the Wikipedia article illustrates the situation. The structure of TE is : TSD+TIR+gene+TIR+TSD. Two inverted tandem repeats (TIR) flank the transposase gene. Two tandem site duplications (TSD) are present on both sides of the insert.

   Transposase makes a staggered cut at the target site with sticky ends and the complex TIR+gene+TIR is transferred to the new site. Gene itself is not duplicated as in the copy and paste process for retrotransposons. TSDs are left at the target site. DNA polymerase fills in the gaps at the target site leading gradually to long repeating sequences. The insertion sites can be identified by short direct repeats followed by inverted TIRs.

3. TEs can also replicate.

TEs can be also classified as autonomous and non-autonomous. Autonomous TEs can move by themselves whereas non-autonomous TEs require other TEs to move.

Horizontal gene transfer

Horizontal gene transfer (HGT) (`https://cutt.ly/zUKTED5`) occurs mostly in prokaryotes but also in some eukaryotes. HGT tends to occur in extreme environments.

Diatoms and algae have received genes from bacteria. For eukaryotes HGT to germ cells is required, which makes the process difficult to realize. Donor and host tend to be closely associated organisms. HGT from bacteria to chordates occurred shortly after this lineage arose.

There are several mechanisms of bacterial HGT.

1. Transformation involves three steps: introduction, uptake and expression.

2. Transduction: DNA is transferred by virus

3. Bacterial conjugation. DNA is transformed in cell-to-cell contact.

4. Gene transfer agents are viruslike elements coded by the host.

Transposable elements (TE) are often involved with HGT. One speaks of the transfer of horizontal TE (HTT). TE transfer occurs also for eukaryotes. This suggests that TEs, which distinguish between prokaryotes and eukaryotes, involve a new transfer mechanism. The mechanism of TE transportation requiring a vector carrying the TE, has not been identified and this allows us to wonder whether only information could be transferred?

9.1.2 General constraints on the model

Consider first general constraints on the model.

1. For eukaryotes, cell and nuclear membranes make HGT difficult if not impossible. The transfer should also occur to germ cells.

2. Water must be essential since in other species than fish the process is much rarer.

3. Sperm cells are analogous to monocellulars, and the HGT occurs for monocellulars. Note however that sperm cells and eggs have a nucleus and chromosomes, which are obstacles for HGT.

4. That HGT would occur during spawning looks a highly plausible hypothesis. This increases the probability of HGT, whatever the mechanism is. Sperm mediated transfer would allow to overcome the basic obstacles and the basic properties of TEs involved would make possible the integration to the host genome.

5. Most of the cells and their DNA degrades during the spawning and the resulting DNA fragments would also contain AFG+TE, which could be transferred to the smelt sperm cells.

How the TE involving the AFG from the sperm of herring could be transported to the sperm of smelt? This is not known.

According to Wikipedia:

Though the actual mechanism for the transportation of TEs from donor cells to host cells is unknown, it is established that naked DNA and RNA can circulate in bodily fluids. Many proposed vectors include arthropods, viruses, freshwater snails, endosymbiotic bacteria and intracellular parasitic bacteria. In some cases, even TEs facilitate the transport for other TEs.

This justifies a heretic question. Could it be only the genetic information, which is transferred and used to construct DNA in the host as a kind of remote replication analogous to quantum transportation?

9.2 Some key ideas of TGD inspired quantum biology

In this section basic notions of TGD inspired quantum biology relevant to the recent article are discussed. The ideas discussed the notion of magnetic body (MB) as a controller of ordinary matter; the hierarchy of effective Planck constants assigned to the hierarchy of extensions of rationals defining a hierarchy of phases of ordinary matter behaving like dark matter; Galois confinement as a universal mechanism for the formation of bound states; dark realizations of genetic code; communications and control in TGD inspired quantum biology. Zero energy ontology (ZEO) [L92] [K93] plays a central role in TGD inspired quantum biology but is not discussed in the sequel.

9.2.1 MB carrying dark matter as controller of ordinary biomatter

MB contains dark matter identified, as phases of ordinary matter characterized by EQ with a dimension $n = h_{eff}/h_0$ serving as a measure of the algebraic complexity of a given space-time region [L112, L113], and interpreted as a universal IQ. The scales of quantum coherence increase with h_{eff}. The layers of MB characterized by the value of n naturally form a master-slave hierarchy in which ordinary matter with the smallest Planck constant is at the bottom, and controlled by higher levels. The energies of systems increase with h_{eff} and since h_{eff} tends to be spontaneously reduced, an energy feed is needed to preserve the distribution of h_{eff}: the interpretation is as an analog of a metabolic energy feed.

MB acts as a "boss" controlling ordinary matter and induces self-organization [L87].

Anatomy of MB

MB has, as its body parts, magnetic flux quanta: flux tubes and flux sheets. There are two kinds of flux quanta. Flux can be vanishing, which corresponds to a Maxwellian regime. Flux can also be non-vanishing and quantized corresponding to a monopole flux. In the monopole case, the

magnetic field requires no current for its creation. This option is not possible in the Maxwellian world. By fractality of the TGD Universe, these flux tubes play a key role at all scales [L80].

Also the Earth's magnetic field with nominal value of $B_E = .5$ Gauss has two parts.

1. The monopole flux part corresponds to the "endogenous" magnetic field $B_{end} = .2$ Gauss and explains the strange effects of ELF EM radiation on the physiology and behavior of vertebrates [J6].

   The presence of this part explains the stability of the Earth's magnetic field. This field should have decayed long ago in a Maxwellian world since it is generated by currents which disappear.The contribution of the molten iron in the Earth's core to B_E decays but the changes of the orientation of B_{end} regenerate it [L24]. Also, magnetic fields that penetrate super-conductors as quantized fluxes and even those of permanent magnets (as opposed to electromagnets) may have a monopole part consisting of flux quanta.

2. The interaction of MB with the gravitational field of Earth is discussed in [L130]. Intriguingly, the metabolic energy currency with the nominal value of .5 eV is rather close to the energy for the escape velocity of a proton. Could the transfer of ions from the surface of the Earth to MB be a standard process?

Communications to and control by MB

Communication from the biological body (BB) to MB and its control by MB would rely on dark photons, which can transform to ordinary photons with a large h_{eff} and vice versa. Molecular transitions would represent one form of control.

1. Cell membranes could act as generalized Josephson junctions generating dark Josephson radiation with energies given by the sum $E_J + \Delta E_c$ of ordinary Josephson energy E_J and the difference ΔE_c of cyclotron energies for flux tubes at the two sides of the membrane. The variation of the membrane potential modulates the Josephson frequency and codes the sensory information at the cell membrane to a dark photon signal sent to MB.

2. The large effects of radiation at ELF frequencies observed by Blackman and others [J6] could be understood in terms of the cyclotron transitions in $B_{end} = .2$ Gauss if "h" in $E = hf$ is replaced with h_{eff}. h_{eff} should be rather large and possibly assignable to the gravitational flux tubes with $\hbar_{eff} = \hbar_{gr} = GMm/v_0$. For the simplest model, M represents the Earth's mass coupling to the small mass m, and v_0 is a parameter with dimensions of velocity expected to have discrete spectrum. The energies $E = h_{eff}f$ of dark photons should be in the biophoton energy range (visible and UV) characterizing molecular transitions [K13, K18].

3. For the value $v_0/c \simeq 2^{-11}$, suggested by the Nottale's model for planetary orbits [E1], the predicted cyclotron energy scale is 3 orders of magnitude higher than the energy scale of visible photons. Several solutions of this problem were considered [L129]. The most plausible solution [L129, L120] is $\beta_0 = v_0/c = 1/2$ for living matter so that gravitational Compton length $\Lambda_{gr} = GM/\beta_0$ equals to Schwartschild radius at the surface of Earth. and brings nothing new to the original Nottale hypothesis.

By its higher level of "IQ", MB would naturally be the master controlling BB by cyclotron radiation - possibly via a genome accompanied by dark genome at flux tubes parallel to the DNA strands.

1. Cyclotron Bose-Einstein condensates (BECs) of bosonic ions, Cooper pairs of fermionic ions, and Cooper pairs of protons and electrons would appear as dark matter in living systems and the $h_{eff} = h_{gr}$ hypothesis predicts a universal cyclotron energy spectrum in the range of bio-photon energies.

2. Dark photons may transform to bio-photons [L9, L8] with energies covering the visible and UV energies associated with the transitions of bio-molecules. This control of biomolecules implies that remote mental interactions are routine in living matter. EEG signals would represent a particular instance of these communications: without the presence of MB it is difficult to understand why the brain would use such large amounts of energy to send signals to outer space.

3. In ZEO, the field body (FB) and MB correspond to 4-D rather than 3-D field patterns and quantum states correspond to quantum counterparts of behaviors and biological functions. Conscious holograms could be generated as a result of interference of a dark photon reference beam from MB and a dark photon beam carrying the sensory information. This hologram would be read by MB using the conjugate of the reference beam.

   In ZEO time reversals of these processes also take place. This makes it possible to understand memory as a result of communications with memory mental images.

9.2.2 Galois confinement

Galois confinement is a universal number theoretical mechanism for the formation of all bound states [L128, L127]. Galois confinement emerged originally in TGD inspired quantum biology but has become a central theme of also the TGD view about condensed matter. Galois confinement provides a purely number-theoretic mechanism for the formation of hierarchies of bound states.

1. Galois confinement involves $M^8 - H$ duality and requires $h_{eff} > nh_0 > h$. M^8 has an interpretation as an analog of momentum space and the points of $X^4 \subset M^8$ assignable to polynomial P with rational coefficients have interpretation as 4-momentum. Monic polynomials P are physically especially interesting [L116]. P defines an algebraic extension of rationals with dimension $n = h_{eff}/h_0$. The physical interpretation is as a hierarchy of phases of ordinary matter with an increasing value of effective Planck constant behaving like dark matter.

2. The roots r_n of P correspond to 3-D mass shells $m^2 = r_n$ in fixed $M^4 \subset M^8$ and X^4 itself contains these mass shells and is determined as a deformation of M^4 which corresponds to an element of local group $SU(3) \subset G_2$, where G_2 is automorphism group of M_c^8 having interpretation as complexified octonions. The condition that $U(2) \subset SU(3)$ leaves the point $g(x)$ invariant implies that one has local CP_2 element defining the $M^8 - H$ duality.$SU(3)$ corresponds to color group physically.

3. Quark states as solutions of algebraic octonionic Dirac equation (all equations are algebraic at M^8 side of $M^8 - H$ duality while everything is differential geometric at H side) correspond to points of M^8 assume to correspond to algebraic integers in the extensions of rationals defined by P so that the points carrying quark define what I have called cognitive representation playing a key role in adelic physics [L50, L51]. For instance, p-adic variants of the cognitive representations make sense.

4. Periodic boundary conditions allow only many-quark states assignable to mass shells for which the total M^4 momentum is an ordinary integer (in suitable units defined by the size scale of CD considered) are possible [L128, L127]. This is the simplest realization of Galois singlet property/confinement. The integer valued total momenta emerge also in the twistorial construction of scattering amplitudes [L116]. This is the simplest realization of Galois singlet property/confinement.

5. This gives rise to an infinite hierarchy of bound states. One can also consider composite polynomials and if they vanish at origin, the roots of composite polynomials contain also the roots of the functional factors of the composite. This is analogous to conservation of genes. All kinds of states: nucleons, nuclei, photons, etc... , can form Galois bound states. It is enough that one deforms the states so that they are not Galois singlets with the original Galois group or to increase the extension so that they are not Galois singlets in the larger extension. From these kinds of states one can form Galois singlets.

9.2.3 Dark realizations of genetic code

The model of bio-harmony [L11] [L78, L107, L121, L122] is essential for the TGD based understanding of what might be called emotional intelligence (whose reality is accepted) and its relations with ordinary intelligence. The surprising outcomes are the connection with genetic code and the key role of bioharmony in quantum information processing in living matter.

1. The notion of bioharmony relies on icosahedral and tetrahedral geometries. The representation of the 12-note scale as a sequence of quints, reduced by an octave equivalence (notes differing by octave are experienced as equivalent) to the basic octave, defines the harmony for a given Hamiltonian cycle: the 20 allowed 3-chords of the icosahedral harmony correspond to the 20 triangular faces. The symmetries of the harmony are defined by some subgroup (Z_6,Z_4, or Z_2) of the icosahedral group.

2. Genetic codons correspond to dark photon triplets (3-chords of light) defined by the triangular faces of an icosahedron and tetrahedron. The counterparts of amino-acids are identified as orbits of 3-chords under the symmetries of a given harmony.

   Any combination of 3 icosahedral harmonies with 20 chords with symmetries Z_6, Z_4 and Z_2 and of the tetrahedral harmony with 4 chords gives a particular bioharmony with 20+20+20+4=64 chords assignable to DNA codons. DNA codons coding for a given amino acid correspond to the chords at the orbit of the symmetry group. Rather remarkably, the numbers of DNA codons coding for a given amino acid come out correctly.

3. Music expresses and creates emotions. Musical harmony codes for moods and emotions as holistic aspects of music. Bio-harmony with 64 3-chords, would assign the binary, local, aspects of information to the 6 bits of the codon and its holistic, emotional aspects to the bio-harmony. A chemical representation of the genetic code can thus correspond to several moods represented by bioharmony. In contrast with physicalism, emotions would appear already at the molecular level, and would have physical effects that are not reducible to bio-chemistry. This understanding is not possible without using the notion of MB.

   The model of bio-harmony requires that the values of B_{end} correspond to those associated with the Pythagorean scale definable by the quint cycle. These frequencies correspond to energies that a molecule must have in order to serve as a basic biomolecule. This criterion could select DNA, RNA, tRNA, and amino-acids.

In the second model of genetic code [L58, L27, L78], codons are represented as dark proton triplets assignable to flux tubes parallel to DNA strands.

1. The numbers of dark proton triplets turn out to correspond to numbers of DNA, RNA, tRNA codons, and amino acids. The numbers of DNA and RNA codons assignable to a given amino-acid in the vertebrate genetic code are correctly predicted. Genes would correspond to sequences of dark proton triplets [L98].

2. Dark proton triplet - dark codon - would be analogous to baryon and Galois confinement [L111] behaving like a single quantum unit. The N dark codons of a dark gene would, in turn, bind to Galois confined states of the Galois group of an EQ associated with the sequence of codons. An entire hierarchy of confinements is possible.

3. Galois confinement can be realized also for dark photon triplets and the sequences of N dark-photon triplets representing genes as dark $3N$-photon states. Genes could serve as addresses for communications based on dark $3N$-photon resonances.

   For communications between levels with the same value of h_{eff} there would be both energy and frequency resonance and for levels with different values of h_{eff} only the energy resonance. It is an open question whether dark $3N$-photons transform to a single ordinary photon or $3N$ ordinary photons (biophotons) in dark-ordinary communications.

4. The basic hypothesis is that both DNA, RNA, tRNA, and amino acids are paired with their dark analogs, and that energy resonance mediates the interaction between the members of pairs.

How could the icosahedra and tetrahedra be realized? Why must one glue them together? This looks aesthetically unappealing. However, surprisingly, both icosahedrons and tetrahedrons appear in, perhaps the simplest honeycomb of the hyperbolic 3-space H^3 (cosmic time = constant hyperboloid). H^3 is also central to special relativity and cosmology [L122]. Dark genetic code can be realized in terms of both dark protons and photons using this particular tessellation and would

be universal. This master tessellation would induce sub-tessellations at the space-time surface, in particular representations of genetic code at magnetic flux tubes. Also 2-D and even 3-D representations of genetic code can be considered (i.e. cell membrane and microtubules) [L124].

9.2.4 Communication and control in living matter

The TGD inspired model for bioharmony suggests a universal communication and control mechanism based on frequency modulation of dark photon radiation and its resonant receival producing a sequence of pulses. The signal sent by the DNA sequence would be resonantly received by a similar DNA sequence as a temporal sequence of resonance peaks determined by the modulation.

An interesting hypothesis is that nerve pulse patterns are basically produced by this mechanism transforming membrane potential oscillations producing Josephson radiation sent to MB and producing pulse sequences initiating nerve pulse pattern at the level of cell membrane.

U-shaped flux tubes serve as the basic tools of communication. Their reconnection replaces U-shaped flux tubes with pairs of flux tubes between two objects and occurs when a resonant dark photon communication between objects is possible. This requires the same cyclotron energy implying identical cyclotron frequencies if the values of h_{eff} are the same: this implies the value of magnetic field and by flux quantization the same thickness of flux tubes.

Galois confinement allows a generalization replacing U-shaped flux tubes with N-flux tubes along which dark N-photons can propagate and to replace dark photon resonance with M-resonance. This communication and control mechanism would be realized at the level of DNA and other biomolecules. The generalization of the notion of genetic code allowing higher dimensional realization of DNA generalizes this communication mechanism further.

Some applications

The proposed general model of communications and control has an impressive number of applications to living matter.

1. The model of water memory involves dark DNA [K41] [L5, L12] assignable to the ordinary DNA and also the dark variants of other biomolecules can be involved. The MBs of water clusters can vary the thickness of their U-shaped flux tubes and therefore their cyclotron frequencies. This makes possible recognition of bio-active molecules with MB involving flux tubes with cyclotron frequencies shared by living matter. When the U-shaped flux tube meets a similar flux tube of a bio-active molecule, reconnection takes place and if it leads to dark photon resonance, a long-lived flux tube pair is formed. The bioactive molecule is "caught".

2. The MB of water clusters can mimic the MBs of invader molecules and this could give justification for the claimed homeopathic effects. Resonant reconnection could be behind water memory, immune system, the claim about homeopathic healing [K41], and the biocatalysis involving the mysterious looking ability of reactants to find each other in dense molecular soup.

3. The most general option is that every polar molecule in living matter is accompanied by a dark nucleon sequence or several of them (as in the case of amino-acids) serving as its "name"". This would also associate a unique dark nucleon sequence with the MB of DNA so that DNA-dark DNA association would be automatic. The same applies to mRNA and tRNA and amino-acids.

The model for the communications also leads to a model for the emergence of language [L163, L164]. Amazingly, only a few point mutations for relatively few genes seem to have led to human languages and transformed biological evolution to cultural evolution? What happened to these genes? In the biochemistry framework it is difficult to imagine an answer to this question. Here TGD could come to the rescue.

One can assign a value of h_{eff} characterizing the evolutionary level also to genes. The genes with larger h_{eff} would serve as control genes and the increase of h_{eff} would mean an evolutionary step. Perhaps a dramatic increase of h_{eff} occurred to FOXP2 and some other genes as human language emerged.

The fundamental language would be defined by genetic code realized in terms of dark $3N$-photons and h_{eff} as a measure of algebraic complexity and a universal "IQ" would characterize the realizations of this language.

What is the role of introns and TEs?

Interesting questions relate to the role of introns and transposons (TEs), which involve introns besides genes.

1. Introns do not express themselves as proteins and their fraction is highest in humans so that the interpretation as junk DNA does not look realistic. TGD inspired quantum biology motivates the proposal that the dark genes could express themselves electromagnetically and that remote replication (and the remote variants of transcription and even translation) could rely on this. This leads to a general model for communications and control.

2. The simplest assumption is that all DNA related structures and also RNA proteins and tRNA, can "talk" by applying these communication mechanisms.

   The difference between TEs and genes not belonging to TEs brings to mind the difference between animals and plants. TEs can move and actively control their environment. TEs are also involved with epigenesis, that is control of gene expression, and modifications of genes.

   Animals and plants differ also in that animals have a nervous system. Could also TEs and ordinary genes have an analogous difference? Animals are thought to represent a level of evolution higher than plants. Could this be true also for TEs? A higher value of h_{eff} for the MBs of TEs would concretize this idea. Nervous system in TGD inspired quantum biology means communications to MB by Josephson radiation. Could one think something like this also now?

   The relation of TEs to genes looks like the relation of a programmer to the program modules of a software. This suggests that the MBs of TEs represent a higher level in the h_{eff} hierarchy than the MBs of genes. The higher value of h_{eff} means also a longer scale of quantum coherence so that TEs might be involved also between communications of even different organisms of the same species.

9.3 Is remote replication of DNA involved with HGT?

In remote replication only the information about TE would be transferred and one would have a biological analog of teleportation.

9.3.1 Is replication of the magnetic body behind biological replication?

The vision [L15] about exclusion zone (EZ) like regions discovered by Gerald Pollack [I53, L15, I89, I76] as primordial life forms and facts about water memory and homeopathy [K41] lead to a vision about how a primitive immune system might have developed and how the recent genetic code might have emerged.

Magnetic bodies and dark analogs of bio-polymers should still play a key role in living matter. The basic idea is that the time evolution of the MB is the template for the time evolution of the biological body. In [K64] [L13] various pieces of evidence for the role of the MB as "morphogenetic field" is discussed. For instance, the replication of DNA and cell would reduce basically to that for corresponding magnetic bodies.

Replication of the MB is analogous to what happens in the 3-vertex of a Feynman diagram. This occurs on several scales. This would make possible dark DNA (dDNA) replication and copying of dDNA to dDNA+dRNA as well as copying of dRNA to dRNA+dark protein.

Replication process should start from the higher levels of dark matter hierarchy and proceed to shorter scales. The basic constraint from ZEO is that the time evolutions of magnetic bodies at various levels of the hierarchy are highly unique as preferred extremals connecting initial and final 3-surfaces. For the maxima of vacuum functional only preferred pairs of 3-surfaces are possible. This gives rise to what might be called "standard behaviors". Also the replication would be this

kind of behavioral pattern. In the context of the positive energy ontology it is extremely difficult to understand the predictability of cell replication or the development of the organism from a single cell by repeated cell divisions.

Remote gene replication [K96] might be one application: the model described was actually developed before the idea that the replication of the MB could be the fundamental mechanism. Its reversal could be a basic mechanism of bio-catalysis and induce the attachment of the bio-molecules together. Also ordinary DNA replication could be induced by the same electromagnetic signal as remote replication.

TGD based model for ordinary DNA replication

Consider first a TGD based model for the ordinary replication of DNA.

1. Assume that the portion of DNA promoting DNA replication is activated by dark radiation at some frequency and that the promoter region emits radiation with the same frequency. This activates further promoter regions -also in other cell nuclei. The replication process is amplified exponentially. The negative feedback is necessary in the general case and is provided by attachment of the produced proteins (basically dark proteins) to the genes making them inactive.

2. This might occur during cell division which might involve irradiation by dark analog of white noise exciting all promoter regions. Certainly the coherence of this process is essential and here the higher levels of the dark matter hierarchy would be essential.

Remote replication in weak sense

Gariaev has reported a phenomenon suggesting remote replication in the sense that the DNA strands exist in B and the irradiation of the DNA at A induces the remote replication in B. In the sequel I will speak about the weak form of remote replication (WRR). We have written together with Peter Gariaev an article discussing a possible TGD based model for the findings [L160].

The work of Gariaev [I40, I39] [I41, I55] provides the experimental guidelines.

1. The phantom DNA [I40] identified as dark nucleon sequences in TGD framework and the evidence for remote activation of DNA transcription [I39] - both discovered by Gariaev's group - are assumed as the first two key elements of the model.

2. The notion of wave DNA introduced suggests that genes express themselves by em radiation and that genetic code is involved. Wave DNA should provide a mechanism of information transfer. Somehow DNA should be encoded to spatial or temporal patterns in turn decoded somehow to DNA. Gariaev has suggested that the modulation of polarization direction for the radiation propagating along the DNA strand could encode for the DNA to a temporal pattern.

The TGD based model for WRR using existing DNA in both A and B is discussed in the article [L160] written together with Peter Gariaev. This discussion and also later developments can be found in [K96, K64].

WRR would use existing DNA strands in B accompanied by dark DNA strands realizing the genetic codons as dark proton triplets. The replication would be remotely induced by the dark radiation from DNA at A possibly arriving to B via the MB having contacts with both A and B. This would be a general mechanism of remote mental interactions in the TGD Universe.

1. WRR becomes possible if the dark radiation exciting promoter region can leak to other cells or even other organisms. Large h_{eff} might make this possible.

2. Also remote transcription is possible by the same mechanism. Actually remote variants of very many basic processes seem to be possible.

3. The observations of Peter Gariaev's group about effects of laser light on genes [I41, I55] could be interpreted as remote replication in this sense.

The analog of this mechanism could make remote transcription and even remote translation at the dark level possible. These processes would induce these processes at the level of biochemistry in accordance with the proposal that biochemistry is quite generally shadow dynamics induced from the level of the MB.

TGD based model for the remote replication in strong sense

For the strong form of remote replication (SRR) only DNA codons are available at B, and under some conditions the presence of DNA at A induces the remote replication at B.

The findings of the group of HIV Nobelist Montagnier [I47, I48] could be interpreted in terms of SRR. In this case the information about DNA at A must be transferred from A to B. Peter Gariaev has reported replication in this sense for years after Montagnier' findings [I72].

1. Montangier's experiment involves two chambers A and B. A contains water plus genes and B contains water plus DNA nucleotides. There were channels between the chambers but so thin that DNA could not get through. Also an em field with 7 Hz frequency was present. Same genes as in A appeared also in B. As if remote replication of genes in A had happened in B. In the TGD framework the presence of 7 Hz frequency suggests that MB was present: the identification either as Schumann frequency or the cyclotron frequency of K ion in the endogenous magnetic field of .2 Tesla is suggestive.

2. Polymerase chain reaction (PCR) [I14] (see `http://tinyurl.com/ybv6mn5l`) is the technique used in the experiments of Montagnier's group and in somewhat modified experiment by Gariaev's group involving irradiation of the second test tube by laser light.

The findings of Montagnier *et al* [I47, I48] can be described in terms of SRR. The model for SRR has developed gradually and the latest version was discussed in 2020 [L108]: this discussion is included also in [K96, K64]. The following describes the definition and development of the model for SRR.

1. Consider two positions A and B. A could be a chamber containing DNA strands and B a chamber containing DNA codons. Assume that DNA to be remote-replicated is in A and the codons producing the replica are in B. The dark flux tubes parallel to ordinary DNA in A and carrying dark codons would be accompanied by dark planar flux tube bundles transverse to them and leading to B. Each flux tube would be analogous to a wave guide for dark photons. In Gariaev's model photons polarized orthogonally to DNA would propagate along these.

2. The planar flux tube bundles extending from A to B would have $h_{eff} > h$. The associated space-time surface which could be seen as a many-valued map from CP_2 or its lower-D surface to M^4 giving rise to a planar bundle of parallel U-shaped flux tubes in M^4 as a quantum coherent structure. DNA codons floating in water in B would reconnect to the ends of these U-shaped flux tubes by resonance mechanism and the resulting DNA strand in B would be the same as in A.

3. The dark photon signal representing DNA sequence could catalyze the formation of conjugate DNA in chamber B from existing DNA sequences in chamber A serving as a template. Since the catalytic interaction of DNA polymerase takes place with already existing DNA sequence, the simplest possibility is that first some conjugate DNA sequences are generated by WRR after which DNA polymerase utilizes these sequences as templates to amplify them to original DNA sequences. Whether the product consists of original DNA or its conjugate can be tested. I have also commented on Montagnier's findings from the TGD point of view [L5, L12].

4. The crucial assumption, which is in conflict with the standard picture, is that the dark DNA nucleotides (dark protons) serving as building bricks of DNA strands do not float freely in water but are already loosely bound to form dark codons.

   The motivation for this assumption is that one cannot assign the frequencies of the 3-chord with different nucleotides of the codon but only to the entire codon. The difference between ordinary codon and dark codon is like that between spoken and written language: in spoken

language word is basically a single entity but in written language it decomposes to letters. Interestingly, in written Chinese the words decompose to syllables but not to letters.

The assumption of effective independence of codons makes sense if the magnetic flux tubes connecting the codons have either value of string tension or larger value of h_{eff} than in the dark codon accompanying the ordinary codon.

Galois confinement allows to generalize the model and gives a justification for the formation of units with increasing complexity and size and behaving quantum coherently.

1. Triplets of dark codons can bind to a single dynamical unit by Galois confinement [L128, L127]. Dark codons can in turn bind to dark genes and even to DNA strands with a larger Galois group. Strands can in turn bind to double strands and double strands to chromosomes. Even larger structures are possible since Galois confinement is hierarchical and new levels correspond to the increase of algebraic complexity associated with the polynomials P defing 4-surfaces in M^8 and by $M^8 - H$ duality in H [L101, L102, L128].

   Biological evolution could be seen as a number theoretical evolution of Galois singlets with increasing size as the algebraic extension and the Galois group associated with space-time regions defined by polynomials would increase and become more complex.

2. Dark codons represented by 3 dark photons would be Galois singlets. From these dark photon genes and even larger dark photon structures can be formed as analogs of dark Bose-Einstein condensates. Photons as particles would be replaced by dark $3N$ photons. Also the planar flux tube bundles would be particle-like entities: $3N$-flux tubes forming quantum coherent structures. The entire gene would use this $3N$-tentacle to build resonant connections to other similar genes or to build similar genes from dark codons to which ordinary codons would be attached.

   The communications between dark proton genes with N codons would be by using dark photon genes involving $3N$-fold cyclotron resonance selecting the receiver. In communications, the simultaneous frequency modulation would yield the message transformed to a sequence of resonance pulses with temporal durations between pulses determined by the modulation.

9.3.2 Could HGT rely on remote replication in strong sense?

Transposons are abundant in eukaryotic cells unlike in prokaryotic cells. This suggests that TEs could make possible SRR and thus allow to circumvent the problems posed by the presence of nuclear membrane and chromosome structure. The reason for this could be simply that the value of h_{eff} is so large for the TEs (or rather, for their MBs) that it makes coherent activities possible in longer length scales and therefore also the control by MB. MB would have a larger size scale and higher "IQ".

Perhaps TE is one particular structure behaving like a unit expressing itself in terms of codons realized as dark photon triplets. TE would be moving gene as an analog of animal. This structure could be essential for SRR. If TE has MB with large h_{eff}, it (or its MB) would be able to behave autonomously: this is what jumping genes are. Genes not associated with TEs would be like plants coding for structure and TEs would be like animals making the structure dynamical.

Therefore the question in the concrete example considered is the following: Could SRR take place and yield a copy of a TE involving the AFG of herring inside the sperm cell or egg of smelt? The TE complex could belong to the sperm cell or egg of herring or their degradation products.

9.3.3 Some reckless speculations

It is interesting to try to see this proposal in a more general context.

1. Introns were for a long time regarded as "junk DNA". Junk interpretation does not resonate with the fact that human genome has the highest portion of introns and humans have also developed culture and language [L163, L164], which in TGD framework would correspond to an evolution of collective consciousness. The reasons for the junk interpretation might

have been the repetitive nature of introns and the belief that genes can be expressed only as proteins or RNA.

TEs as jumping genes are now known to have many important functions: they make the genome dynamic and affect its identity and size and can lead to a duplication of pieces of the genome. They are involved with the control of gene expression and epigenesis (amusingly they are still regarded as selfish genes!).

DNA is interpreted as information theoretically and one can wonder whether TEs might play an essential role in the communications at molecular level. Magnetic body (MB) and the hierarchy $h_{eff} = nh_0$ of effective Planck constants are a central element in TGD inspired quantum biology. The larger the value of h_{eff}, the longer the quantum coherence length and time scales are and genes could be classified using the value of h_{eff} for their MB as a criterion, a kind of universal IQ.

2. TEs dominate also in the genomes of crops (see `https://cutt.ly/5UZGvbY` and `https://cutt.ly/QUZG8qa`) and trees. It has become clear that trees are not isolated entities but know each other and take this into account in their behavior. Forest is not a collection of isolated trees, but a highly refined self-organizing social structure. For instance, conifers have a high amount of TEs, which suggests that forest is a conscious entity, which has MB controlling the forest at the level of the ordinary biomatter.

   Concerning crops, at least 35 % of the rice genome % of the sorghum genome [3], and nearly 85 % of the maize genome is made up of transposable elements (TEs). It is difficult to avoid seeing an analogy between human community and crop field or forest. Could TEs make possible communications in the scale of the crop field and forest and make it, or rather, its MB, a conscious intelligent creature?

3. I know that I should overcome the temptation of mentioning crop circles although most mainstream biologists certainly regard crop circles as human made. I cannot. It is also better to immediately confess that I have even written two articles about crop circles about a quarter century ago [K26, K27]. I of course know that there is no statute of limitations for this kind of science crimes so that this is not intended to be a defense for what I have done.

   Are the crop circles really human made? Some biologists have risked their career by studying them and have found that the folded straws of crops of the crop circle have the appearance of being affected by microwave radiation (think of a tomato, which has exploded in a microwave oven). Also light balls have been reported around crop circles as well as glass balls resulting from molten quartz.

   Microwave photons are known to induce "burning" of water, an effect which is poorly understood. If microwave photons are dark with energy $E == h_{eff}f$, say in biophoton range, this might be understood. One can also create in a microwave oven small light balls consisting of plasma.

   This raises questions: Could TEs make possible communications between individual plants of the crop field? Could TEs make it possible for the MB of the crop field to control the field? Could MB of the crop field of some other conscious entity use dark microwave photons to induce the formation of crop circles. Could the crop circles be interpreted as an expression of an intelligent conscious entity (not necessarily the MB of crop field) and analogs of patterns of neural activity as I proposed years ago [K26, K27]?

4. Cannabis is one of humanity's oldest crops and has a high proportion of TEs `https://cutt.ly/8UZW5v1`. Could this relate to its dramatic effects on human consciousness?

   Usually these effects are interpreted as being due to the biochemistry of cannabis (`https://cutt.ly/8UZET6t`). In the TGD framework, the idea that the binding of various psychoactive molecules on synaptic contacts activates flux tubes to MBs, even those in outer space, is attractive. The book "Inner paths to Outer Space" [J17] by Rick Strassman, Slawek Wojtowicz, Luis Eduardo Luna and Ede Frecska inspired an model [K82] for the possible mechanism of the action of psychedelics.

Could also the TEs in the DNA of cannabis play some role? Could they have MBs with especially high h_{eff}? Could it make sense to speak of co-evolution of the human consciousness and cannabis-consciousness (or crop-consciousness in general) based on interactions not directly conscious to us?

Chapter 10

Gene tectonics and TGD

10.1 Introduction

Quantamaganize articles are often highly inspiring. At this time the article "Secrets of Early Animal Evolution Revealed by Chromosome 'Tectonics'" (`https://cutt.ly/OOJbxUz`) provide food for TGD inspired thoughts about genetics.

This led to a little intellectual adventure leading to a proposal for a general answer to two questions. What is the physical counterpart of biological function at fundamental level? How do genes code for biological functions?

10.1.1 Gene tectonics

Due to the technical restrictions, the research of evolutionary history is strongly concentrated on point mutations so that one has not learned much about the evolution in the scale of the entire genome. This kind of research tries to understand what differentiation to new species and lineages involves at the. level of genes.

In a paper appearing in Science Advances [**?**] (`https://cutt.ly/LOJbaH0`), an international team of researchers led by Daniel Rokhsar has tracked changes in chromosomes that occurred as 800 million years ago. They identified 29 big blocks of genes that remained recognizable as they passed into three of the earliest subdivisions of multicellular animal life. Using those blocks as markers, the scientists deduced how the chromosomes fused and recombined as those early groups of animals became distinct.

The researchers call this approach "genome tectonics". What Rokhsar intuited was that blocks of genes in a given lineage were in good approximation conserved apart from the reshuffling of the genes inside the blocks. One can speak of conservation of chromosomes. This intuition could be tested recently, when enough chromosome-scale genomic information about diverse animal groups became available.

What causes the blocks of genes to stay together? One explanation for the conservation of the blocks is that physical nearness facilitates co-operation in the basic genetic processes such as transcription. This functional explanation applies to Hox genes, which is however a small part of the genome.

An alternative explanation is in terms of genomic inertia. There are only very few mechanisms of genetic reorganization.

1. Remixing occurs within chromosomes so that genes remain linked over the time.

2. In the terminal fusion chromosomes A and B are fused along their ends but genes remain linked with their original fragment.

3. Chromosome A is inserted inside chromosome B.

4. Fusion with mixing involves blending of genomes of the chromosomes A and B. The simultaneous fusion and mixing does not sound plausible whereas fusion followed by mixing is natural and this is what is meant as one learns from the original article [I50]. One speaks

about mixing as inversion mutations in this case. If so, only the first three mechanisms serve as basic mechanisms.

Interestingly, the second and third mechanism correspond to basic topological reactions for strings involving reconnection. The mixing within a chromosome corresponds to a permutation of genes within the genome, and the question is whether it could have some natural mathematical description.

Genomic rearrangements are not easy to spread in the population. During meiosis and the formation of gametes all chromosomes must pair with a matching partner. In absence of a partner, odd-sized chromosomes cannot pass to the next generation. Hence broken and fused chromosomes tend to be dead ends. The reshuffling of genes within chromosomes is however possible. There is also a competition with the existing genomes so that the rearrangements have small changes except in small populations.

This picture allows us to make conclusions about genetic evolution. If two species share a similar mixture of two gene blocks, the mixing very probably occurred in the common ancestor. It is also possible to make testable predictions.

Simakov, Rokhsar and their colleagues [**?**] (`https://cutt.ly/7OJbE8U`) used genetic tectonics to learn more about the emergence of some of the earliest animal groups about 800 million years ago. Chromosome fusions in early evolution were studied. How conserved genes passed into early animal lineages during the animals evolution from a common ancestor. Three early lineages represented by demosponges (21 chromosomes), cnidarians (23 chromosomes) cnidarians, bilaterians (24 chromosomes). The researchers found 29 blocks of genes that were highly conserved among their chromosomes.

Using the rules of chromosome fusing and gene mixing that they had identified, the researchers reconstructed the chromosome-level events that accompanied the evolution of these three lineages from a common ancestor. They showed that the chromosomes of sponges, cnidarians and bilaterians all represent distinctive way of combining elements from the ancestral genome.

10.1.2 How does gene tectonics relate to the TGD view about genome and its evolution?

Key notions of TGD inspired quantum biology

For several reasons, the proposed mechanisms of evolution at the level of chromosomes are highly interesting from the point of view of TGD.

TGD inspired quantum biology relies on the following key ideas.

1. The view about space-time as 4-surface in $H = M^4 \times CP_2$ leading to the notion of magnetic cody (MB).

2. Number theoretical (adelic) physics predicting the hierarchy of phases of ordinary labelled by the effective Planck constant h_{eff} and behaving like dark matter, p-adic physics as correlates for cognition, and $M^8 - H$ duality predicting that space-time regions are coded by polynomials.

   Number theoretic vision associates evolutionary hierarchies to the inclusion hierarchies of extensions of rationals associated with polynomials P, which at the fundamental level determine space-time via holography. The degree of the polynomial defines effective Planck constant $h_{eff} = nh_0$ serving as a kind of universal IQ characterizing the system.

   MB has large value of h_{eff} serving as a universal IQ, and serves the master and controls the biological body in the role of slave. This leads to the proposal that genetic code has fundamental realization at the level of dark matter in terms of dark proton and dark photon triplets and biochemical realization is a secondary realization.

3. Quite generally, biochemistry emerges as a kind of shadow dynamics. The controlling dynamics of MB is much simpler and control and communications is based on dark photon signalling. Biophotons can be identified as ordinary photons produced from dark photons.

Resonance is the general communication mechanism. The frequencies associated with the signal select the receiver via resonance condition and the signal itself represented as a frequency modulation is transformed to a sequence of resonance peaks.

Genetic codons are realized as dark proton and dark photon triplets, which correspond to Galois singlets in a number theoretic picture. Quite generally, bound states correspond to Galois singlets and codons could combine to form genes and larger quantum coherent structures by Galois confinement somewhat analogous to Bose-Einstein condensates.

4. Zero energy ontology (ZEO) in which the quantum state is identified as a superposition of deterministic time evolutions analogous to biological functions or computer programs.

   Polynomials determine space-time surfaces, which in turn are correlates for biological functions so that the notion of biological function reduces to a function as a polynomial with rational coefficients. Functional composition is analogous to a composition of a computer program from modules or of a biological function from simpler ones. The natural proposal is that genes correspond to compositions of polynomials with codons and letters perhaps identifiable as generating functions.

   ZEO provides a new view about quantum measurement theory and predicts that the arrow of time changes in ordinary, "big", state function reductions (BSFRs) and predicts also the occurrence of "small" SFRs (SSFRs) as counterparts of "weak" measurements. This leads to a generalization of thermodynamics and time reversal provides a general mechanism of self-organization and of homeostasis.

Questions

This picture allows us to consider answers to several questions inspired by the article.

What could be the mathematical description for the mixing of genes inside the chromosomes? Why does it have no dramatic effects unlike the recombinations of chromosomes? What does the mixing mean for the biological functions associated with the genes?

What is the fundamental mathematical counterpart for the biological function of a gene? What does construction of chromosomes from genes and various recombinations of chromosomes correspond to in terms of biological functions?

In meiosis chromosomes re-arrange in a new way. What does this mean at the level of the biological functions?

10.2 Key ideas of TGD and TGD inspired quantum biology

To consider the questions posed above, one must first introduce some key ideas and notions of TGD.

10.2.1 Duality between geometric and number theoretic physics

The TGD based view of fundamental physics and also of quantum biology involves in an essential manner the duality of the two visions about physics behind TGD. The geometrization of physics involves generalization of Einstein's program from the geometrization of classical physics to that for the entire quantum physics. Number theoretical vision about physics, which I call adelic physics, brings in number theoretical notions [L50, L51, L101, L102, L128].

1. In the physics as geometry vision [L128], space-time at the fundamental level is identified as a 4-surface in $H = M^4 \times CP_2$, in a loose sense an orbit of 3-surface.

   General Coordinate Invariance (GCI) requires that the dynamics associates to a given 3-surface a highly unique 4-surface at which the 4-D general coordinate transformations act.

   This 4-surface is a preferred extremal of the action principle determing space-time surfaces in H and analogous to Bohr orbit. GCI gives Bohr orbitology as an exact part of quantum theory and also holography. The space-time surfaces turn out to be minimal surfaces with singularities analogous to the frames spanning the soap film [L132].

2. In the physics as number theory vision, one considers 4-surfaces in complexified octonionic M^8 determined by octonionic continuations of real polynomials P with rational coefficients. The dynamics reduces to the condition that the normal space of 4-surface is associative (quaternionic). M^8 is analogous to momentum space so that a generalization of momentum-position duality of wave mechanics is in question.

10.2.2 Space-time surfaces are coded by roots of polynomials

The roots of an irreducible polynomial P continued to a complexified octonionic polynomial, code for a 4-surface in M^8 in turn mapped by $M^8 - H$ by duality to a space-time surface in H [L133, L134, L101, L102].

1. The algebraic roots of P (having rational coefficients) define mass shells $H^3 \subset M^4 \subset M^8$ and these mass shells serve as holographic data defining $M^8 - H$ duality. The duality is defined in terms of a deformation of the real projection M^4_c defining 4-D surface connecting the real projections of the mass shells.

2. The deformation is local $SU(3)$ element g for the subgroup $SU(3) \subset G_2$ of octonionic automorphisms satisfying the condition that the image points $g(m)$ are invariant under $U(2)$. This deformation maps M^4 to CP_2 and defines $M^8 - H$ duality explicitly. An alternative, purely geometric manner to define the duality is by assigning to the normal space of X^4 containing a preferred plane E^2 a point of CP_2 characterizing it.

3. The construction of scattering amplitudes [L133, L134] based on this picture leads to the proposal that by the conservation property the interaction many-particle systems with external particles characterized by polynomials P_i corresponds to a functional decomposition of P_i. The permutations of P_i give rise to different compositions but conserve the roots. There are good reasons to assume that only cyclic permutations can appear in the quantum superposition to which cognitive measurements [**?**] producing as a final state a collection of disjoint surfaces as external particles of the reaction and described by the product of polynomials can be applied.

   Scattering amplitudes are assumed to be dictated by a number theoretic dynamics defined by re-combinations of Galois singlets of many quark states consisting of free quarks with total momenta, which are ordinary integers (quarks have momenta which are algebraic integers) in a unit defined by p-adic length scale associated with the largests ramified prime of P.

10.2.3 Space-time surfaces and quantum computer programs

The interaction by the formulation of the functional composite has also cognitive interpretation [**?**]: Nature would be doing quantum computations by performing functional compositions.

1. In zero energy ontology (ZEO) [L92] [K93, K95], quantum states are quantum superpositions of deterministic time evolutions analogous to computer programs, biological functions or behaviors.

2. The functional composite would correspond to a decomposition of a computer program to sub-modules, and for rational or even integer coefficients one has a quantum analog of the Turing machine.

   The hierarchy of algebraic extensions of rationals however extends the Turing paradigm. Physical states are however Galois singlets with momentum components, which are integers in suitable scale.

3. The state function reduction (SFR) cascade process reducing the entanglement between different relative Galois groups in the hierarchy of Galois groups defined by the polynomials can be identified as a physical correlate of cognitive analysis [L110]. SFR cascade would be analogous to a halting of a quantum computer program.

4. Biological functions are analogous to (quantum) computer programs. They could be realized as topological quantum computations [K4, K87]. The braids connecting DNA and nuclear membrane or microtubules could code for these programs.

10.3 The new findings about genes and TGD

In this section the findings of [I50] and their possible implications are considered in the conceptual framework discussed above.

10.3.1 Dark realizations of the genetic code

The realization of the genetic codons in terms of dark proton - and dark photon triplets [L11, L78] leads to a profound generalization of the notion of the genetic code suggesting a new realization as which could be 2- and even 3-D (the MB of the cell membrane could realize genetic code). Dark DNA codons coding for the same amino-acids differ and the proposal is that dark photons realizations are responsible for what could be called emotional intelligence realized as bioharmony [L11, L78, L122]. The realization in terms of codons and frequencies would be behind the reductionistic "bit" intelligence and holistic and intuitive, emotional intelligence [L42].

The vision about biological control and communications using genetic code realized as 3-chords brings to mind computer language LISP [L122]. Dark codons represented as 3-chords serve as addresses and the message would be coded as frequency and amplitude modulations. The cyclotron resonance sequence at the receiving end transforms the message to a sequence of pulses and also nerve pulse patterns could be produced in this manner.

Codons would correspond to either dark 3-protons or 3-photons identifiable as Galois singlets. Also genes, gene pairs in double DNA strand, and even to chromosomes could be Galois singlets behaving like a single quantum unit having dark proton and perhaps even dark photons counterparts.

Quite generally, these realizations of the genetic code would be induced from the so-called icosa-tetrahedral tessellation of the hyperbolic space H^3 (mass shell) [L122]. The chemical realization of the genetic code would be only a secondary realization. The dynamics of the MB would induce biochemistry as a shadow dynamics of the MB serving as the "boss".

10.3.2 Genes as composite functions?

There is an intriguing analogy with genetics inspired by the idea that functional compositions define analogs of quantum computer programs.

1. One might say that the roots of P determine the genome of the 4-surface since they fix the boundary data as 3-D mass shells specifying the holographic data fixing $X^4 \subset M^8$ and its image as a minimal surface in H.

2. If the polynomials P of a real variable with rational coefficients (possibly monic polynomials with integer coefficients) satisfy the condition $P(0) = 0$, the compositions of polynomials inherit the roots of the factors in the composition. One can speak of analogs of conserved genes.

3. These analogies inspire the question whether genes or their MBs could indeed correspond to functional composites of polynomials characterizing the 4-surfaces determining the space-time surfaces assignable to genes or their magnetic bodies carrying dark genes as dark matter in TGD sense and controlling the genes. A stronger condition would be that the genes correspond to polynomials and the linear sequence of n genes to the composition $P = P_n \circ ... \circ P_n$. In principle, this would provide a solution to the fundamental question of how genes code for biological functions.

4. The remixings of genes within chromosomes would correspond to permutations of the polynomials P_i in their functional composite. In this picture the mixtures of genes inside the chromosome would correspond to the permutations of polynomials P_i representing genes in the functional composite: $P = P_n \circ ... \circ P_n$ representing chromosomes. The fusion of two chromosomes would in term correspond to the functional composite of $P \circ Q$ of composites of this kind. The simplest genes would correspond to a functional composites of polynomials representing codons, which in turn would correspond to functional composites of 4 polynomials.

5. Suppose that the 64 codons correspond to functional composites of 4 polynomials P_i allowing all permutations. One cannot however assume that the functional composites differing by a cyclic symmetry are equivalent so that the Z^3 equivalence class for the functional composites corresponds to the same amino-acid. One would have $N = 24$ non-equivalent composites corresponding to 24 codons of 3 different polynomials coding for 8 amino-acids, 36 codons with 2 different polynomials coding for 12 amino-acids, and 4 codons containing only a single polynomial coding for 4 amino-acids. The prediction would be unrealistic.

   The letters of codon could however correspond to 4 basic functions and their functional decomposition having codon as its counterpart indeed implies that their order in the composition matters. It is interesting to interpret the symmetries of the genome in terms of functional compositions. The most notable symmetry is almost perfect doublet symmetry with respect to the last letter.

   This symmetry suggests that the basic functions correspond to 2 doublets $D_1 = (f_1, f_2) and D_2 = (f_3, f_4)$ and that the members of the doublet $D_1 \circ f \circ g$ are almost equivalent as also the members of the doublet $D_2 \circ f \circ g$ at the biochemical level (protein transcription).

10.3.3 Why the reshuffling of genes need not have dramatic effects?

What is the effect of a permitatopm on a general composite polynomial $P_n \circ ... P_1$ at the fundamental level? The functional composite changes in the permutation of the composing functions. In particular, the root spectra of two composites with different order differ. They correspond to inverses of the roots of composites P^k under $(P_k \circ ... P_1)^{-1}$, $k = 1, ..., n$ so that the spectra are not identical although they can be mapped to each other in 1-1 manner. The permutation of genes in chromosomes or codons in genes would correspond to this kind of change for the root spectrum.

At the fundamental quark level this kind of permutation would affect the discrete virtual quark spectrum given by the roots of P appearing as virtual masses in the scattering amplitudes defining zero energy states, and also in the spectrum of Galois singlets [L133, L134] since the sum of quark momenta would be ordinary integer by Galois confinement.

Also the reshuffling of genes could corresponds to permutation of polynomials. Unless the 4 polynomials are commutative, this need not cause too dramatic effects.

This could have an interesting interpretation inspired by the TGD based view of the brain. The sensory data, in very general sense, from the biological body, in particular the brain, are communicated to MB. There is evidence that the brain obeys effective hyperbolic geometry in statistical sense [J11]. Neurons close to each other functionally, but not necessarily physically, are near to each other in this effective geometry.

The TGD inspired explanation [L103] is that these neurons correspond to nearby points at the magnetic body (MB) assignable to mass shell H^3 in H, which indeed obeys hyperbolic geometry. H^3 plays a fundamental role in the number theoretical physics at the level of M^8. This would explain the mysterious looking fact that salamander survives in reshuffling of its neutrons [J26] since this reshuffling does nothing for the image points at MB.

Could the situation be almost similar at the level of genes? Could the reshuffling of genes alter the situation at the level of chemical realization of chromosomes but not at the level of MB. Could this be tested?

10.3.4 How do the findings relate to Cambrian Explosion

The evolution of chromosomes was studied in a time scale of 500 million years. Interestingly, Cambrian Explosion (CE) took place roughly 500 million years ago and plays a key role in the TGD based view about biological evolution [L65, L131] . The TGD based view about pre-Cambrian evolution proposes that multicellular life evolved in underground oceans and bursted on the surface of Earth in CE about 500 million years ago.

Amusingly, the plate tectonics would have emerged at that time if TGD is right. Before that the surface of Earth would have been like the surface of Mars now.

The finding that multicellulars have started to evolve already 800 million years ago does not conflict with the TGD picture. The evolution would have occurred underground and its outcome would have bursted to the surface of Earth 500 million years ago.

Monocellulars could have drifted to the surface of Earth much before CE, say 800 million years ago, and managed to survive. For the multi-cellulars, the Earth's surface was however too harsh a place. Their sudden appearance in the CE would have brought to surface genomes, which had experienced fusions followed by mixing. Unless one is ready to believe that the fossils of the intermediaries have disappeared, the interpretation would be that fusion and almost simultaneous mixing must have occurred.

Part III

NUMBER THEORETICAL VISION AND GENES

Chapter 11

Philosophy of Adelic Physics

11.1 Introduction

I have developed during last 39 years a proposal for unifying fundamental interactions which I call "Topological Geometrodynamics" (TGD). During last twenty years TGD has expanded to a theory of consciousness and quantum biology and also p-adic and adelic physics have emerged as one thread in the number theoretical vision about TGD.

Since Quantum TGD and physical arguments have served as basic guidelines in the development of p-adic ideas, the best way to introduce the subject of p-adic physics, is by describing first TGD briefly.

In this article I will consider the p-adic aspects of TGD - the first thread of the number theoretic vision - as I see them at this moment.

1. I will describe p-adic mass calculations based on p-adic generalization of thermodynamics and super-conformal invariance [K46, K19] with number theoretical existence constrains leading to highly non-trivial and successful physical predictions. Here the notion of canonical identification mapping p-adic mass squared to real mass squared emerges and is expected to be key player of adelic physics and allow to map various invariants from p-adics to reals and vice versa.

2. I will propose the formulation of p-adicization of real physics and adelization meaning the fusion of real physics and various p-adic physics to single coherent whole by a generalization of number concept fusing reals and p-adics to larger structure having algebraic extension of rationals as a kind of intersection.

   The existence of p-adic variants of definite integral, Fourier analysis, Hilbert space, and Riemann geometry is far form obvious, and various constraints lead to the idea of NTU and finite measurement resolution realized in terms of number theory. Maybe the only way to overcome the problems relies on the idea that various angles and their hyperbolic analogs are replaced with their exponentials and identified as roots of unity and roots of e existing in finite-dimensional algebraic extension of p-adic numbers. Only group invariants - typically squares of distances and norms - are mapped by canonical identification from p-adic to real realm and various phases are mapped to themselves as number theoretically universal entities.

   Another challenge is the correspondence between real and p-adic physics at various levels: space-time level, embedding space level, and WCW level. Here the enormous symmetries of WCW and those of embedding space are in crucial role. Strong form of holography (SH) allows a correspondence between real and p-adic space-time surfaces induced by algebraic continuation from string world sheets and partonic 2-surface, which can be said to be common to real and p-adic space-time surfaces.

3. In the last section I will describe the role of p-adic physics in TGD inspired theory of consciousness. The key notion is Negentropic entanglement (NE) characterized in terms of number theoretic entanglement negentropy (NEN). Negentropy Maximization Principle (NMP) would force the growth of NE. The interpretation would be in terms of evolution as increase

of negentropy resources - Akashic records as one might poetically say. The newest finding is that NMP in statistical sense follows from the mere fact that the dimension of extension of rationals defining adeles increases unavoidably in statistical sense - separate NMP would not be necessary.

In the sequel I will use some shorthand notations for key principles and key notions. Quantum Field Theory (QFT); Relativity Principle (RP); Equivalence Principle (EP); General Coordinate Invariance (GCI); World of Classical Worlds (WCW); Strong Form of GCI (SGCI); Strong Form of Holography (SH); Preferred Extremal (PE); Zero Energy Ontology (ZEO); Quantum Criticality (QC); Hyper-finite Factor of Type II_1 (HFF); Number Theoretical Universality (NTU); Canonical Identification (CI); Negentropy Maximization Principle (NMP); Negentropic entanglement (NE); Number Theoretical Entanglement Negentropy (NEN); are the most often occurring acronyms.

Chapter 12

ZEO, Adelic Physics, and Genes

12.1 Introduction

Zero energy ontology (ZEO) solving the basic problem of quantum measurement theory has become a cornerstone of quantum TGD, and together with the vision about physics as infinite-D geometry of the "world of classical worlds" (WCW) [K72] and number theoretical vision about physics as adelic physics [L50, L51] fusing the real number based physics of sensory experience and the p-adics physics of cognition and intentionality dictates to high degree the key structures of TGD.In this chapter the implications of the ZEO for the understanding of genetic code are considered.

12.1.1 Summary of Zero Energy Ontology (ZEO)

Zero energy ontology (ZEO) [L92] lies behind TGD based quantum measurement theory in turn giving rise to a theory of consciousness by making observed part of system as a conscious entity - self. ZEO solves the basic paradox of quantum measurement theory forcing to give up ontology altogether in the Copenhagen interpretation. ZEO has become a key aspect of the entire TGD based physics.

In this section I will consider more precise mathematical formulation and physical interpretation of ZEO. ZEO forms also the cornerstone of TGD inspired theory of consciousness and quantum biology. I will consider also some related aspects of ZEO such as the notions of free will and intentionality, the notions of memory and precognition as its time reversal, intuitive in contrast to formal reasoning, and remote metabolism as a universal thermodynamical mechanism of metabolism in ZEO based thermodynamics.

12.1.2 About quantum measurement theory in ZEO

The relation between zero energy ontology (ZEO) based quantum measurement theory and adelic vision is clarified. The considerations suggest a more precise picture about cognitive representations and formulation of quantum measurement theory for them. One can generalize classical cognitive representations as number theoretical discretizations of space-time surfaces in the extension of rationals considered to their quantum counterparts as wave functions in the Galois group of the extension and introduce also fermions as spinors in the group algebra of Galois group. The strongest option is purely number theoretical representations of fermionic Fock spaces in terms of spinors in this group algebra. Presumably however M^8 spinors are required as basic building bricks and have interpretation in terms of octonion structure.

An attractive vision is that number theoretical quantum measurements reduce to measurement cascades involving a sequence of state function reductions reducing the entanglement between wave functions in sub-Galois group H and group G/H and ends up to a prime Galois group for group algebra has prime dimension and represents Hilbert space prime not decomposable to tensor product.

Also time measurement is considered from the number theoretic perspective assuming $M^8 - H$ duality. Clock readings are realized as roots of the rational polynomial determining the space-time surface. Time measurement would involve a localization to a definite extension of rationals,

whose dimension n must be proportional to the temporal distance T between the tips of causal diamond (CD) to guarantee fixed time and energy resolution.

12.1.3 The dynamics of SSFRs as quantum measurement cascades in the group algebra of Galois group

Adelic physics, M^8-H duality, and zero energy ontology lead (ZEO) to a proposal that the dynamics involved with "small" state function reductions (SSFRs) as counterparts of weak measurements could be basically number theoretical dynamics with SSFRs identified as reduction cascades leading to completely un-entangled state in the space of wave functions in Galois group of extension of rationals identifiable as wave functions in the space of cognitive representations. As a side product a prime factorization of the order of Galois group is obtained.

The result looks even more fascinating if the cognitive dynamics is a representation for the dynamics in real degrees of freedom in finite resolution characterized by the extension of rationals. If cognitive representations represent reality approximately, this indeed looks very natural and would provide an analog for adele formula expressing the norm of a rational as the inverse of the product of is p-adic norms. The results can be applied to the TGD inspired model of genetic code.

12.1.4 DNA and time reversal

The recently (towards end of year 2020) added section about DNA time reversal is written together with Reza Rastmanesh and devoted to the view about DNA inspired by zero energy ontology (ZEO) forming the basis of the quantum measurement theory of Topological Geometrodynamics (TGD) and by the notion of dark DNA inspired by the TGD view about dark matter as phases of the ordinary matter with effective Planck constant $h_{eff} = nh_0 > h$ at magnetic body (MB) - the third key notion distinguishing TGD from standard model. The basic prediction of ZEO is that "big" (ordinary) state function reduction (BSFR) changes the arrow of time meaning "death" and "reincarnation" with opposite arrow of time. This leads to a new view about self-organization.

The time reversals of the basic processes like transcription and replication turn out to be possible only for the conjugate (passive) strand - this is basically due to th CPT theorem in TGD context and chiral selection. By chiral selection enzymes can catalyze processes but not their time reversals. For instance, conjugate strand polymerizes in reverse time direction - this looks like depolymerization in standard time direction. Polymerization of the conjugate strand however occurs in standard time direction but in reverse direction along strand.

The recombination of DNA strands during meiosis is poorly understood. This could correspond to reconnections for the flux tubes associated with the active DNA strands. Time reversal would occur in BSFR and formerly passive conjugate DNA strands would depolymerize to "loose" codons (not independent letters) by the time reversed polymerization, the flux tubes associated with the formerly active strands would suffer reconnections inducing recombination without assistance of enzymes, second BSFR would occur, and be followed by the replication of recombined active strands.

According to the findings of Becker, the direction of the electric field along the body axis determines whether the system is awake or sleeps. By the properties of electric field under time reflection, the arrow of time correlates also with the direction of the electric field. TGD predicts that consciousness is possible even at the level of DNA. Could also DNA have a longitudinal electric field with direction correlating with the arrow of time of DNA at the (magnetic body) MB of DNA. Could there be a switch changing the direction of this electric field?

This inspires a model for the DNA as ferro-electret based on the properties of the negatively charged sticky ends of chromosome and dark DNA codons as proton triplets along a magnetic flux tube parallel to DNA strand. A simple proposal for the time switch based on the analog of Becker's DC currents emerges: proton flow of the dark protons of sticky end to the opposite sticky end would change the arrow of time. The model could generalize also to proteins known to be ferro-electrets and could be accompanied also by their dark analogs.

12.2 Some comments related to Zero Energy Ontology (ZEO)

Zero energy ontology (ZEO) lies behind TGD based quantum measurement theory in turn giving rise to a theory of consciousness by making observed part of system as a conscious entity - self [L53]. ZEO solves the basic paradox of quantum measurement theory forcing to give up ontology altogether in the Copenhagen interpretation. ZEO has become a key aspect of the entire TGD based physics.

The basic prediction of ZEO is that ordinary ("big") state function reductions (BSFRs) involve change of the arrow of time. There is a lot of support for this prediction. The recent highly counterintuitive findings of Minev *et all* provided support for the time reversal in atomic systems [L79] [L79]. Fantappie [J20] proposed decades ago time reversal in living systems and introduced syntropy as time reversed entropy. In living matter the generation of more complex molecules from their building bricks can be seen as decay in time reversed direction. Phase conjugate laser beams are known to obey time reversed second law.

Also Libet's findings [J3] related to the active aspects of conscious experience find a nice explanation in terms of the time reversal. The latest application is to the understanding of the mysterious looking findings about earthquakes and volcanic eruptions suggesting that macroscopic quantum jumps involving time reversal are in question [L81]. This suggest that experimental verification of the time reversal and occurrence of macroscopic quantum jumps is possible by studying causal anomalies. For these reasons is important to try to develop the details of the view about ZEO as precise as possible.

In the sequel I will consider more precise mathematical formulation and physical interpretation of ZEO. ZEO forms also the cornerstone of TGD inspired theory of consciousness and quantum biology and I will consider also some related aspects of ZEO such as the notions of free will and intentionality, the notions of memory and precognition as its time reversal, intuitive in contrast to formal reasoning, and remote metabolism as a universal thermodynamical mechanism of metabolism in ZEO based thermodynamics.

12.2.1 General view about ZEO

The details of ZEO - in particular the technical details related to the conservation laws BSFR and SSFR - are from well-understood and the following is an attempt to fix these details by using analogy with cosmology.

Rough view about ZEO

Consider first what ZEO roughly means.

1. The realization of ZEO [L94, L53, L66, L91] involves besides the notions of "small" (SSFR) and "big" state function reduction (BSFR) also the notion of causal diamond (CD). CD defines perceptive field of conscious entity as a 8-D region $cd \times CP_2$, where cd is the 4-D causal diamond of M^4 defined as the intersection of future and past directed light-cones.

2. At the classical level the basic entity is space-time surface connecting 3-surfaces at the opposite boundaries of CD. The space-time surfaces inside sub-CD continue outside and there is a hierarchy of CDs with largest CD beyond which space-time surfaces do not continue. This defines a space-time correlate for the hierarchy of selves.

   Space-time surfaces are preferred extremals of the basic action principle defined by the twistor lift of TGD [L72]. Minimal surfaces with 2-D string world sheets as singularities would be in question. They connect 3-surfaces at the boundaries of CD and are analogous to Bohr orbits so that not any pair is possible and the conditions characterizing preferred extremal property might even imply 1-1 correspondence between these 3-surfaces.

3. Zero energy states are superpositions of preferred extremals. One can also understand zero energy states as superpositions of deterministic programs - quantum programs, functions in the sense of quantum biology, or quantum behaviors. ZEO allows to solve the basic paradox of quantum measurement theory since the non-determinism of quantum jump between zero energy states corresponds to the causality of free will and is not in conflict with the classical

determinism realizing the causality of field equations. Experienced time and geometric time are not same but there is a strong correlation between them.

4. In SSFRs the active boundary of CD shifts to future - at least in statistical sense. This is preceded by a unitary time evolution generating superposition of CDs with different sizes but having fixed passive boundary and same superposition of 3-surfaces at it. SSFR involves time-localization to single CD with fixed temporal distance between its tips. Essentially time measurement is in question.

5. In BSFR the arrow of time changes and one can say that state function reduction measuring set of observables takes place at the active boundary of CD, which becomes a passive boundary at which state does not change during subsequent SSFRs in which CD increases in opposite direction with the former passive boundary becoming an active boundary. The change of the arrow of time in BSFR creates the illusion that instantaneous quantum jump corresponds to a smooth and deterministic time evolution leading to the final state [L79] [L79].

The mathematical and physical details of the picture are not completely nailed down, and the best manner to proceed is to return to basic questions again and again and to challenge the details of the existing picture. In the following I will do my best to invent nasty arguments against ZEO.

ZEO and conservation laws

The geometry of CD breaks Poincare invariance. Lorentz invariance with respect to the either tip of CD is exact symmetry and is extremely attractive in the construction of members of state pairs in ZEO. Classically Poincare invariance is exact and one can deduce expressions for conserved quantities for both bosonic and fermionic sector: the latter have interpretation as operators, whose eigenvalues in Cartan algebra are by quantum classical correspondence (QCC) identified as classical values of conserved quantities.

ZEO involves the somewhat questionable assumption that one can assign well-defined Poincare quantum numbers to both boundaries and that these quantum numbers are opposite: this motivates the term ZEO.

1. M^8-H duality [L86] allows to assign to CDs with either boundary fixed a moduli space, which corresponds to Poincare group. The proposal is that Poincare invariance is realized at this level and that the values of conserved charges in Cartan algebra correspond to the Poincare quantum numbers labelling these wave functions. The wave functions at the boundaries of CD could be arranged in representations of Lorentz group acting as exact symmetry of the boundary.

2. There is further little nuisance involved. Only time translations, which correspond to a non-negative time value as distance from the fixed boundary of CD are possible. One would obtain momentum eigenstates restricted to a future or past light-cone. This is of course what happens in TGD based cosmology. Maybe one must just accept this as a physical fact forcing to give up mathematical idealization.

   Formally one would replace the plane wave basis with a basis multiplied by characteristic function for future or past light-cone equal to 1 inside the light-cone and vanishing elsewhere. This basis is closed with respect to summation. This would mean that the states are not anymore exact eigenstates of momentum globally but superposition of Lorentz boosts of the basic momentum obtained by Fourier expanding the characteristic function of future/past light-cone.

   But what about CD which is intersection of future and past directed light-cones? Can one really assign to both boundaries wave functions defined in entire future (or past) directed light-cone? It seems that this is the case. Zero energy state would be entangled state as a superposition of products of boosted momentum eigenstates with opposite momenta representing the characteristic function of CD.

   The usual idea about unitary time evolution for Schrödinger amplitude would be given up inside CD, and replaced by a sequence of unitary time evolutions producing de-localization of the active boundary of CD and followed by a localization.

3. There is still a problem. A complete de-localization for the boundaries of CD is not consistent with the intuitive idea that CD has definite size scale. In wave mechanics the plane waves are only idealizations and in the real world one replaces plane waves with wave packets. Gaussian wave packets have the nice feature that they remain Gaussian in Fourier transformation.

   If one has Gaussian wave packet for the temporal distance between the tips of CD concentrated on certain value of time, the Fourier transform for this is Gaussian wave packet concentrated around certain relative energy, which is two times the energy assignable to say passive boundary of CD. Instead of sharp value of time as distance between the tips of CD one would have Gaussian distribution for its value. This is consistent with Lorentz invariance since zero energy states allow superposition over states with varying momenta assignable to say active boundary. The wave function would be essentially Gaussian in energy in the rest system and one can consider also wave functions in Lorentz group leaving the passive boundary of CD invariant.

SSFRs in ZEO

In the proposed picture the sequence of SSFRs could mean gradual widening of the Gaussian wave packet for the value of measured time as the temporal distance between the tips of CD by discrete steps.

The basic condition is that the states at passive boundary of CD identified as superpositions of 3-surfaces remain unaffected during the sequences of SSFRs increasing the size of CD. This corresponds to generalized Zeno effect and in consciousness theory thr unchanging part of zero energy state corresponds to unchanging part of self, one might call it soul. One can imagine two options.

Option I: CD increases statistically in SSFRs but classical energy is conserved for space-time surfaces connecting its boundaries. Energy density would decreases as CD increases. This does not seem too bad actually: it would be analogous to matter dominated cosmology.

Not only superpositions of 3-surfaces at passive boundary of CD would be conserved but also their 4-D tangent spaces would be unaffected: this is unnecessarily strong a condition for generalized Zeno effect.

Option II: CD increases but classical energies decrease. This looks more plausible- if not the only - option and is strongly favoured by the analogy of CD with expanding cosmology. It also conforms with uncertainty principle. The process would be essentially quantum analog of cooling or analog for what happens for particle in a box expanding adiabatially. The classical energies of the space-time surfaces in zero energy state would thus decrease as CD increases.

Also this option allows the states as superpositions of 3-surfaces to at passive boundary of CD to remain unffected in expansion of CD. The classical energies can however decrease because the space-time surfaces - tangent spaces of space-time surfaces at passive boundary - can change so that also energies can change.

This option is completely analogous to quantum adiabatic change in which the coefficients in the superposition of energy eigenstates are unaffected but energies change.

Option II looks more natural and will be considered in more detail.

1. The constraint that SSFRs as quantum measurements are for observables, which commute with observables, whose eigenstate the state at the passive boundary is, poses very strong constraints on what happens SSFR. Furthermore, preferred extremal is analog of Bohr orbit and cannot cannot be arbitrary pair of 3-surfaces. Therefore, when the CD changes, the preferred extremal also changes as a whole meaning also that also energy changes. These conditions could force adiabatic picture and the analog of Uncertainty Principle for classical energies as function of CD size.

2. The sequence of SSFRs could be also analogous analogous to what happens for a particle in box as the size of the box increases adiabatically: adiabaticity would actually be a hypothesis about what happens in the steps consisting of unitary evolution and SSFR. In adiabatic approximation the coefficients in the superposition of the energy eigenstates do not change at all: only the energies would change.

3. In thermodynamics this kind of process would correspond to a cooling, which could serve as a natural quantum correlate for the cooling in cosmology. In accordance with the idea that quantum TGD in ZEO corresponds to a complex square root of thermodynamics, one could interpret zero energy state as complex square root of thermal partition function for cosmology assignable to CD. The hierarchy of CDs would define Russian doll cosmology.

4. A further manner to understand this is in terms of Uncertainty Principle. As the size scale of CD given by temporal distance between its dips increases, the classical energy decreases. Intuitively the reduction of the classical energy is easy to understand. Increasing CD and keeping the 3-surface as such at passive boundary reduces time gradients at the passive boundary and space-time surface becomes more flat. Energy density is proportional to time gradients of coordinates and its therefore reduced. This argument is also used in inflation theories.

5. Change is the prerequisite of conscious experience and there would be indeed change also at the passive boundary of CD contributing to conscious experience. But in some sense this contribution - the "soul" - should *not* be changing! "Adiabaticity" would translate this idea to the language of physics.

What happens to CD in long run? There are two options.

1. The original assumption was that the location of formerly passive boundary is not changed. This would mean that the size of CD would increase steadily and the outcome would be eventually cosmology: this sounds counter-intuitive. Classically energy and other Poincare charges are conserved for single preferred extremal could fail in BSFRs due to the fact that zero energy states cannot be energy eigenstates.

2. The alternative view suggested strongly $M^8 - H$ duality [L43] is that the size of CD is reduced in BSFR so that the new active boundary can be rather near to the new passive boundary. One could say that the reincarnated self experiences childhood. In this case the size of CD can remain finite and its location in M^8 more or less fixed. One can say that the self associated with the CD is in a kind of Karma's cycle living its life again and again. Since the extension of rationals can change in BSFR and since the number of extensions larger than given extension is infinitely larger than those smaller than it, the dimension of extension identifiable in terms of effective Planck constant increases. Since $n = h_{eff}/h_0$ serves as a kind of IQ, one can say that the system becomes more intelligent.

   Also the temperature assignable to CD remains finite. In cosmological scales it could correspond to the analog of the temperature assignable to CMB. TGD based view about stars as blackhole like entities [L80] leads to the identification of the Hagedorn temperature assignable to the volume filling flux tube giving rise to star with the Hawking temperature of dark radiation at gravitational flux tubes. Even CMB temperature could be assigned with dark photons at gravitational flux tubes. The asymptotic temperature for CD before BSFR could correspond to this temperature.

   One expects that the center of mass coordinates of cm do not appreciably change during the quantum evolution. The hierarchy of CDs would imply that the Universe decomposes effectively to sub-Universes behaving to some degree independently. The view about Karma's cycles provides a more precise formulation of the pre-ZEO idea that systems are artists building themselves as 4-D sculptures. In particular, this applies to mental images in TGD based view about brain. The assumption that stars correspond to repeatedly re-incarnating conscious entities allows to solve several time anomalies in cosmology [L80] so that there would be a direct connection between cosmology and theory of consciousness.

There could be a relationship between quantal flow of geometric time by SSFRs and p-adic variant of time coordinates giving a reason why for p-adicity.

1. TGD predicts geometric time as a real variant and p-adic variants in extensions of various p-adics induced by given extension of rationals (adelic space-time and adelic geometric time). Real and p-adic times share discrete points in the extension of rationals considered: roots of

octonionic polynomials defining space-time surfaces as roots for their "real" and "imaginary" parts in quaternionic sense [L84]. The roots of the real polynomial with rational coefficients giving octonionic polynomial as its continuation define space moments of M^4 linear time assignable to special SSFRs. p-Adic time associated with the p-adic balls assignable the points are not well-ordered. One cannot tell about two moments of time which is earlier and which later.

2. This could relate to the corresponding lack of well ordering related to "clock time" associated with self at given level of evolutionary hierarchy defined by the extension of rationals. The increase of "clock time" as a distance between tips of CD for a sequence of small state function reductions (weak measurements) occurs only in statistical sense and "clock time" can also decrease. The moments of time correspond to roots of the real polynomial define "special moments in the life of self", one might say.

   At the limit of infinite-D extension the roots of the polynomial define algebraic numbers forming a dense set in the set of reals. Cognitive representation becomes dense set. These "special moments" need not however become dense.

3. One can raise an interesting question inspired by self inspection. As one types text, it often happen that the letters of the word become in wrong order, change places, and even jump from a word to another one. The experienced order of letters assignable to a sequence of SSFRs is not the same as the order of letters representing the order for the moments of geometric time. When one is tired, the phenomenon is enhanced.

   Neuroscientists can certainly propose an explanation for this. But could this be at deeper level quantum effect based on the above mechanism and have a description in terms of p-adicity assignable to prime p defining a ramified prime for the extension of rationals involved? When one is tired the metabolic resources have petered out and the IQs $n = h_{eff}/h_0$ defined by dimensions of extensions of rationals for the distribution of extensions tend to reduce, cognitive resolution for time becomes lower and mistakes of this kind become worse.

There is a further technical detail involved. For SSFRs the temporal distance between active boundary and passive boundary increases at least in statistical sense. It seems that one must define the inner product in S-matrix elements for the unitary step preceding SSFR using the previous state basis as sub-basis of the new state basis in the case that CD increases. In adiabatic approximation the S-matrix elements would be overlaps for the states with different size of CD and analogous to matrix elements between states of particle in boxes with the same fixed end but different moving end.

BSFRs in ZEO

Details of BSFR are not completely fixed. One can consider two options. Both options must satisfy the condition that the states at passive boundary of CD identified as superpositions of 3-surfaces remain invariant during the sequence of SSFRs. The tangent space-to the space-time surfaces need not however remain invariant. Therefore the classical energies of space-time surfaces can change since the energy densities are proportional to time derivatives of embedding space coordinates.

1. The size of CD increases steadily as was the original proposal and is thus not reduce in BSFRs. The problem with the steady increase seems to be that the size of CD becomes infinite eventually and the state evolves to what looks like cosmology. If the energy assignable with zero energy state is conserved, the energy density of matter inside CD increasing without limit becomes arbitrarily small. Is this a catastrophe?

   For TGD inspired cosmology this is the case at the limit of big bang in the sense that the energy density goes like $1/a^2$ (cosmic string dominance) and energy in a co-moving volume vanishes like a, where a is light-cone proper time. One can think that CD defines only perceptive field and that space-time surfaces continue also outside CD up to the maximal size of CD in the hierarchy of selves involved. The zero energy state would have finite energy energy but density of energy would go to zero at the boundary of CD. The perceptive field of conscious entity would increase steadily in size.

As found, energy need not be conserved in the subsequence SSFRs because Gaussian wave packets of CDs around given size are required so that eigenstates of energy are not in question and the reduction of the width of Gaussian in the sequence of SSFRs implies reduction of average energy. Only the superpositions of 3-surfaces at the passive boundary of CD would be conserved.

Even the conservation of energy combined with the increase of CD need not be a catastrophe. In matter dominated cosmology the conservation of mass takes place with respect to cosmological time which corresponds to the proper time measured as temporal distance from the passive tip of CD. This cosmological mass is not energy but closely relates to it. What looks of course counter-intuitive is that every self would evolve to a cosmology.

2. The size of CD could be also reduced in BFSR [L84]. $M^8 - H$ duality and existence of "braney" solutions encourages to take this option serious. The 6-D brane like entities correspond to $t = constant$ sections for linear M^4 time t. They would represent special moments in the life of self. The exceptional 6-D roots of octonionic polynomials as branes would emerge to the perceptive field conscious entity at these moment. Discontinuity of classical space-time evolution as SSFR. Every time-reversed re-incarnation of self would have have "childhood" and experience increase of CD from some minimal size to maximal size.

   Since the size of CD can be reduced, it could happen that the CD remains stuck below certain maximal size for ever. The associated mental images would continue living in the geometric past of bigger CD associated with self. The sub-CDs in past would represent memories of self. Cosmos in 4-D sense would be full of life. The interpretation of CD as perceptive field allows this. CD could also increase and become even a cosmology! This picture looks attractive from the view point of consciousness.

3. One can however invent an objection against ZEO, one might even speak about paradox.

   (a) Suppose that in biological death I indeed re-incarnate with opposite arrow of time and continue to live towards geometric past. Suppose also that I re-incarnate as more advanced human being - at least in statistical sense. Human beings have parents. But how can I have parents in the former geometric future, if my parents how have already died live in the former geometric past?

   (b) The only solution of the paradox seems to be that the magnetic body (MB) - the boss - does not disappear in the death of biological body (BB). The MBs of my parents continue their existence and in my biological death means their separation in stanard time direction and meeting in the new time direction. They meet, fall in love, and give rise to my birth but all this in opposite time direction.

   This would provide an answer to a long-standing question about whether MBs are preserved in biological death or not. My view has been that biological death is more or less that MB loses interest in my BB and directs attention to something more interesting. One could however argue that also MB is generated in birth and genes code also for it so that it would die. If directing attention corresponds to BSFR MB would continue to exist after biological death. This particular reincarnation - CD - would be like vortex in the flow of time.

   (c) Can one find any support for this crazy looking proposal? TGD Universe is fractal and lower levels in the length scale hierarchies are slaves. In particular, bio-chemical level serves as the slave of MB expected to obey kind of shadow dynamics. If the proposed topological dynamics of MBs solving the above paradox has a miniature representation at the level of DNA, one could take the proposal with some seriousness.

   In meiosis (`http://tinyurl.com/n5eqkdn`) germ cells, whose chromosomes are coctails of paternal and maternal chromoses (PCs and MCs), are formed. In fertilization (`http://tinyurl.com/ngzwhcq`) - in some sense a (time?) reversal of meiosis - pairs of PCs and MCs are formed. The fusion of paternal and maternal germ cells could be indeed seen in topological sense as a time reversal of replication. The replication of soma cells

involves mitosis (http://tinyurl.com/p35lkwr) forming pairs of chromosomes of PCs and MCs.

Could the chromosomal dynamics be a miniature version of the proposed dynamics at the level of MB even at the level of organisms? If so, mitosis at the level of MB would correspond to a loose pairing of paternal and maternal MBs - formation of a relationship. Our personal MBs as analogs of germ cells would be coctails of MBs of PCs and MCs formed by reconnection process.

What about replication? In the case of asexual reproduction (http://tinyurl.com/y8odomtf) one could speak about replication at the level of MB of the entire organism. Also cell - and DNA replication would represent examples of asexual reproduction and in meiosis sexual reproduction of also DNA would take place.

When does BSFR occur? I have imagined several options, which need not exclude each other.

1. Could BSFR occur, when there are no observables at the active boundary commuting with those diagonalized at passive boundary. Measurement of observable at means generation of eigenstate in the extension of rationals and it typically occurs that the resulting state is outside the extension. Could BSFR occur when there are no observables in the extension of rationals in question.

2. $M^8 - H$ duality predicts universal special solutions besides 4-D space-time surfaces. These 6-D analogs of branes correspond to n moments of linear M^4 time, where n is the polynomial whose octonionic continuation defines space-time surfaces in M^4 as roots of its real or imaginary part in quaternionic sense. At these branes 4-D space-time surfaces are glued together along their ends- space-time looks is analogous to piecewise continuous curve in time direction - and they would correspond to "special moments in the life of self" [L84]. When all these moments as special roots of the octonionic polynomial are experienced, BSFR would be the only possibility. The polynomial with rationals coefficients defining the octonionic polynomial defines the extension of rationals used so that this option could be consistent with the first option.

3. Is BSFR is forced to occur because there are no preferred extremals connecting the pairs of 3-surfaces exists anymore. Could it happen that the state becomes increasingly classical during the sequence of SSFRs and thus becoming more and more local in WCW (the "world of classical worlds", which is essentially the space of 3-surfaces at either boundary of CD). The unchanging part of the zero energy state associated with the time-reversed state as outcome of BSFR at the new passive boundary would be maximally classical. This might relate to the fact that the world looks so classical. Also the fact BSFRs themselves look classical smooth time evolution ending to the outcome of BSFR, creates the illusion of classicality [L79].

12.2.2 ZEO, life, and consciousness

The most important implications of ZEO relate to consciousness and quantum biology. One can understand act of free will and motor action in terms of BSFR. BSFR corresponds to motor action and its time-reversal. SSFRs correspond to sensory perception in either direction of time [L70]. Model for memory is one prediction and predicts precognition as time reversal of memory [K70] [L95]. Also the relationship between generation of insight and mechanical logic deductions can be understood. In biology ZEO leads to remote metabolism as a universal purely thermodynamical mechanism of metabolism. One can also understand zero energy states as superpositions of deterministic programs - quantum programs, functions in the sense of quantum biology, or quantum behaviors.

Act of free will, intentionality, and ZEO

Act of free will would correspond to BSFR that is quantum jump leading to final state with opposite arrow of time. Final state is a superposition of deterministic time evolution connecting

the 3-surfaces in the superpositions defining initial and the final states. In this picture state function reduction leads to final state inducing time reversed time evolution so that classically the causal order is changed. What in standard picture - say neural activities - causes the outcome, is caused by the outcome. Could it be that mere volitional act with sharp enough intention is needed? The correct deterministic time evolution is dictated by intention as consequence rather than cause!

Here I cannot avoid the temptation to tell about my own strange experiences. At this age one must remember to take the pills every morning. I have the habit of filling my pill dispenser every Monday morning. I do not bother to count the pills one by one. I just take randomly a bunch of them hoping that their number is correct. And it is! Quite too often! Similar thing happens in market when I pay with coins: I do not count the coins but just take a handful of them. The sum of the coins is correct quite too often! Could a mere sharp intention dictate the outcome. Could one learn gradually this kind of sharp intentions.

Could this be crucial for various skills like playing tennis or computer game, where one simply cannot react rapidly by computing the outcome since time does not allow it? Could this explain also mathematical/physical/.. intuition as skill to solve problems by making quantum jump directly to the solution of the problem.

Precognition and ZEO

It seems that neuroscientists are beginning to take remote mental interactions such as precognition, telepathy, and psychokinesis seriously. The popular article entitled "*Scientists Discover That The Heart & Brain Respond To Future Events – Before They Happen*" (see `http://preview.tinyurl.com/y494hw5u`) describes changing views of neuroscientists towards precognition.

In ZEO precognitions are naturally time-reversed memories. Classical signals giving rise to sensory experience arrive from geometry future in the standard frame. During sleep state precognition should be possible if sleep corresponds to time-reversed state for the self.

In the associative and computational models of brain our ability to predict the future is taken to be an extrapolation based on memories and experience of earlier life. This looks very reasonable but when one asks how these memories are represented, problems begin to appear. In TGD framework ZEO predicts that memories correspond to mental images in geometric past, in the simplest case, when the original event took place. This solves a huge problem of standard since memory storage becomes brain in 4-D sense rather than in 3-D sense [K70].

ZEO however implies that also time reversed memories are possible. If sleep state correspond to time reversed self about which we do not have direct memories, memories with reversed arrow of time would be possible in this state. Precognition becomes possible if these memories can be communicated to the wake-up state with the ordinary arrow of time. In dreams some parts of brain are awake and they could make possible this communication. The communicated information could be also conscious to some selves above or below us in the hierarchy. Dreams can indeed predict what happens during the next day. The classical book "*An Experiment with Time* " (see `http://tinyurl.com/jtqysty`) of J. W. Dunne tells about precognitive dreams that he experienced.

Intuitive and formal logical reasoning in ZEO

The basic vision is that adelic space-time geometry provides correlates for sensory experience and cognition/imagination. Fermionic degrees of freedom would represent quantal Boolean mind. In ZEO given deterministic time evolution for 3-surface and induced spinor fields would give rise to sensory and cognitive time evolution and to Boolean evolution having interpretation as analog of logical deduction leading from premises to conclusions.

1. The basis of fermionic Fock states can be regarded as Boolean algebra. Superpositions and thus entanglement of fermionic qubits are however possible and one can speak about quantum Boolean logic. In standard view concepts are formally regarded as sets containing the instances of concept as elements. Quantum concepts could be superposition of quantum states representing the instances so that quantum abstraction would be much more complex notion than ordinary abstraction. Non-classical Boolean states would be superpositions of statements identifiable as abstractions. Schrödinger cat would be seen abstraction. "Dead" and "alive" would represent instances of this abstraction.

2. Zero energy states are superpositions of initial and final fermion states and there is also a superposition over 3-surfaces, and could be interpreted as representations for implications. The sum $\sum_n S_{mn}|n\rangle$, where S denotes unitary S-matrix, represents a superposition over all transitions $|m\rangle \to |n\rangle$ allowed by laws of physics. These transitions could be interpreted as logical implications.

   One could argue that by diagonalizing S-matrix one obtains only diagonal transitions and the situation is rather trivial: just logical identities. The point is however that in number theoretical physics the diagonalization of S would in general lead outside the extension of rationals determining the adele and is therefore not possible. Same number theoretical mechanism would also stabilize negentropic entanglement and could force BSFR. Only state big state function reduction extending the extension of rationals can reduce this kind of entanglement.

3. Probably every mathematician has pondered the mystery of mathematical insight. How for instance mathematical insight is generated? What eureka experience is basically? Insight would correspond naturally to a big state function reduction leading to a new state reversing the arrow of time.

   Truth can be deduced in given system of axioms also mechanically - at least in principle. How does insight relate to a logical deduction leading to a theorem? The final state of quantum jump is superposition of classical time evolutions leading from the final state to geometric past. With respect to standard arrow of time it is superposition of logical deductions leading from various initial states- initial assumptions - to the final state - to the outcome of the deduction. Superposition of states at boundary of CD could be seen as an abstraction. Deterministic time evolutions would represent the mechanical deductions.

   Note however that in the time reversed state arbitrary long time evolution in opposite time direction is in principle possible and would correspond to an arbitrary long ordinary deduction or computation [L32]. After that a return to the original arrow of time would take place and provide the solution. The formal deduction leading to the outcome would be indeed forced by the outcome rather than vice versa?

Metabolism in ZEO

ZEO has also deep implications for biology. As already explained, ZEO allows to understand what behaviors, biological functions are at fundamental level.

Why metabolism is needed can be understood in TGD view about dark matter as phases of ordinary matter labelled by the value of effective Planck constant $h_{eff} = n \times h_0$, where n has also interpretation as dimension of extension of rationals giving rise to the extension of adeles [L51, L50]. n serves as a kind of IQ labelling different evolutionary levels and is bound to increase in statistical sense. Not only biology but also self-organization involving also energy feed could be understand in terms of the hierarchy of Planck constant.

In ZEO remote metabolism suggests itself as a completely universal purely thermodynamical mechanism of metabolism. Usually system loses its energy by dissipation. If the arrow of time is non-standard, systems seems to receive energy from environment. Note that the duration of time spent in time reversed state does not matter! What matters is the increment of time between states with same arrow of time! Sleep state could be seen also as a way to collect metabolic energy. BSFR can be seen as an act of free will - motor action and sucking of metabolic energy from "environment" would be very natural.

The interpretation for the return to the original time direction by second BSFR would be as beginning of sensory perceptions in standard arrow of time as sequences of SSFRs. During this period subsystem would be dissipating energy to environment.

12.2.3 Under what conditions does BSFR take place and what happens in it?

In the following the question under what conditions "Big" state function reduction (BSFR) takes place and what happens in it.

Two kinds of state function reductions

The discussion however requires the basic ideas of ZEO as background.

1. "Small" state function reductions (SSFRs)

Small state function reductions (SSFRs) are counterparts of so called "weak measurements", which are rather near to classical measurements in the sense that nothing drastic happens.

1. The passive boundary of CD does not shift but changes in size because active boundary shifts and this induces change of size. For state pairs defining zero energy states the members at passive boundary do not change and the coefficients of possibly time-entangled state defined as their superposition do not change. The members of state pairs at active boundary change and this change is induced by unitary time evolution between too SSFRs. This time evolution could be regarded as a generalization of adiabatic time evolution.

2. In statistical sense the active boundary shifts towards future and the size of CD increases. The temporal distance between the tips defines clock time in one-one correspondence with SSFRs. Note that the unitary evolution forms a superposition of CDs with different sizes and SSFR means localization to single CD size.

3. The moment "Now" of self would naturally correspond to the M^4 hyper-plane dividing CD into two pieces of identical size. The radius of this 3-ball would be $r = T/2$, where T is the temporal distance between the tips of CD. At this hyperplane expansion of 3-ball with light-velocity would transform to contraction.

4. The mental images of self would correspond sub-CDs and also they would shifts towards geometric future in the sequence SSFRs. They would form a kind of log file about the life history of self such that geometric time order would be opposite to subjective time order. Self could remember these experiences by sending signals to geometric future reflecting back in time direction - seeing in time direction would be in question.

   What is in sharp conflict with natural expectation is that the memories would be stored in geometric future and part of them would become un-changing permanent part for the time reversed re-incarnation of self- kind of Karma.

   Note however that self might have also mental images represented as sub-CDs in geometric past.

$M^8 - H$-duality suggests space-time picture about the "log files".

1. 4-D space-time surfaces in complexified M^8 having interpretation as complexified octonions are 4-D roots for octonion valued polynomial obtained as an algebraic continuation of a real polynomial with rational or even algebraic coefficients. $M^8 - H$ correspondence maps thee surfaces to minimal surfaces with 2-D singularities in H [L86, L84].

2. Besides this one obtains for any polynomial also special solutions as analogs of branes in M-theory. They have topology of 6-D ball and their projection to M^4 is $t = r_n$ hyperplane intersecting CD and with topology of 3-ball. r_n is a root of P and thus an algebraic number. I have called $t = r_n$ "very special moments in the life of self". Generalized vertices for particle reactions would correspond to partonic 2-surfaces localized at these 6-surfaces. At these surfaces incoming and outgoing partonic orbits would be glued together along their ends. The roots define positions of external particles at the boundaries of CD.

3. In SSFRs these balls at the active half of CD would shift towards future and new roots would emerge. These roots wold define a geometric representation of the memories of CD as "log file" increasing in size. If there are sub-CDs associate with them, one would have mental images shifting towards future.

2. "Big" state function reductions (BSFRs)

"Big" state function reductions (BSFRs) correspond to ordinary state function reductions (SFRs) in ZEO. In BSFR the roles of active and passive boundaries of CD are changed and the

arrow of geometric time changes since the formerly passive boundary starts to shift to opposite time direction. State function reduction not commuting with the observables defining states at passive boundary as their eigenstates would takes place and the state at passive boundary would be changed. It would be however fixed by quantum dynamics. The findings of Minev *et al* provide support for the change of the arrow of time in ordinary SFR [L79].

The passive boundary can be shifted towards future so that the size of CD would decrease. One can say that the re-incarnate would be experience childhood. Note that also part of the "log file" about often personal experiences of self towards end of its life defining the permanent part of self-hood of the re-incarnate would disappear. The interpretation in terms of Karma is suggestive.

Remark: During a discussion with Marko Manninen, Marko noticed that people who have had near death experience often report that they experienced their entire life like a film during these moments. Could the "log file" representing stored mental images give rise to this experience at the moment of death?

What happens in biological death from TGD perspective?

What happens in biological death can be taken as a guideline in attempts to understand what happens in BSFR.

1. Death certainly occurs if there is no metabolic energy feed to the system. Metabolic energy feed is guaranteed by nutrition using basic molecules as metabolites. Since the increase of h_{eff} quite generally requires energy if other parameters are kept constant and since the reduction of h_{eff} can take spontaneously, the metabolic energy is needed to keep the distribution of values of h_{eff} stationary or even increase it - at least during the growth of organism and perhaps also during the mature age when it would go to increase of h_{eff} at MB.

   If the size of CD for at least MB correlates with the maximum value of h_{eff} or its average, the size of CD cannot grow and can be even reduced if the metabolic energy feed is too low. The starving organism withers and its mental abilities are reduced. This could correspond to the reduction of maximum/average value of h_{eff} and also size of CD.

   One can argue that if the organism loses metabolic energy feed or is not able to utilize the metabolic energy death and therefore also BSFR must take place.

2. In ZEO self-organization reduces to the second law in reversed direction of geometric time at the level of MB inducing effective change of arrow of time at the level of biological body [L87]. The necessary energy feed correspond to dissipation of energy in opposite time direction. In biological matter energy feed means its extraction from the metabolites fed to the system. One could say that system sends negative energy to the systems able to receive it. A more precise statement is that time reversed subs-system dissipates and metabolites receive the energy but in reversed time direction.

   In living matter sub-systems with non-standard arrow of time are necessary since their dissipation is needed to extract metabolic energy. The highest level dissipates in standard time direction and there must be a transfer of energy between different levels. This hierarchy of levels with opposite arrows of geometric time would be realized at the level of MB.

Death as a re-incarnation with opposite arrow of time

These observations suggest that one should consider the reincarnation with opposite arrow of time with wisdom coming from the death of biological systems.

1. We know what happens in death and birth in biological systems. What happens in biological death should have analogy at general level. In particular, in death the decay of the system to components should occur. Also the opposite of this process with reversed arrow of time should take place and lead at molecular level to the replication of DNA and RNA and build-up of basic biomolecules and at the cell level to cell replications and development of organs. How these processes could correspond to each other?

2. The perceived time corresponds to the hyperplane $t = T/2$ dividing CD to parts of same size. Here T is the distance between the tips of CD and therefore to maximal diameter of

temporal slice of cd, which is 3-ball. The part of CD above it shifts towards future in SSFRs. In BSFR parts of the boundary of space-time surfaces at the active boundary of CD become unchanging permanent parts of the re-incarnate - kind of log file about the previous life. One can say that the law of Karma is realized.

If CD decreases in size in BSFR the former active boundary keeps its position but its size as distance between its tips is scaled down: $T \to T_1 \leq T$. The re-incarnate would start from childhood at $T - T_1/2$ and would get partially rid of the permanent part of unchanging self-hood corresponding to interval $[T - T_1/2, T/2]$ so that the permanent part of reincarnate would correspond to $[T - T_1/2, T]$. Reincarnate would start almost from scratch, so to say. The part between $T - T_1/2$ and T would be preserved as analog of what was called BIOS in personal computers.

3. At the moment of birth CD possibly would thus decrease in size and the former passive boundary now in the range $[T - T_1/2, T - T_1]$ and lower tip of new CD at $T - T_1$ would become active and the seat of sensory experience. Arrow of time would change. Where the analog of biological decay is located? The region of CD in the range $[T/2, T - T_1/2]$ disappearing from "log file" is the natural candidate. This region is also the place, where the events related to birth in opposite time direction should take place.

4. The decay of the organism should therefore correspond to the development and birth of re-incarnated organism at the level of MB (it must be also remembered that genuine time reversal takes place at the level of MB and induces only effective time reversal at the level of ordinary bio-matter). The decay of organism dissipates energy in standard time direction: this energy could used by the re-incarnate as metabolic energy. How long lasting biochemical processes have effective time reversals depends on the quantum coherence scale determined by the size scale of corresponding CD.

Could the re-incarnations with opposite arrow of time be seen in bio-chemistry?

The possible occurrence of effective time reversals at the level of bio-chemistry could be perhaps tested experimentally.

1. Could the replication of DNA and RNA and build-up of various bio-molecules be effective time-reversals for their decays. Could the same apply to the replication of cells and generation of organs. Replication of DNA is self-organization process in which second DNA strand serves as a template for a new one. The decay of DNA should therefore involve two DNA strands such that the second DNA strand serves as a template for the effectively time reversed replication. The double strand structure indeed makes possible for the other strand to decay first. Cell replication should use another cell as replicate and same would happen in the cell decay.

2. An interesting mental exercise is to imagine the time reversals of various basic processes like transcription and translation. In the time reversal of translation of mRNA to amino-acid sequence the amino-acid sequence and mRNA would return to ribosome machinery, and amino-acid and tRNA codon associated with tRNA would return to form tRNA. mRNA strand would shift one step backwards and the process would repeat itself and finally mRNA strand would return to open DNA strand. In the time reversal of transcription of DNA to mRNA, mRNA strand would return to open part of DNA strand, decay to RNA codons and eventually DNA strand would close. It should be easy to check whether these processes really occur in the decay process.

3. The formation of stem cells involves de-differentiation. Could it mean time reversal of the entire process leading to a differentiated cell? Also this idea could be tested.

In biology pairs of various structures often occur. Could they correspond in some sense to effective time reversals of each other whereas at the level of magnetic body one would have genuine time reversals

1. Could the opposite inherent chiralities of MBs of DNA strands correspond to opposite arrows of time at the level of MB of DNA realizing dark genetic code [L27]? Could this be seen as a kind of explanation for the double strand structure of DNA. Could the passivity of DNA strand with respect to transcription correspond to opposite arrow of time at the level of MB? Could the passive strand become active in time reversal?

2. Even brain has this kind of pairing. Right brain hemisphere is passive in the sense that it does not seem to contribute to wake-up intelligence (presumably identified as analytic intelligence). Could either hemisphere serve as a template in the development of brain or could this happen only at the level of MB of brain? Could different time arrows at the level of MB be used to understand the strange passive character of right brain and could one one understand the holism of right brain *viz.* analytic reductionism of left brain as reflection of the fact that dissipation as decay corresponds to time reversal for self-organization generating structures at the level of MB.

What about ordinary re-incarnation?

A couple of comments relating to the notion of re-incarnation in standard sense are in order.

1. Eastern philosophies talk about the possibility of liberation from Karma's cycle. Can one imagine something like this? The above picture would suggest that in this kind of process the reduction of the size of CD does not occur at all and therefore there would be no decay process equivalent to the growth of time reversed organism. This would serve as an empirical signature for the liberation - if possible at all. CD would continue to increase in size or perhaps keep its size. It would seem that a new kind of non-biological source of metabolic energy would be needed.

2. Reincarnation is a basic notion in Eastern philosophies. In ordinary reincarnation person has memories about life of a person, who lived earlier. There is evidence for this. This cannot be understood in terms of time reversed re-incarnation.

   Recall that there would be a hierarchy of selves and corresponding CDs within CDs. It has remained an open question whether CDs could also overlap? Could re-incarnation in ordinary sense be explained in terms of this kind of overlap?

   Suppose that one has two overlapping CDs: CD_1 and CD_2 and that CD_2 extends farther to the future of CD_1. The sub-CDs of CD_1 shift to future as the active part of CD_1 shifts to future and increases in size giving rise to a kind of log file defining the personal memories of CD_1. In this kind of situation the mental images of CD_1 can enter to CD_2 and become mental images of CD_2. This would be sharing of mental images but in different sense as compared to the fusion of mental images by entanglement, which could also require intersection of sub-CDs of mental images.

   Could one imagine that the cosmos is full of selves serving as counterparts of memes wandering around and finding for selves hosting them by providing metabolic energy? Note that ZEO means that CD center of mass degrees of freedom do not carry any conserved quantum numbers so that the motion of these lonely CDs would not be restricted by conservation laws!

3. This picture suggests that CD:s form a conscious fractal atlas consisting of charts with various resolutions analogous to the atlas defining a covering of manifold by open sets. The earlier proposal was that in biological death MB redirects its attention to a new system. This picture would be modified: the MB of of CD_1 would still attend the time-reversed system and experience time-reversed life. Some sub-CDs of CD_1 would however belong to a new CD in its geometric future - CD_2. This conforms with the intuitive expectation that space-time surfaces continue outside CD and only the perceptive field of conscious entity is restricted to CD.

4. Mental images should correspond to sub-selves and therefore sub-CDs of CD. Contrary to what I have proposed earlier, it seems that after images cannot correspond to BSFR type re-incarnations of mental images nor re-incarnations in standard sense.

Mental images would shift towards the future together with active part of CD and form a kind of log file. Could after images be memories of previous mental images involving a signal time reflect from the the mental image in log file and creating the after image as a sensory memory of the earlier visual mental image? Or could one understand after images in terms of propagation of dark photon signals along closed magnetic loops giving rise to periodically occurring mental images.

In [L104] I discussed how the evolution of self by BSFRs could correspond to a transition to chaos as iteration of the polynomial defining the space-time surface. The proposed picture was that the evolution by SSFRs corresponds to iteration of a polynomial P assignable to the active boundary of CD. This would predict a continual increase of the degree of the polynomial involved. This is however only one possibility to interpret the evolution of self as iteration leading to chaos.

1. One could argue that the polynomial $P_{nk} = P_n \circ .... \circ P_n$ associated with the active boundary remains the same during SSFRs as long as possible. This because the increase of degree from nk to $n(k+1)$ in $P_{nk} \to P_{nk} \circ P_n$ increases h_{eff} by factor $(k+1)/k$ so that the metabolic feed needed to preserve the value of h_{eff} increases.

   Rather, when all roots of the polynomials P assignable to the active boundary of CD are revealed in the gradual increase of CD preserving P_{nk}, the transition $P_{nk} \to P_{nk} \circ P_n$ could occur provided the metabolic resources allow this. Otherwise BSFR occurs and self dies and re-incarnates. The idea that BSFR occurs when metabolic resources are not available is very natural for this option.

2. Could $P_{nk} \to P_{nk} \circ P_n$occur only in BSFRs so that the degree n of P would be preserved during single life cycle of self - that n can increase only in BSFRs was indeed the original guess.

While preparing this contribution I learned about a highly interesting claim (`https://tinyurl.com/yap8ss4p`) made by the research group led by Harold Katcher. The claim is that the epigenetic age (there are several measures for it such as methylation level of DNA) of rats has been reduced up to 50 percent. The theory goes that epigenetic age of molecules would be controllable by hormonal signalling globally.

BSFR would mean death of conscious entity and its reincarnation with opposite arrow of time. The system would rejuvenate in the transition starting a new life in opposite time direction from childhood so to say - rejuvenation would be in question. Doing this twice would lead to life with original arrow of time but starting in rejuvenated state. The claim of the group suggests that living matter could do this systematically using hormonal control.

Tukdam and TGD

This piece of text was inspired by a document (`https://rb.gy/abt8za`) about a strange phenomenon known as Tukdam. What happens is that in Tukdam the person is physically dead but is believe to be in a continued meditation. There is no EEG, the heart does not beat, and there is no normal metabolism. However, the decomposition processes do not start. The condition can last up to a couple of weeks. Similar longer-lasting ones have been reported: a yogi can be buried underground for months in an oxygen-free state and then wake up.

This challenges neuroscience's view of the brain as the seat of consciousness. According to reports there could be awareness and a sensory experience consisting of different light sensations. The Tibetan Book of the Dead describes these experiences. Near-death experiences have many similar features [L119].

In the body in Tukdam, the area of the heart is reported to feel warmer to the touch than the rest of the body, but the thermometer does not detect this difference. This would indicate that the body receives metabolic energy at the cellular level from some other source than in the normal metabolism, and that living matter can detect what measuring devices based on the recent knowledge provided by modern physics cannot detect. Where could this energy come from? If one wants to answer this, one must also ask what happens in death and what is consciousness and what is life.

1. Dark energy and matter are the two basic puzzles of recent day physics. In the TGD approach, I have identified dark matter as a phase of ordinary matter, for which the effective Planck constant h_{eff} is much larger than normally.

   In particular, the gravitational Planck constant $h_{eff} = h_{gr}$ assignable to gravitational flux tubes can be very large and makes quantum coherence possible even on astrophysical scales. Large Planck constants would be associated with the dark matter magnetic body, which would be the TGD counterpart to the magnetic field of Maxwell's theory, but would differ from it in many respects. As a quantum coherent unit, this magnetic body would control the ordinary biological body and induce its coherence. The classical energy of a magnetic body, consisting of volume energy and magnetic energy, would be dark energy.

2. In the TGD Universe dominated by zero energy ontology, consciousness is a universal phenomenon and present on all scales, from elementary particles to the level of the cosmos. Even galaxies, stars and planets would be conscious beings. Also life and death would be universal phenomena. Likewise, the biological decomposition process associated with death would correspond to the universal decomposition process, which would essentially correspond to the decomposition of magnetic monopole flux tubes (magnetic catabolism), which would induce the catabolism of the breakdown of biomolecules. Its time-reversed version would be magnetic anabolism and induce the building of bio-structures such as molecules.

3. The fundamental metabolic processes would be essentially magnetic anabolism and catabolism induced by "big" state function reductions (BSFRs) changing the arrow of time and inducing the biological anabolism and catabolism. Death would mean reincarnation with the opposite arrow of time.

In Tukdam, the biological body would be dead, but the magnetic body would still be alive and prevent the biological decay from starting. The disintegration of the magnetic body would start in Tukdam much later than normally, and initiate the disintegration of the biological body. The content of the conscious experience in Tukdam, light sensations and deep peace, would come from the magnetic body. The dead biological body would not provide contribution from sensory input, motor activity, and cognition.

By a strange accident, just before seeing the document about Tukdam, I wrote an article [L147, L150] about a seemingly completely unrelated topic, solar flares related to the reversal of the direction of the sun's magnetic field in the solar cycle, which has a period of 11+11 years.

The reversal of the Sun's magnetic field would correspond to magnetic catabolism as the breakdown of long monopole flux tubes into very short parts. It would be followed by magnetic anabolism as their re-fusion into long flux tubes. The solar cycle would correspond to the sleep-wake cycle, or more precisely: a series of lives in different directions of time. Death would only be a change of time's arrow, nothing final.

The model unexpectedly leads to a biological analogy and to understanding what might happen to the magnetic body in biological death.

12.2.4 Conditions on the periods with reversed arrow of time

In zero energy ontology (ZEO) falling asleep (death at"my" level of self the hierarchy) corresponds to ordinary - or "big" - state function reduction (BSFR) and also means a reincarnation with opposite arrow of time. We would be therefore conscious during sleep and wake-up would correspond to falling sleep of that other, time reversed self.

When I fall asleep, I wake-up later tomorrow morning for instance, not yesterday morning. It is interesting to see what kind of conditions this implies and whether it is possible to satisfy this easily and even more interesting is to see whether a time travel to the geometric past - maybe the Golden Youth - could be possible.

The following assumptions are made about what happens in BSFR.

1. Causal diamond (CD) is a correlate for self. CD is obtained by gluing together two identical half-cones along their bottoms. Moment "Now" corresponds to the largest hyperplane $T_{now} = T$ (origin of time coordinate is at either (call it "lower") tip of CD) .

2. During the sequence of SSFRs defining self, the 3-surfaces at the passive boundary of self are fixed although their 4-D tangent space changes and corresponds to the unchanging part of selfhood - soul one might say. The opposite active boundary of CD and 3-surfaces at it change and shift towards geometric future.This gives rise to wake-up consciousness involving sensory input and thoughts, emotions etc. induced by it. Each SSFR is preceded by the analog of unitary time evolution.

3. BSFR means a death of self (subself) and its reincarnation with an opposite arrow of time. One can equally well speak about the analog of falling in sleep and waking up after that for some level of hierarchy of selves. The self born in the death of the self with an opposite arrow of time self has no direct memories about the state. Self can however have memories about dreams in which part of say brain is awake. These memories store information about what self experienced during the sleep.

   In BSFR the active boundary of the CD becomes passive and is frozen. The size of CD is scaled down so that CD becomes small: this implies that the reincarnated self has a childhood and much of the memories - often not pleasant - stored near the active boundary as subselves living forth and back as conscious entities disappear. The surviving memories of self become "silent wisdom" of the reincarnated self.

4. If CD belongs to a larger CD, call it CD_{super} representing a larger unit of consciousness, the sub-CDs must shift to the same direction as the active boundary of CD_{super}. Otherwise the sub-CDs would drop from the flow of consciousness. This is analogous to co-movement of matter in cosmology.

   Note that the mental images of self correspond to sub-CDs around T_{now} and shift towards geometric future as CD increases and new mental images emerges at T_{now} plane: by $M^8 - H$ correspondence these special moments in the life of self correspond to roots of the polynomial defining space-time surface and reside are the upper half-cone of the CD. As CD increases, new roots pop up inside the upper half-cone near the T_{now} hyper-plane for some particular SSFRs. Completely counterintuitively, the mental images about past experiences are therefore in the geometric future of T_{now} hyperplane!

The proposed picture must be consistent with everyday experience. Call the two periods of self sleep wake-up and sleep label the two different BSFRs by "sleep" and "wake-up".

1. In each SSFR CD size increases - at least in statistical sense this implies that T grows. Each SSFR corresponds to a scaling for the CD shifting its active boundary towards the geometric future. During its life cycle CD experiences scaling Λ:

$$T_{now} \to T_{now,sleep_1} = \Lambda(SSFR) T_{now} \quad , \quad \Lambda(SSFR) > 1 \quad .$$

2. When the system falls in sleep the size of CD is scaled down so that also the value of T_{now} is scaled down by $\Lambda_{BSFR} < 1$:

$$T_{now,sleep_2} = (1-\Lambda(BSFR)) 2T_{now,sleep_1} = (1-\Lambda(BSFR))\Lambda(SSFR) 2T_{now} \quad , \quad \Lambda(BSFR) < 1 \quad .$$

   After that the CD begins to increase in size by small scalings in SSFRs to opposite time direction and T_{now} begins to decrease from its value $T_{now,sleep}$ begins to decrease.

3. If CD belongs to a bigger CD - call it super-CD - representing a larger unit of consciousness with a longer life cycle, one can argue that the CD must shift to the same direction as the larger CD increases. Otherwise the CD would drop from the flow of consciousness defined by super-CD. This is analogous to co-movement of matter in cosmology. Therefore a given life cycle corresponds also a shift ΔT of sub-CDs towards the growth direction of super-CD takes place and one has for the time coordinate $T_{super,now}$ of the super-CD. Therefore one must perform shift$T \to T + \Delta T$ for $T_{now,sleep_1}$ and $T_{now,sleep_2}$ to take into account the drifting. This gives for the moments "Now" before ad after the shrinking of CD in BSFR (falling asleep):

$$T_{super,now,sleep_1} = T_0 + T_{now,sleep_1} + \Delta T \ ,$$

$$T_{super,now,sleep_2} = T_0 + (1 - \Lambda(BSFR))2T_{now,sleep_1} + \Delta T \ .$$

4. Similar formula holds true for the moment of wake-up. In the previous formula T_{now} is replaced with $T_{now,sleep_2}$ and one has

$$T_{super,now,wakeup_1} = T_0 + \Lambda^{1)}(SSFR)T_{now,sleep_2} + \Delta T^{1)} \ ,$$

$$T_{super,now,wakeup_2} = T_0 + (1 - \Lambda^{1)}(BSFR))\Lambda^{1)}(SSFR)2T_{now,sleep_2} + \Delta T^{1)} \ .$$

The parameter T_0 depends on the choice of the origin of time for super-CD but is irrelevant.

One can deduce a consistency condition for the parameters of the model.

1. During the sleep period the time coordinate $T_{super,now}$ for moment "Now" in the coordinates of larger CD changes in the following manner:

$$T_{super,now,sleep} = T_0 + T_{now,sleep_1} \to T_{super,now,wakeup}$$

$$= T_0 + \Lambda^{1)}(BSFR)T_{super,now,sleep_2} + \Delta T^{1)} \ .$$

T_0 is an irrelevant parameter associated with super-CD. Note that there is breaking of time reversal symmetry since self associated with CD_{super} has fixed arrow of time unlike CD. Hence ΔT has at least in a statistical sense the same sign irrespective of the arrow of time of self.

2. This picture should be consistent with what we observe. When the tired average self fall a sleep at the evening, it wakes wake-up at the morning and is full of energy. Quite generally, wake-up occurs after time $\Delta T(sleep)$ meaning that the value of time T_{super} has increased by

$$T_{super,now,wakeup} = T_{super,now}(sleep_1) + \Delta T(sleep) \ .$$

These two expressions for the value of $T_{super,now}(wakeup)$ must be consistent and this gives a conditions on the parameters involved:

$$(1 - \Lambda^{1)}(BSFR))\Lambda^{1)}(SSFR)2T_{now,sleep_1} + \Delta T^{1)}$$

$$= T_{now,sleep_1} + \Delta T + \Delta T(sleep) \ .$$

$\Delta T(sleep)$ is given by

$$\Delta T(sleep) = [(1 - \Lambda^{1)}(BSFR))\Lambda^{1)}(SSFR)2 - 1]T_{now,sleep_1} + \Delta T^{1)} - \Delta T \ .$$

Intuitively it seems clear that for a given arrow of time it is not possible to wake-up before one falls asleep, and the condition $\Delta T(sleep) > 0$ for the standard arrow of time gives a constraint on the parameters. One cannot however exclude the possibility of time travel without dying or falling asleep first of the duration of time travel is much longer than that of wave-up period: $\Delta T^{1)} - \Delta T$.

A special solution corresponds to $\Delta T(sleep) = \Delta T^{1)} - \Delta T$ and $(1 - \Lambda^{1)}(BSFR))2\Lambda^{1)}(SSFR) = 1$ giving $T_{now,sleep_2} = T_{now}$.

12.3 Still about quantum measurement theory in ZEO

The relation between zero energy ontology (ZEO) based quantum measurement theory and adelic vision could be much clearer. The following considerations suggest a more precise picture about cognitive representations and formulation of quantum measurement theory for them.

In the sequel ZEO based theory of consciousness [L53, L92] as quantum measurement theory is discussed first by starting with a criticism of physicalism and after that introducing ZEO based view about consciousness as quantum measurement theory as a solution to the problems of physicalism.

After this the relation between zero energy ontology (ZEO) based quantum measurement theory and adelic vision [L50, L51] is discussed. The considerations suggest a more precise picture about cognitive representations and formulation of quantum measurement theory for them. One can generalize classical cognitive representations as number theoretical discretizations of space-time surfaces in the extension of rationals considered to their quantum counterparts as wave functions in the Galois group of the extension and introduce also fermions as spinors in the group algebra of Galois group. The strongest option is purely number theoretical representations of spinors as spinors in this group algebra. Presumably however M^8 spinors are required and have interpretation in terms of octonion structure.

An attractive vision is that number theoretical quantum measurements reduce to measurement cascades involving a sequence of state function reductions reducing the entanglement between wave functions in sub-Galois group H and group G/H and ends up to a prime Galois group for group algebra has prime dimension and represents Hilbert space prime not decomposable to tensor product.

Also time measurement is considered from the number theoretic perspective assuming $M^8 - H$ duality [L84]. Clock readings are realized as roots of the rational polynomial determining the space-time surface in M^8. Time measurement would involve a localization to a definite extension of rationals, whose dimension n must be proportional to the temporal distance T between the tips of causal diamond (CD) to guarantee fixed time and energy resolution.

12.3.1 ZEO based theory of consciousness as quantum measurement theory

Consider first zero energy ontology (ZEO) based quantum measurement theory as a theory of consciousness.

Criticism of physicalism

It is good to start with a criticism of physicalism.

1. In physicalism consciousness would reduce to a physical property, like energy, momentum or charge and one would have the hard problem. There would be absolutely no idea why for instance sensory qualia emerge and how they correspond to sensory input. For instance, the assignment of sensory qualia to brain regions leads to a mystery: auditory, visual, etc. areas look exactly the same. How they can give rise to so different qualia?

   Remark: The answer to the question is that this is not possible. I n TGD framework macroscopic quantum coherence and ZEO allow to assume that sensory qualia are seated at sensory organs [L42].

2. This is not the only problem: free will is not possible and we must stop talking about ethics and moral as we have indeed done in modern free market economy, which threatens to destroy our civilization.

3. The third problem of physicalism and also idealism is that conscious experience is about something: it carries information about something, external world, my body, even about my thoughts. It is associated with a pair of systems- me and the rest of the world - rather than single system as consciousness as a physical property implies. This "aboutness", kills the physicalistis view and actually idealism and under reasonable assumptions also dualism. Standard ontologies of consciousness fail.

Physicalistic approach has also problems with quantum measurement theory. The basic problems are basically due to the fact that observer as a conscious entity remains an outsider: observations affect the measured system but theory cannot say anything about observer as subjective entity. In ZEO the situation is different [L92] (`http://tinyurl.com/wd7sszo`) .

1. Quantum jump defines the basic building brick of conscious experience. It is something between two different quantum worlds, not in the world as a physical property of quantum system. Consciousness is a moment of re-creation. This a solves the hard problem and problem of free will.

2. Also the paradox of state function reduction can be solved if one can understand the problems related to the notion of time. There are two times: experienced time and geometric time, or the clock time. They are very different. Experienced time irreversible and has preferred moment "Now". Geometric time reversible and without preferred "Now". For some reason these times have been however identified.

ZEO based quantum measurement theory

In ZEO physical states as time= constant snapshots are replaced by pairs of "initial" and "final" states A and B or - by holography - with superpositions of deterministic time evolutions from A to B with respect to geometric time - note the analogy with computer program in computer science, behavior pattern in neuroscience, and function in biology.

1. In "small" state function reductions (SFRs) -"weak" measurements - the superposition of time evolutions from A to B is replaced with a new one such that states A at passive end - "initial state" - are not changed. Classical determinism is respected although one has quantum jump and generalization of quantum measurement theory. Two times - two causalities. The temporal distance T between A and B increases in statistical sense and this gives the correspondence between experienced time as sequence of state function reductions and geometric time is identified as T. These measurements changing B correspond to "weak" measurements analogous to classical measurements and to sensory input. A represents permanent part of selfness, "soul" one might say.

2. In "big" (ordinary) state function reductions (BSFRs) the roles of "initial" and "final" states change and the arrow of geometric time changes. Self dies and reincarnates with an opposite arrow of geometric time.

3. In more precise view the pairs of time=constant snapshots are replaced with what I call causal diamonds (CDs). The assumption that the size of CD is preserved In BSFR as assumed originally leads to some paradoxical looking implications. For instance, the size of CDs assignable to our sub-selves identifiable as mental images would increase without bound. $M^8 - H$ duality suggests strongly that the sizes of CDs can decrease in BSFR: the formerly active boundary would be frozen but the temporal distance of formerly passive boundary would be reduced so that the size of CD would decrease. One could say that self has childhood and starts from scratch with all sins of previous life forgiven.

This picture about state function reduction finds considerable empirical support.

1. The paradoxical experimental findings of Minev *et al* in atomic systems challenging standard quantum measurement theory give strong support for the reversal of the arrow of time in BSFR [L79] [L79] (`http://tinyurl.com/yj9prkho`).

2. Also Libet's finding that experience of free will [J3] seems to be preceded - caused - by neural activity, can be understood. It is not anymore support for the claim that free will is an illusion. State function reduction changing time order happens, and free will causes neural activity in the geometric past.

3. There is are lot of support for the new view about time from biology. For instance, self-organization - not only biological - could be understood as involving time reversal meaning that the time reversed reduction of order implied by generalization of second law looks

from standard observer's viewpoint like increase of order. Self-assembly and generation of structures in long scales would involve increase of time order. Evolution is second aspect of self-organization and reduces to the unavoidable increase of h_{eff} as dimension for extension of rationals. Also the need for energy feed - metabolic energy feed in living matter - can be understood because the increase of h_{eff} keeping other parameters constant, increases energy scale. Dark matter would be visible everywhere in sharp contrast with standard prejudices.

4. There is support even from cosmology and astrophysics, where TGD predicts quantum jumps in macroscopic scales. For instance, stars older than Universe can be understood in more detailed picture about ZEO [L80, L81] (`http://tinyurl.com/tf38xnx`).

One can of course criticize the view about the role of clock time as the distance T between the tips of CD as over-simplified [L92].

1. The state function reductions preceding SSFRs are preceded by unitary processes U. What one can say about "time evolution" U. First of all, U is assumed to produce a zero energy state de-localized in the space of CDs - in particular with respect to the distance T between the tips of CD.

   The simplest guess is that in SSFR a complete localization in T - measurement of T - and other moduli of CD (say boost with respect to the lower tip of CD) occurs. Can one reduce the localization in T to a SSFR reducing quantum entanglement or is time measurement something different? What entanglement of CD sizes with different values of T with the measurement apparatus could mean? What the presence of a measurement apparatus for time T - the clock at fundamental level, could mean mathematically? Later also the question whether one could reduce this measurement to pure number theory emerges?

2. The notion of completely localized state is over-idealization and also mathematically poorly defined. Gaussian wave packet over classical states with well-defined classical conserved energy (by Poincare invariance) with respect to T localized around some value T_0 is a more realistic notion and time measurement would mean localization to a wave packet around T_0.

   In [L92] the proposal that the time evolution of self could be seen an analog of cooling process analogous to cosmic cooling is considered. This would correspond to an adiabatic time evolution happening for a particle in box whose size increases slowly. In this process the coefficients in a superposition of states with given classical energy remain unaffected but the classical energies of the states themselves decrease. This would conform with Uncertainty Principle stating that the classical energies scale as $1/T$.

A more detailed view about quantum measurement in ZEO

Consider next in more detail what state function as quantum measurement means in TGD.

1. In standard quantum measurement theory quantum measurements are often thought to be performed by humans only. In TGD one assumes that state function reduction as analog of quantum measurement is universal and can take place for any pair of mutually entangled systems unentangled from its complement.

2. Density matrix for the entangled pair of systems is the fundamental observable. This applies to both BSFRs and SSFRs at active boundary of CD, which correspond to "weak" measurements commuting with the observables diagonalized at the passive boundary of CD and thus leaving the states at it invariant.

3. Quantum measurement involves typically measurement of several observables. This is realized as a measurement cascade. First the quantum measurement of density matrix occurs for some pair formed sub-system S_1 and its complement S_2 forming together system S. After the same occurs for S_1 and S_2. Observables correspond to density matrices in this cascade. One proceeds as along as new decompositions are found. If the final state belongs to a sub-space with prime dimension the cascade stops since there is no further decomposition to tensor product.

4. The density matrix for subsystem in general case decomposes to a sum of projectors t subspaces and the state function reduction takes to one of them. The outcome of the measurement can be sub-space rather than ray.

   Number theoretic vision suggests also a second possibility. The SSFR would take place only if the eigenvalue of density matrix having probability interpretation associated with the subspace or ray is in the extension of rationals associated with the matrix elements of the density matrix and space-time surfaces considered (defining the cognitive representation). If one assumes frequency interpretation of probability theory, this probability must be rationals. Entanglement can be number theoretically stable. This would that one can have stable entanglement.

   It is natural to assume that BSFR can can increase the extension of rationals associated with the eigenvalues of density matrix in the extension of the extension associated with its matrix elements.

5. Stable entanglement could be crucial for quantum computation as also the possibility of large values of h_{eff} and of time reversal. One can also assign to entanglement with coefficients in an extension of rationals p-adic variant of entanglement entropy by replacing logarithms of probabilities with the logarithms of their p-adic norms. These p-adic entanglement negentropies can be positive so that the entanglement carries information. This negentropy is different from the real negative entropy due to the loss of precise knowledge about entangled states. Quite generally, the sum of p-adic negentropies can be larger than real entropy. This would explain the paradoxical looking fact that highly evolved biological systems are highly entropic [I73] [L21]. england

12.3.2 The relationship between adelic physics and ZEO based quantum theory

The challenge is to formulate quantum measurement theory taking into account the constraints from adelic physics [L50, L51]. One can consider the possibility is that the quantum physics could reduces at the level of cognitive representations to purely number theoretic physics. This would mean huge simplification. I have considered quantum theory at the level of cognitive representations from the point of view of number theory in [L89] and from the perspective of scattering amplitudes in [L88].

Two kinds of cognitive representations

One can consider two kinds of cognitive representations. The cognitive representations considered hitherto correspond to number theoretical discretization of space-time surface determined by an extension of rationals, they are "classical". The bosonic wave functions in Galois group of extension acting on cognitive representations and their fermionic counterparts based on fermionic dynamics in the group algebra of Galois group and its normal subgroups (Galois groups too) would define quantal cognitive representations.

1. There are cognitive representations both at the classical level in terms number theoretical discretizations of space-time surfaces defined by the extension of rationals and at the quantum level based on spinorial wave functions in Galois group of the representation. Also the spinorial wave functions in factor sub-groups and normal subgroups of Galois group are involved.

2. One can assign preferred primes p_{pref} to the classical space-time dynamics as ramified primes p_{ram} of the extension. For these the polynomial defining extension has double root in $O(p) = 0$ approximation. This would be the realization of quantum criticality for cognition: criticality is typically in potential models a situation in which two or more extrema of the potential function coincide - catastrophe theory of Thom is classical example.

3. At the level of state (spinorial) space wave functions in Galois group acting on cognitive representations are natural candidate for a bosonic state space. Quantum states would be

wave functions in Galois group G with normal subgroup H acting as a Galois group of lower-D extension.

G/H is group itself and one can express wave functions in G as superpositions of products wave functions in G/H and H. The wave functions in G/H and H define naturally a tensor product and an attractive idea is that state function reduction can be regarded as measurement in G/H or equivalently in H. When H has prime order further reduction is not possible since Hilbert spaces with prime dimension are primes of tensor product.

A natural candidate for preferred primes p_{pref} is as orders of smallest possible normal subgroups of Galois group, kind of primitive generating Galois groups.

Remark: One must consider also the possibility that quark and possibly also leptonic degrees of freedom are present as additional spinor indices. The fact that M^8 has octonionic structure could require also M^8 spinor structure.

4. In TGD dark matter is identified as $h_{eff} = n \times h_0$ phases of ordinary manner. n is identified as the order of Galois group of Galois extensions and thus of the extension itself. For ordinary value of Planck constant empirical inputs suggests the identification $h = 6h_0$ [L31, L63].

   Quite interestingly, one has $6 = 2 \times 3$ so that there is factorization to 2-D and 3-D subspaces assignable to massless particles, and massive gauge bosons. This indeed suggests that number theoretical vision could allows to represent all many-particle states in terms of wave functions (spinor fields) in the group algebra of Galois group.

5. How to construct cognitive representations for fermions? A natural generalization of the bosonic dynamics in n-D group algebra of Galois group is introduction of spinor structure in terms of 2^k-dimensional spinors in the group algebra. For $k = n$ both chiralities are present and for $k = n-1$ only second chirality. In fact, one could pose even more chirality conditions giving $2^{n/2}$-D ($[n+1]/2$-D) spinors for even (odd) n. Indeed, the recent view about SUSY in TGD framework suggests that only quarks - second embedding space chirality - appear as fundamental fermions and that leptons are local composites of 3 quarks - spartners of quarks in well-defined sense [L93] (`http://tinyurl.com/y4pdb2xz`).

   The simplest option is that at the level of cognitive representations the fermionic oscillator operator algebra corresponds to the oscillator operator algebra creating fermions states having at most $k = n$, $k = n-1$,...$n/2$ ($[n+1]/2$) fermions assignable to these spinors in finite measurement resolution. Entire quantum dynamics at the level of cognitive representations would reduce to the dynamics of fermions in the group algebra of Galois group and its Galois sub-groups.

6. There is also question about the Galois groups of the extensions of various p-adic number fields Q_p induced by the extension of rationals with dimension n. For p-adic numbers in approximation the extension reduces to a finite field $G(p,k)$, $k \leq n$, and one has k-dimensional extension. Galois group G_p is smaller than the Galois group G for rationals. G_p would act naturally in the p-adic counterparts of cognitive representations and the representations of G would reduce to direct sums of representations of G_p. Note that the distinction between sensory and cognitive (real and p-adic) would emerge only at the quantum level.

   For $p < n+1$ the fact that one has $x^{p-1} = 1$ for $G(p)$ implies that the irreducible polynomial P defining the extension Q reduces to a polynomial with degree $nmodp-1 \leq p-1$. Information is lost for $p < n+1$. For $p \geq n+1$ situation is different but also in this case the reduction occurs for ramified primes since polynomial P as in this case multiple roots. This would be the counterpart of quantum criticality at the level of cognitive representations.

7. Could the primes appearing as factors of n be preferred p-adic primes? Since these primes as p-adic primes mean a loss of information, they are distinguished but hardly preferred in p-adic evolution. Ramified primes larger than n are more plausible candidates and can be assigned even with polynomials of order 2. The preferred p-adic primes assignable to elementary particles are indeed large: electron would correspond to $M_{127} = 2^{127} - 1 \sim 10^{38}$ [K46].

Quantum measurement theory for cognitive representations

What can one say about quantum measurement theory for cognitive representations? The basic questions concern the tensor products. How many tensor factorizations there are and can one pose some conditions on them? Assume that fermionic Fock states for second quantized spinor fields in n-D group algebra are enough for quantum physics at the level of cognitive representations.

1. Tensor product decomposition for n-D group algebra corresponds to the factorization $n = k \times l$. All factorizations of n define a possible quantum measurement situation and state function reduction can take place in bosonic sector to k or equivalently l-dimensional space. These factorizations would be highly unique since they correspond to pairs of Galois group G and its Galois subgroup H. They are defined modulo discrete automorphism of G. It is not clear whether the choice of this automorphism has physical content: one might consider a discrete variant of gauge invariance.

   For the fermionic oscillator algebra analogous statement holds true. Now the decompositions are induced by $n = k \times l$ decompositions.

2. State function reduction cascades would correspond to sequences of Galois subgroups $G \supset G_1 \supset ....G_k$ such that G_k corresponds to either trivial group of group with prime order. In this case the final state would be reached by a factorization in which the density matrix for G_k does not allow eigenvalues in the extension considered. This extension could be G, G_1 or perhaps rationals (frequency interpretation for probabilities).

$M^8 - H$ duality and measurement cascade

$M^8 - H$ duality [L84] suggests much more concrete picture about the measurement cascade.

1. $M^8 - H$ duality predicts that the roots r_n of a rational polynomial defining the space-time surfaces at the level of M^8 correspond "very special moments in the life of self" $t = r_n$ for the M^4 linear time in the rest system of CD, and that once these moments have been experienced, BSFR can take place. This is possible but not the only possible interpretation.

2. $M^8 - H$ duality and the view about evolution as analog of genetic evolution in which genes are conserved suggests that the polynomials can be regarded as functional composites of simple polynomials $P = P_{n_1} \circ P_{n_2} \circ ...P_{n_k}$ satisfying $P_{n_r} = 0$ (n_i refers to the degree of the polynomial). P possesses the roots of P_i and the corresponding Galois groups as normal subgroups as the counterpart for the conservation of genes in evolution.

   One can distinguish also primitive polynomials as those defining extensions which do not decompose further. Galois groups with prime number of elements corresponds to such extensions. Note that the same extension can appear at several levels in hierarchy and would correspond to a realization of extension at different hierarchy level defining a kind of abstraction level.

3. Intuitively the measurement cascade should correspond to a cascade proceeding to shorter time and length scales by increasing the resolution and also to a process in which abstraction is gradually concretized.

   Could the measurement cascade for a state localized to a given extension of rationals start with the measurement of the root set $X_1 = \{r_{1,1}\}$ of P_{n_1} corresponding to the lowest time resolution. After than P_2 and the root set $X_2 = \{r_{2,i}\}$ would be measured meaning a refined of time resolution replacing $r_{1,i}$ with as subset of X_2 around it.

   Here one must be however very cautious: one could also consider a hierarchy of CDs with decreasing size scales as the counterpart of the measurement cascade. I do not understand well enough the scale hierarchy to answer the question whether these two views might relate.

Measurement of time number theoretically

Could the measurement of clock time T as (average) distance between the tips of CD [L92] be understood as number theoretical measurement?

1. What about the measurement of time as the distance T between tips of CD or more generally as the center of mass value T_0 of T in the case that one has Gaussian wave packets localized around varying T_0? How could one realize the measurement apparatus - the clock - in terms of entanglement?

   Suppose that the superposition over CDs with different values of T corresponds at the level of space-time surfaces in M^8 to that for space-time surfaces determined by polynomials P_n with varying degrees and rational coefficients. The measurement fixing the extension and Galois group would not fix P_n since there is a large number of polynomials with rational coefficients but same Galois group. The measurement fixing the extension leads to a partial (at least) localization in T or T_0 but this is not expected to be enough.

2. A stronger localization in the state function reduction measuring n would require that T or T_0 correlates with the degree n. How could this be achieved in a natural manner? Intuitively the requirement of some fixed time resolution based on the preferred moments $t = r_n$ interpreted as clock readings has fixed resolution as the average time lapse $\Delta T = \langle \Delta T_{i,i+1} = r_{i+1} - r_i \rangle$ would require $n \propto T$ or $n \propto T_0$. How could this be achieved concretely? Could one specify the zero energy states by giving the time resolution as ΔT and being equivalent to energy resolution. This would also dictate the resolution of the cognitive representation as the set of space-time points in the extension.

12.4 Some questions concerning zero energy ontology

Zero energy ontology (ZEO) [L92] gives rise to quantum measurement theory, which naturally extends to a theory of consciousness. In this article also consciousness aspect is central and my sincere hope is that it would not expel those physicist readers for whom consciousness still remains an unscientific notion.

Zero energy ontology (ZEO) briefly

ZEO provides a new ontology solving the key problem of the standard quantum measurement theory and quantum theory itself. It must be emphasized that ZEO is not a new interpretation created to put under the rug the logical paradox due to the conflict between non-determinism of state function reduction (SFR) and the determinism of unitary time evolution. Also the problem about the scale in which quantum world becomes classical disappers: the Universe is quantal im all scales and ZEO view about quantum jump makes the Universe to look like classical.

1. At the level of space-time dynamics, the notion of preferred extremal (PE) as a space-time surface is central: PE is an extremal of an action principle, which by general coordinate invariance must be highly unique once its intersection with either boundary of causal CD $= cd \times CP_2$ (cd is the intersection of future and past directed light-cones of M^4) is given. In the ideal situation this implies holography. Space-time surface is an analog of Bohr orbit and classical theory is an exact part of quantum theory.

   There is probably a finite and discrete non-determinism analogous to that associated with soap films spanned by a frame: space-time is indeed a minimal surface as also soap films, and the 3-surfaces at its ends at boundaries of CD are part of the frame. Besides space-time surface is an extermal for Kähler action analogous to Maxwell action. The challenge is to interpret this finite non-determinism.

2. Quantum states, which I call zero energy states, can be interpreted as pairs of analogs of ordinary 3-D quantum states with positive energy. The members of the pair are at the opposite boundaries of CD. The convenient convention used also in quantum field theories (QFTs) is that the conserved quantum numbers at opposite boundaries sum up to zero classically: this brings in nothing new. At quantum level, 4-momenta are conserved only at the limit when CD has infinite size whereas classically the conservation holds true for all CD sizes: this reflects the Uncertainty Principle [L128]. Also in QFTs exact momentum conservation is obtained only at the limit of infinite quantization volume.

At the space-time level, zero energy states can be regarded also as superpositions of deterministic time evolutions: this is central for the interpretation.

3. SFRs are quantum jumps between zero energy states. SFR does not affect any deterministic time evolution but only replaces their superposition with a new one. This solves the paradox that was one of the key motivations for ZEO.

4. Zeno effect strongly suggests that there are 2 kinds of quantum measurements assignable to SFRs. For "weak measurements", "small" SFRs (SSFRs), the component of zero energy state at the either boundary of CD, to be called passive boundary (PB), is unaffected. Also the PB is unaffected apart from scaling. At the active boundary (AP) state changes and AP is scaled up (at least in statistical sense) and due to the scaling shifts to the geometric future.

   The unitary time evolution preceding each SSFR corresponds to a scaling of CD (or rather, its M^4 projection cd) rather than time translation as its counterpart in string models. In A unitary evolution B between two SSFRs a superposition of CDs with varying sizes is formed and SFR localizes CD to a fixed size, which means the measurement of geometric time identifiable as the distance between the tips of CD. This geometric time correlates with the subjective time defined by the sequences of SSFRs. Subjective and geometric times are not identical as in standard ontology but only correlated.

5. "Big" SFRs (BSFRs) are the counterparts of ordinary quantum measurements. In the BSFR the roles of AB and PB of CD change so that the arrow of time changes since CD increases in the opposite direction of time (at least in statistical sense). For an observer with an opposite arrow of time, BSFR looks like an average deterministic time evolution leading to the final state of BSFR as observed experimentally by Minev *et al* [L79] [L79]. This illusion makes BSFR look classical in all scales although the TGD based dynamics is quantal in all scales due to the hierarchy of Planck constants predicted by TGD.

   The possibility of time reversal forces a generalization of thermodynamics to allow both arrows of time: this kind of generalization was proposed long ago by Fantappie [J20] with motivation coming from biology. Quite generally, self-organization processes seem to violate the arrow of time. External energy feed explains this partially but BSFR would be an important additional element of self-organization [L87, L125], especially so in living matter.

   The assignment of "free will" to BSFR allows us to understand how free will can be consistent with the classical non-determinism of physics which would be exact.

ZEO based quantum measurement theory and therefore also physics naturally extends to a theory of consciousness, and one cannot avoid using this word, which is still a cursed word in the physicalistic camp.

Problems related to the mathematical realization of ZEO

There are several open questions related to ZEO and TGD inspired theory of consciousness and the existing view involves several working hypothesis which should be reduced to deeper principles or shown to be wrong.

At least the following questions related to physical interpretation of ZEO are still waiting for a detailed answer.

1. Preferred extremal (PE) property of space-time surfaces is central for quantum TGD [L109]. It follows from holography forced by general coordinate invariance (GCI), which however need not be ideal. How uniquely does the PE property of the space-time surface fix the space-time surface inside a given CD? The simplest situation is that the data at the end of the space-time surface at either boundary of the CD,fixes it completely. Space-time surface would be an analog of Bohr orbit.

   Full determinism would imply that WCW for CD effectively reduces to the space of 3-surfaces assignable to either end of CD. The dynamics of SSFRs would reduces to that in fermionic degrees of freedom assignable to Boolean cognition since WCW degrees of freedom assignable to sensory perception would be fixed.

However, the dynamics of soap films spanned by frames suggests that this is not the case. The 3-D ends of the space-time surface define a frame and also dynamically generated portions of frame are allowed by the variational principle defined by the sum of a volume term and Kähler action as an analog of Maxwell action. The coefficient of the volume term has an interpretation in terms of a length scale dependent cosmological constant Λ.

Outside the frame space-time surface would be at least for a very large portion of extremals an analog of complex surface and therefore a minimal surface [L132] and also an extremal of Kähler action. At the frames only the equations for the entire action (sum of volume term and Kähler action) would be satisfied. The divergences of the conserved isometry currents for the volume term and Kähler action would have delta function type singularities but they would cancel each other. The portions of the frame could be analogous to singularities of analytic functions such as cuts and poles.

2. Number theoretic universality [L51, L50] in turn suggests that the inherent non-determinism of p-adic differential equations [K56] [L92] proposed to be a correlate of imagination could also relate to this non-determinism. How do the non-determinism of space-time surface, p-adic non-determinism, and non-determinism of the state function reduction relate to each other: could they be even one and the same thing?

ZEO based quantum measurement theory defines a theory of consciousness. How unique is the interpretation of zero energy ontology (ZEO) [L92]? Here 3 options suggest themselves corresponding to "western" and "eastern" world views and their hybrid.

1. For the western option, the space-time surface continues outside any CD as external world, in particular sub-CD and sub-CD is a correlate for the perceptive field of self.

2. For the eastern option, space-time ends at the boundary of any CD and sub-CD is not a correlate for the perceptive field of self and there is no constraint from the external world at boundaries of CD.

3. For the hybrid of these two options, conscious entity corresponds to a hierarchy of CD for which the highest level corresponds to CD for which space-time does not continue outside the CD. The highest level represents a God-like entity.

Problems related to ZEO based theory of consciousness

The new picture about sub-CDs at WCW level raises questions related to the TGD inspired theory of consciousness. This view involves several ad hoc assumptions related to the notions such as attention, mental image, memory, volition and intentions. Do these assumptions follow from more general assumptions or can some of them be simply wrong?

1. CD is a correlate for the perceptive field of self. Sub-CDs of CD define perceptive fields of subselves identified as mental images. What is the precise definition of sub-CD? Can one say that a sub-CD is created when a mental image is created. How does this happen? What determines the position and size of the sub-CD?

   The sub-CD is defined by the restriction of zero energy state to sub-CDs so that sub-CDs are induced by CD. This condition is analogous to boundary condition in classical physics and freezes WCW degrees of freedom of sub-CD at the passive boundary (PB) but the failure of determinism leaves discrete degrees of freedom at the active boundary (AB) so that the dynamics of SSFRs is restricted to these sub-WCW degrees of freedom and fermionic degrees of freedom.

2. Where sub-CDs and subselves are located? The natural location for a minimal sub-CD and mental images is around 3-surface at which the classical non-determinism fails: the frames of the soap film in soap film analogy. One can develop a rather detailed picture about frames [L132] based on number theoretic vision realized in terms of $M^8 - H$ duality [L101, L102, L117].

3. How sub-selves (sub-CDs) are created? Can they disappear? The notion of attention as generation of sub-CD achieved by a location of WCW ("world of classical worlds") spinor field at spacetime surfaces having their intersection with the PB of CD in a fixed set of 3-surfaces defining the sub-WCW is highly suggestive. This also affects the WCW spinor field of CD.

   The attention can be directed in several ways. Redirection of attention means a movement of the region defining the content of mental images in the interior of a CD. Entanglement and classical communications would be naturally associated with attention defined in this manner. If minimal subselves are associated with the frames as loci of classical non-determinism, the set of targets of attention is discrete and finite.

   This view about attention makes it possible to see also memory, anticipation, and intentions as special cases of attention.

4. The time evolution of CD itself would correspond to a scaling of CD (rather than translation), which by the failure of strict determinism brings in new discrete degrees of freedom related to the new frames becoming into the daylight as space-time surfaces increase. In the new picture, the sub-WCW property poses strong restrictions to the earlier picture about the development of sub-CD. The idea about silent wisdom as mental images preserved from the previous life after BSFR is not lost but is considerably modified.

   In this picture, the small failure of classical determinism would be an absolutely essential element in that it makes possible a non-trivial theory of consciousness at the level of CD and at space-time level. Otherwise would have only fermionic degrees of freedom forgiven sub-CD. What is intriguing is that everything would be finite. SFRs would involve choices between finitely many alternatives and in this respect the theory would be analogous to the computationalistic approach: in fact, preferred extremals are analogous to computer programs.

12.4.1 Some background

In the sequel, some understanding of the basic ideas and notions of TGD proper [L109] is needed. Also ZEO as the target of critical discussion is briefly summarized.

TGD view briefly

Very concisely, TGD emerges as fusion of special and general relativities and has Poincare invariance of special relativity and General Coordinate Invariance (GCI) and Equivalence Principle (EP) as basic principles. Also the interpretation as a generalization of string models is possible: point-like particles are replaced by 3-surfaces instead of strings and world lines become space-time surfaces.

The notion of induction makes it possible to eliminate classical boson fields as primary dynamical variables and reduce them to the sub-manifold geometry of the space-time surface. For the simplest option, free second quantized quark fields of the embedding space $H = M^4 \times CP_2$ induced to the space-time surface remain as fundamental fermion fields and quarks serve as basic building bricks of both bosons and fermions as elementary particles [L93, L118].

Some understanding of notions such as the "world of classical worlds" (WCW) [K72], preferred extremal (PE) [K9], and various variants of holography [L101, L102] implied by general coordinate invariance (GCI) in TGD framework is assumed. Inclusions of hyperfinite factors of type II_1 (HFFs) [K90, K36] are central elements of quantum TGD proper.

Adelic physics [L50, L51] replacing real number based with number theoretical universal physics based on the hierarchy of adeles defined by extensions of rationals (EQs) and $M^8 - H$ duality (see Appendix 12.4.6) allowing number theoretic and geometric views about physics dual to each other is also assumed as the background.

Hierarchy of Planck constants $h_{eff} = n \times h_0$, with n identified as dimension of EQ, is the basic implication of adelic physics and central for quantum TGD. The phases labelled by h_{eff} behave like dark matter [K22, K23, K24, K25]. This hierarchy serves as a correlate for quantum criticality in arbitrarily long length scales.

Cognitive representations identified as points of space-time surface for which preferred coordinates of embedding space are in an extension of rationals are also central for the construction of the theory using M^8-H duality [L101, L102].Galois group of EQ becomes number theoretical symmetry and is central in the description of quantum variants of cognitive representations [L6, L110].

Zero energy ontology (ZEO) [L92] is a key notion of quantum measurement theory. The basic prediction is that time reversal occurs in the ordinary state function reduction (SFR). This has profound implications for the interpretation of the quantum measurement theory [L79].

TGD inspired theory of consciousness can be seen as an extension of quantum measurement theory and relies on Negentropy Maximization Principle (NMP) as a basic dynamical principle [K50] [L125] implying second law for ordinary entanglement entropy.

M^8-H duality as it is towards the end of 2021

The view of M^8-H duality (see Appendix 12.4.6) has changed considerably towards the end 2021 [L128] after the realization that this duality is the TGD counterpart of momentum position duality of wave mechanics, which is lost in QFTs. Therefore M^8 and also space-time surface is analogous to momentum space. This forced us to give up the original simple identification of the points $M^4 \subset M^4 \times E^4 = M^8$ and of $M^4 \times CP_2$ so that it respects Uncertainty Principle (UP).

The first improved guess for the duality map was the replacement with the inversion $p^k \to m^k = \hbar_{eff} p^k/p^2$ conforming in spirit with UP but turned out to be too naive.

The improved form [L128] of the M^8-H duality map takes mass shells $p^2 = m^2$ of $M^4 \subset M^8$ to cds with size $L(m) = \hbar_{eff}/m$ with a common center. The slicing by mass shells is mapped to a Russian doll like slicing by cds. Therefore would be no CDs in M^8 contrary to what I believed first.

Quantum classical correspondence (QCC) inspires the proposal that the point $p^k \in M^8$ is mapped to a geodesic line corresponding to momentum p^k starting from the common center of cds. Its intersection with the opposite boundary of cd with size $L(m)$ defines the image point. This is not yet quite enough to satisfy UP but the additional details [L128] are not needed in the sequel.

The 6-D brane-like special solutions in M^8 are of special interest in the TGD inspired theory of consciousness. They have an M^4 projection which is $E = E_n$ 3-ball. Here E_n is a root of the real polynomial P defining $X^4 \subset M^8_c$ (M^8 is complexified to M^8_c) as a "root" of its octonionic continuation [L101, L102]. E_n has an interpretation as energy, which can be complex. The original interpretation was as moment of time. For this interpretation, M^8-H duality would be a linear identification and these hyper planes would be mapped to hyperplanes in $M^4 \subset H$. This motivated the term "very special moment in the life of self" for the image of the $E = E_n$ section of $X^4 \subset M^8$ [L84]. This notion does not make sense at the level M^8 anymore.

The modified M^8-H duality forces us to modify the original interpretation [L128]. The point $(E_n, p=0)$ is mapped $(t_n = \hbar_{eff}/E_n, 0)$. The momenta (E_n, p) in $E = E_n$ plane are mapped to the boundary of cd and correspond to a continuous time interval at the boundary of CD: "very special moment" becomes a "very special time interval".

The quantum state however corresponds to a set of points corresponding to quark momenta, which belong to a cognitive representation and are therefore algebraic integers in the extension determined by the polynomial. These active points in E_n are mapped to a discrete set at the boundary of cd(m). A "very special moment" is replaced with a sequence of "very special moments".

So called Galois confinement [L117] forces the total momenta for bound states of quarks and antiquarks to be rational integers invariant under Galois group of extension of rationals determined by the polynomial P [L128]. These states correspond to states at boundaries of sub-CDs so that one obtains a hierarchy. Galois confinement provides a universal number theoretic mechanism for the formation of bound states.

ZEO

The TGD based view of consciousness relies on ZEO solving the basic paradox of quantum measurement theory. First, a brief summary of the recent view of ZEO [L92] is required. Some aspects of this view will be challenged in the sequel for sub-CDs.

1. The notion of a causal diamond (CD) (see **Fig. 20**) is a central concept. Its little cousin "cd" can be identified as a union of two half-cones of M^4 glued together along their bottoms

(3-D balls). The half-cones are mirror images of each other. CD=$cd \times CP_2$ is the Cartesian product of cd with CP_2 and obtained by replacing the points of cd with CP_2. The notion of CD emerges naturally in the number theoretic vision of TGD (adelic physics [L51])via the $M^8 - H$ duality [L86, L101, L102].

2. In the ZEO, quantum states are not 3-dimensional if the classical determinism does not fail as it actually does, but superpositions of 4-dimensional deterministic time evolutions connecting ordinary 3-dimensional states. By holography forced by general coordinate invariance, time evolutions are equivalent to pairs of ordinary 3-D states identified as initial and final states of time evolution.

   Quantum jumps replace this state with a new one: a superposition of deterministic time evolutions is replaced by a new superposition. The classical determinism of individual time evolution is not violated. This solves the basic paradox of quantum measurement theory. There are two kinds of SFRs: BSFRs (counterparts of ordinary SFRs) changing the arrow of time (AT) and SSFRs (analogs of "weak" measurements) preserving the arrow of time that give rise to an analog of the Zeno effect (`https://cutt.ly/yl7oIUy`) [L92]. The findings of Minev *et al* [L79] provide strong support for ZEO [L79].

To avoid confusion, one may emphasize some aspects of ZEO.

1. ZEO does not mean that the physical states identified in standard quantum theory as 3-D time= constant snapshots - and assigned in ZEO to the opposite boundaries of a causal diamond (CD) - would have zero energy. Rather, these 3-D states have the same conserved quantities, such as energy. Conservation laws allow us to adopt the convention that the values of conserved quantities are opposite for these states so that their sum vanishes.

   This is not new: in quantum field theories (QFTs), one speaks, instead of incoming and outgoing particles, external particles arriving from the geometric past and future and having opposite signs of energy. That conserved quantities vanish in the *4-D* sense, expresses only the content of conservation laws. A weaker form of this condition [L123] states that the total conserved Poincare charges are opposite only at the limit of infinitely large CD. CD would be an analog of quantization volume in QFTs, whose finiteness implies a small conservation of momentum.

2. ZEO implies *two* times: subjective time as a sequence of quantum jumps and geometric time as a space-time coordinate: for instance, the proper time of the observer. Since subjective time does not correspond to a real continuum, these times are not identifiable but are strongly correlated. This correlation has led to their identification although they are different.

12.4.2 How uniquely PE property fixes the space-time surface?

How uniquely the PE property fixes the space-time surface if its 3-D intersections with the boundaries of CD are given? This is the key question in this section.

Various variants of holography

General coordinate invariance (GCI) forces holography in the TGD framework. One can however consider several variants of holography [L101, L102, L125].

1. Holography in the standard sense would fix the space-time surface from the data of its intersection with either boundary of CD or the data associated with the light-like 3-surfaces at which the signature of the induced metric changes.

2. Strong form of holography (SH) states that 2-D data at the intersections of the light-like 3-surfaces and boundary of CD are enough to determine the space-time surface.

3. The strongest form of holography inspired by $M^8 - H$ duality [L101, L102, L123] states that space-time region is determined by a rational value coefficients of a real polynomial extended to an octonionic polynomials, whose "root" is the space-time surface in M^8. The n roots of a real polynomial would determine a 4-D region in M^8 and its image in $H = M^4 \times CP_2$ would be interpreted as space-time surface.

4. There is a variant of holography, which gives up the full determinism of classical field equations and gives rise to what look like classical topological analogs of Feynman diagrams.

   (a) Consider first the particle level at the level of H. Particle lines generalized to 4-D orbits of 3-D surfaces representing particles. Particles as 4-D orbits of 3-surfaces contain light-line 3- D orbits of partonic 2-surfaces.

   (b) Partons as building bricks of particles in the information theoretic sense, and correspond to partonic 2-surfaces at which the orbits of partonic 2-surfaces meet. Their orbits are 3-D light-like surfaces at which the signature of the induced metric of the space-time surface changes.

   The partonic 2-D surfaces defining topological vertices belong to the 3-D sections of space-time surface with a constant value of M^4 time coordinate t to which one can map the 6-D brane-like entities of M^8 predicted by $M^8 - H$ duality [**?**]

This picture suggests that, besides the data at the boundaries of CD, also the data at the partonic 2-surfaces in the interior of CD are needed. This failure of classical determinism brings in the failure of the strongest form of holography. There would be a large number of PEs connecting the 3-surfaces at the ends of CD and they would correspond to the analogs of Feynman diagrams.

Zero energy state as a scattering amplitude would be a superposition over these diagrams. This superposition would not be however pre-determined as in the path integral but the zero energy state would define the superposition of paths in question.

Is the failure of classical determinism possible?

The possibility of classical non-determinism is suggested by the interpretation of space-time surfaces as generalized Feynman diagrams. These Feynman diagram entities would not however define an analog of path integral in TGD framework. Classical non-determinis would be a space-time correlate for the non-nondetermism at quantum level.

In this framework partonic 2-surfaces or equivalently the 3-D sections of the space-time surfaces with constant value of M^4 time would act as 3-surfaces at which the deterministic time evolution as a minimal surface would fail.

Another option is that light-like 3-surfaces containing the partonic 2-surfaces at very special moments of M^4 time define frames. These special values $t = t_n$ of M^4 time would be associated with 6-D branes predicted by M^8 picture as universal special solutions and their images in H would define "very special moments in the life of self" defined by the sequences of SSFRs defining the self.

1. The first hint comes from the dynamics of soap films. Soap films are minimal surfaces. The soap films spanned by 1-D frames consist of minimal surfaces glued together at the frames and this dynamics is non-deterministic in the sense that it allows several soap film configurations due to the different branchings at frames. At frames the minimal surface equations fail.

2. In TGD framework space-time surfaces as PEs are both minimal surfaces and extremals of Kähler action. In this case the 3-surfaces associated with "very special moments of time" $t = t_n$ could define an analog of a dynamically generated frame defining a 4-D soap film. The 3-surfaces at the ends of the CD would be fixed frames like those for soap films.

   This realizes quantum criticality in the sense that the field equations outside frame do not involve the parameters of the action which sum of volume term and Kähler action. The interpretation as a non-linear analog of massless free field theory outside the frame conforms with the basic spirit of quantum field theory. These solutions of field equations rely on a a generalization of holomorphy to 4-D situation so that field equations reduce to purely algebraic conditions involving only the first derivatives of embedding space coordinates. The analogy is defined by the solution of 2-D Laplacian equation in terms of real or imaginary part of an analytic function.

Field equations consist of two terms, which are divergences for the conserved currents (4-momentum currents plus color currents) defined by the induced metric in the case of volume term. In the interior of the space-time surface these divergences vanish separately for the volume term and Kähler action but not at the frame.

3. The field equations must hold true also at the 3-D frame but this need not be true for both volume term and Kähler action separately. The coupling parameters of the theory make themselves visible only via the frame. For the volume action the divergences of the conserved currents are orthogonal to the space-time surface. For K "ahler action, the divergences of the conserved currents contain to terms. The first term is proportional to the energy momentum tensor of Kähler action and orthogonal to the space-time surface.

   Second term is not orthogonal to the space-time surface. For twistor lift the Kähler also has an M^4 part with a similar decomposition.

   The sums of the parts of divergences orthogonal to the space-time surface and parallel to it must sum up to zero separately. This gives 8 conditions altogether so that the number of field equations is doubled at the frame.

4. Could it happen that the divergences of these two isometry currents are singular and proportional to 3-D delta function but that their sum vanishes and conservation laws are respected? The part of the frame in the space-time interior would be dynamically generated whereas the part of the frame at the ends of CD would be fixed.

5. The restriction to 3-D frames is not the most general option. The delta function singularities could be located also at 2-D partonic 2-surfaces, at light-like 3-surfaces at which the induced metric changes its signature, and at string world sheets which connect these light-like 3-surfaces and have 1-D light-like boundaries at them. The light-like 3-D surfaces would be analogs of the cuts for analytic functions. Partonic 2-surfaces at the ends of light-like 3-surfaces could be analogs for the ends of the cuts. String world sheets could serve as analogs of poles.

6. The non-determinism associated with the soap films and with frames suggests that there is a large number of 4-D "soap films with a given frame", which is fixed at the boundaries of CD but not in the interior of CD.

12.4.3 Questions related to the theory of consciousness

At the level of TGD inspired theory of consciousness theory, causal diamond (CD) defines a correlate of self or of its perceptive field. CD has sub-CDs which correspond to subselves experienced by self as mental images [L92, L125].

Concerning the evolution of self, the basic notions of "small" state function reduction (SSFR) as an analog of "weak measurement" and "big" SFR (BSFR) as an analog of ordinary SFR.

1. The first deviation from the standard ontology is that BSFR changes the arrow of time defined by the selection of PB of CD at which 3-D part of zero energy states remains unchaged during SSFRs.

2. The second deviation is that either boundary of CD and states at it remain unaffected in SSFRs whose sequence defines self as a conscious entity. This is the TGD counterpart for the Zeno effect of ordinary quantum theory in which repeated measurements of the same observable leave the state unaffected.

The details of the evolution of self are not fully understood and the proposed general view can be criticized.

1. How the constraint that sub-CD serves as a correlate for a classical perceptive field can be taken into account?

2. What is the precise definition of mental images as subselves? Are they at some special positions inside space-time surface?

3. What are the precise definitions of memories and conscious memory recall? The same question applies to the notions of intention, anticipation and attention.

4. Can the mental images be destroyed or do they only experience BSFR and continue to live with an opposite arrow of time and become unconscious to self? If a mental image can completely disappear, what could be the physical mechanism leading to its disappearance?

5. One can challenge the detailed picture of the notion of time evolution by SSFRs. The assumption about the drift of mental images towards future in the second half-cone of CD is ad hoc. Should it be replaced with a deeper assumption. Could one simply assume that they are stationary.

Three ontological options

The basic problem of ZEO is whether the causal diamond (CD) represents a perceptive field in the sense that the space-time surface continues outside the CD or whether CD is an independent entity in the sense that space-time surfaces do not continue outside CD. Conservation laws do not exclude either option.

ZEO allows 3 ontological options which might be called easter, western, and intermediate views.

Option I: Space-time surfaces are restricted inside CDs. Quantum universe is a collection of CDs containing space-time surfaces, which have ends at the boundaries of CD.

In this framework, space-time in cosmological scales is an idealization and could be perhaps explained in terms of the correlations between CDs. CDs do not form a fractal atlas of something unless one says that the atlas *is* the territory. CD is an independent entity rather than a perceptive field of sub-self.

One can argue that for sub-CDs this picture is problematic since it seems that one loses totally the notion of objective reality as something existing outside CD. There are no sensory perceptions. Could the overlaps with other CDs create the experience about the existence of the external world?

Cosmology would be a mental construct and correspond to a very large CD. One would have a multiverse but only at the level of conscious experience. Option I is consistent with the eastern view that only subjective experience exists but not with the western view.

Option II: Space-time surface continues always outside all CDs and CDs can be interpreted always as perceptive fields. Option II conforms with the westerm option and implies that cosmology is something real.

Option III: Self is a hierarchy of CDs such that for sub-CDs the space-time surfaces continue outside the CD but for the largest CD this would not be the case. Sub-CDs would represent perceptive fields but the largest CD would be a God-like entity experiencing itself as the entire cosmos.

Meditators report altered states of consciousness in which the separation to self and external world ceases and the mind is empty. Also the experience of timelessness is mentioned. Could these states correspond to experiences without mental images (sub-CDs) created by SFRs at this highest level?

Option III is roughly consistent with both western and eastern views about consciousness. If one requires the notion of the external world as objective reality and accepts the proposed explanation of altered states of consciousness, option III remains the only possible option.

A general picture about the dynamics of sub-CDs

The ZEO based view of quantum measurement theory and the theory of consciousness inspired by it have not been precisely formulated for sub-CDs. In particular, the question of how sub-CDs as mental images are created, has remained unanswered.

The following proposal provides such a formulation and is consistent with Options I and III.

1. CDs form a fractal atlas of conscious maps but the map would be the territory since in general the space-time surfaces need not continue outside the CD. There would be no external particles as 4-D lines for generalized Feynman diagrams outside CD.

2. Sub-CDs correspond to mental images of CD as a conscious entity. From the point of view of consciousness theory, there are only experiencers (CDs) which can have experiences as mental images (have sub-CDs), be mental images of experiencers (be sub-CDs) and share mental images (intersecting CDs with common sub-CDs).

3. Consistency conditions for the quantum dynamics of CDs and sub-CDs and for the overlapping CDs give rise to correlations between the regions of the map. The shared regions are geometrically analogs for the intersections of the intersections of a covering of a manifold by open sets.

4. For sub-CD the interpretation of sub-CD as a perceptive field would be natural.

The first question is what does one really mean with sub-CD at the level of space-time surfaces.

1. Do the space-time surfaces of sub-CD continue outside sub-CD as space-time surfaces of CD? Does this imply that the quantum dynamics of sub-CDs in ZEO is completely dictated by that of CD? This is certainly not the case. Fermionic zero energy states associated with the sub-CD are possible and are analogous to quantum fluctuations. Note that in the TGD framework all elementary particles can be constructed from fundamental fermions (quarks).

2. If the PE (PE) property fixes completely the space-time surface, its intersections with the boundary of CD, this seems to be the case. If the classical dynamics is not completely deterministic, as suggested by the analogy with minimal surfaces spanned by frames, the situation changes.

   Sub-CD defines a subsystem of CD with boundary conditions at the boundary of CD which do not completely fix the quantum dynamics of sub-CD. Quantum states as WCW spinor fields inside sub-CD could change in SFRs of sub-CD.

   The tensor product of sub-CD with CD would not be ordinary tensor product but much more restricted one and Connes tensor product, related to inclusions of HFFs, would be a possible identification. A sub-system would be like an included hyper-finite factor of type II_1 (HFF).

Suppose that the classical dynamics is indeed non-deterministic and sub-CDs are defined in the proposed manner. How the view about WCW spinor fields changes as one restricts the consideration to sub-WCW.

1. The failure of the classical determinism forces to replace each 3-surface at PB with a discrete tree-like structure consisting of all PEs connecting it to AB. Sub-WCW as the space of PEs is larger than the space of 3-surfaces X^3 at PB. Zero energy states are defined in this sub-WCW and assign to a given X^3 a wave function in this discrete set allowing interpretation as wave function in a set of paths of the tree.

   One cannot avoid the association with cognitive representations of adelic physics involving the number theoretic degrees of freedom characterized by Galois group of the extension of rationals associated with the polynomial defining the space-time region [L38, L110].

2. The activation of sub-WCW would mean an SFR selecting in WCW of CD such sub-WCW for which the space-time surfaces are such that their ends at sub-CD are fixed. This would correspond to SFR creating a sub-CD and corresponding mental image. This would answer the long standing question whether and how mental images can appear as if from scratch. This SFR would also represent a third kind of SFR having interpretation as a partial localization in WCW associated with CD. This also suggest that mental images could disappear suddenly. This "activation" could be seen as a directed attention.

3. WCW degrees of freedom at the boundaries of sub-CD are fixed. Also sub-WCW spinor fields make sense. One can allow the tensor product of Fock spaces of many-fermion states associated with the boundaries of CD. One would have a QFT like picture with sub-WCW degrees of freedom fixed at boundaries of sub-CD.

4. The tensor product of fermionic state spaces at the boundaries of sub-WCW makes sense and one can define zero energy states in the same manner as proposed hitherto. The only difference is that WCW degrees of freedom are frozen at the boundaries of sub-CD. At the level of conscious experience this means that the subself experiences the external world as fixed. This would be by definition the meaning of being subself.

   The fermionic Fock state basis has an interpretation as a Boolean algebra so that fermionic zero energy states have an interpretation as Boolean statements of form $A \to B$. This would mean that consciousness of the subself would be Boolean, cognitive consciousness, thinking. This conforms with the Eastern view that ordinary consciousness is essentially thinking and that the higher level of consciousness as that associated with the highest level of the CD hierarchy of self is pure consciousness. Thinking assignable to the fermionic degrees of freedom would be seen as an endless generation of illusions. "Reality" in this interpretation would correspond to WCW degrees of freedom.

What restrictions must one pose on the quantum dynamics of CDs in the case of sub-CDs? Does the subjective evolution of sub-CD states by SSFRs and BSFRs make sense for sub-CDs?

1. The increase of the size of sub-CD makes sense and the proposed subjective evolution by scalings and SSFRs makes sense. The time evolution is also now induced by the increase of the perceptive field of a subself defined by the WCW associated with increasing sub-CD bringing in new 4-surfaces due to the classical non-determinism.

2. What about the interaction between CD and sub-CDs. Does this time evolution respect the condition that the space-time surfaces meet the fixed 3-surfaces at boundaries of sub-CD or is it possible that the SSFRs of CD destroy the subself by delocalization so that sub-CD as a mental images must be regenerated by localization in WCW.

3. Also the interaction between overlapping CDs and the sharing of mental images can be understood in this framework.

12.4.4 Comparison of the revised view of self with the earlier one

The revised view about TGD inspired theory of consciousness relies on the definition of subself at the level of WCW unlike the older view. In the following the new view is compared with the old view.

The view about SSFRs

Earlier picture

The earlier view about SSFRs was inspired by the M^8 picture.

1. The dynamics was assumed to involve both scaling of CD with respect to either tip of CD. The lower half-cone was only scaled whereas the upper half-cone was also shifted as required by the stationarity of the passive boundary. Dynamics at PB was passive in the sense that only a portion of the space-time surface became visible making also new states visible at it (Zeno effect) in the sequence of SSFRs . The idea about scaling leads to a rather concrete proposal for the S-matrix characterizing the scalings of CD.

2. The surfaces inside CD (or sub-CD) were assumed to be mirror symmetric with respect to the middle plane of CD. This assumption does not conform with the assumption that these surfaces define a perceptive field in the sense that they are parts of large space-times and continue outside CD.

The old view had several ad hoc features.

1. The creation of mental images was implicitly assumed without specifying what this could mean mathematically. These mental images were assumed to be created in the upper half-cone just above the $t = T$ mid-plane of CD and shift to the geometric future with the upper half-cone of CD. The asymmetry between upper and half-cone could be seen as reflecting geometrically the future-past asymmetry but was ad hoc.

2. One can criticize the assumption that the memories about the events of the subjective past are located in the geometric future with respect to the mid-plane of CD.

3. Whether mental images can disappear or only die and reincarnate by BSFR, was not specified.

New picture
In the new picture the situation is the following.

1. Also in the new picture, the time evolution by SSFRs would be a sequence of scalings of CD. The assumption about reflection symmetry of space-time surfaces is given up since it is inconsistent with the identification of sub-CD as a perceptive field. Also now the time evolution is passive in the sense that only a new portion of the space-time surface extending outside sub-CD is revealed at each step.

2. As in the previous picture, new discrete WCW degrees of freedom appear during the sequence of SSFRs and complexity increases. For both options only fermionic degrees of freedom remain if full determinism is assumed and if QCC is required also at the level of SFRs.

3. In the new view both directed attention, memory, and intention correspond to a generation of sub-CD by a localization in WCW fixing a subset of 3-surfaces at the PB of CD. Redirecting of attention would allow apparent movement of the sub-CD in the interior of CD and as a special case shifting the mental images in the time direction assumed in the earlier picture.

4. In the new view the loci of mental images are naturally associated with the loci of classical non-determinism that is 3-surfaces at the 4-D minimal surface branches.

5. $M^8 - H$ duality suggests that the branchings occur at H image points of the M^8 cognitive representation defined by the quark momenta which are algebraic integers for the extension of rationals defined by the polynomial defining $X^4 \subset M^8$. The non-determinism at $X^4 \subset H$ point set would correspond to non-determinism assignable to a bound state of quarks at corresponding point of M^8.

   Note that physical states correspond to total quark momenta which are rational integers, one can speak of Galois confinement meaning that physical states are Galois singlets. This gives an infinite hierarchy of bound states formed by a universal, purely number theoretical mechanism. All bound states could be formed in this manner.

   The non-determinism at $X^4 \subset H$ point which corresponds to a subset of points as images of quark momenta composing the bound state would correspond to non-determinism assignable to a bound state of quarks at corresponding point of M^8. There would be a hierarchy of CDs within CDs and hierarchy of mental images corresponding to the hierarchy of bound states.

   The bound state momenta are mapped to $X^4 \subset H$ by $M^8 - H$ duality already described. In particular, the positions of quarks contained in 6-branes X^6 with a constant energy $E = E_n$ are mapped to a sequence of points at the boundary of cd of the system by M^8-duality and it can be said to represent the positions of these quarks. These point sets define sequences of "very special moments in the life of self".

   The targets of attention would therefore form a discrete set assignable to bound states of quarks and antiquarks. Note however that each 3-surface X^3 in the superposition defining the WCW spinor field at the PB of CD has its own discrete set loci of non-determinism. BSFRs can change the superposition of these 3-surfaces. The selection between branches is possible in BSFR but not in SSFRs.

6. An attractive idea motivated by ZEP is that volitional action could be interpreted in the new view as an SFR selecting one path at the node of a tree characterizing the non-determinism. Single deterministic time evolution analogous to a computer program would be selected rather than modifying the deterministic time evolution as in standard ontology. In the M^8 picture, the very special moments $t = r_n$ in the life of self correspond to the roots of a real polynomial. What happens when all roots have been experienced? Does NMP force the BSFR to occur since nothing new can be learned?

Comparison of the views about BSFR

Those aspects of BSFR in which old and new views differ are of special interest.

Earlier view

The fact that the notion of sub-CD and mental image were not properly formulated led to several ad hoc assumptions.

1. The possible failure of a strict determinism was realized. The failure of strict determinism was assigned to "very special moments in the life of self" associated with the images $E = E_n$ planes of $M^4 \subset M^8$ at which the partonic vertices as loci of non-determinism were assigned.

2. The mental images of previous life near the AB of CD were assumed to be inherited as "silent wisdom". Their contents was from the early period of life with opposite arrow of time and one can of course ask whether they were really "wisdom".

3. There were also assumptions about the change of the size scale of CD in BSFR. The idea that the reduction of the size scale guarantees that re-incarnate has childhood was considered. This assumption also prevents unlimited increase of the size scale of sub-CD.

New view

The new view makes it possible to develop a more detailed picture of what happens in BSFR.

1. The WCW localization at the AB of CD selects one of the branches of the space-time surface beginning at the PB. This selection of the branch happens to each 3-surface in the superposition of 3-surfaces at the PB defined by the WCW spinor field before BSFR.

2. The future directed tree becomes a past directed tree beginning from one particular branch at the AB. The initial and final space-time surface share a common space-time surface connecting the roots of the old and new trees. This is essential for having a non-trivial transition amplitude for BSFR at WCW level.

In the earlier view, the mental images interpreted as memory mental images and located near the boundary of CD were assumed to be inherited as "silent wisdom" by the time-reversed reincarnate. What happens now?

The notion of "silent wisdom" as inherited information still makes sense.

1. The new space-time surfaces originate from 3-surface which was selected by WCW localization in BSFR. Therefore the new space-time surfaces carry classical information about previous life.

2. The space-time surfaces originating from the new root are near to the space-time surface connecting the old and new roots. The WCW spinor field before and after BSFR musthave a strong overlap in order to make the transition amplitude large. This implies that information about previous life is transferred to the new life.

3. The nearness property could imply that they are easily re-created as perceptions by directed attention so that they would indeed be "silent" wisdom. These mental images are from the later part of the life cycle rather than from the early life as in the earlier picture. If aging means getting wisdom, then silent wisdom would be in question.

Does the notion of "silent wisdom" as mental images make sense?

1. Mental images - this includes both sensory and memory mental images and intentions) are naturally assignable to the loci of classical non-determinism at the images of the planes $E = E_n$ of the branched space-time surfaces associated with the new root ("very special moments in the life of self").

   For the special space-time surface connecting the roots of old and new space-time surface, the surfaces $E = E_n$ in M^8 would not change and the mental images would carry information about previous life. Could one talk about potentially conscious "silent wisdom".

2. What happens to the mental images of self in BSFR? Can they be preserved or do they disappear or do they reincarmate by BSFR? The idea about preservation makes sense only for space-time surfaces connecting the roots.

3. What can happen to the size scale of CD in BSFR? The extreme option that CD decreases in size by shift of the formerly PB such that the time evolutions are fully determinimistic in the superposition of 3-surfaces. There would be no inherited silent wisdom and the self would start from scratch, live a chilhood. Otherwise these loci would define candidate for inherited silent wistom.

In the earlier picture the mental images corresponding to sub-CD could not disappear although it could die by BSFR and reincarnate with a reversed arrow of time. Can the mental image disappear now? Creation of mental image require metabolic energy feed: this explains 7 ± 2rule for the number of simultaneous mental images. Could this happen when attention is redirected? Therefore one could argue that mental image must totally disappear when the attention is redirected.

On the other hand, time reversed mental image apparently feeds energy to the environment in the original arrow of time, i.e. apparently dissipates. Could this dissipation be interpreted as an energy feed for its time reversal.

Note that the total disappearance of the mental image means delocalization at the level of WCW and seems possible. The new view clearly challenges the idea about the Karma's cycle of self. This cycle appears in many applications of BSFR.

12.4.5 Conclusions

Also the article *Some comments related to Zero Energy Ontology (ZEO)*" [L92] written for few years ago challenged the basic assumptions of ZEO. One tends to forget the unpleasant questions but now it was clear that it is better to face the fear that there might be something badly wrong. ZEO however survived and several ad hoc assumptions were eliminated.

Progress at the level of basic TGD

The basic goal is to improve the understanding about quantum-classical correspondence. The dynamics of soap films serves as an intuitive starting point.

1. In TGD frame 3-surfaces at the boundaries of CD define the analog of frame for a 4-D soap film as a minimal surface outside frame. This minimal surface would be an analog of a holomorphic minimal surface and simultaneous exremal of Kähler action except at the frame where one would have delta function singularities analogous to sources for massless d'Alembert equation.

2. There is also a dynamically generated part of the frame since the action contains also Kähler action. The dynamically generated parts of the frame would mean a failure of mimimal surface property at frame and also the failure of complete determinism localized at these frames.

3. At the frame only the equations for the entire action containing both volume term and Kähler term would be satisfied. This guarantees conservation laws and gives very strong constraints to what can happen at frames.

   The frame portions with various dimensions are analogous to the singularities of analytic functions at which the analyticity fails: cuts and poles are replaced with 3-, 2-, and 1-D singularities acting effectively as sources for volume term or equvavelently Kähler term. The sum of volume and Kähler singularities vanish by field equations. This gives rise to the interaction between volume and Kähler term at the loci of non-determinism.

4. H-picture suggests that the frames as singularities correspond to 1-D core for the deformations of CP_2 type extremals with light-like geodesic as M^4 projection, at partonic 2-surfaces and string world sheets, and at 3-D $t = t_n$ balls of CD as "very special moments in the life of self" which integrate to an analog of catastrophe. T

Deformations of Euclidean CP_2 type extremals, the light-like 3-surfaces as partonic orbits at which the signature of the induced metric changes, string world sheets, and partonic 2-surfaces at $r = t_n$ balls taking the role of vertices give rise to an analog of Feynman (or twistor -) diagram. The external particles arriving the vertex correspond to different roots of the polynomial in M^8 picture co-inciding at the vertex.

The proposed picture at the level of $H = M^4 \times CP_2$ has dual at the level of (complexified) M^8 identifiable as complexified octonions. The parts of frame correspond to loci at which the space-time as a covering space with sheet defined by the roots of a polynomial becomes degenerate, i.e. touch each other.

Concerning the physical interpretation, a crucial step of progress was the interpretation of M^8 as analog of momentum space allowing to interpret $M^8 - H$ duality as an analog of momentum-position duality and of complementarity principle of wave mechanics [L128]. This forced to modify $M^8 - H$ duality in M^4 degrees of freedom to satify the constraints posed by UP.

There is a nice analogy with the catastrophe theory of Thom [A42, A27]. The catastrophe graph for cusp catastrophe serves as an intuitive guide line. embedding space coordinates serve as behaviour variables and space-time coordinates as control variables. One obtains a decomposition of space-time surface to regions of various dimension characterized by the degeneracy of the root.

Progress in the understanding of TGD inspired theory of consciousness

The improved view about ZEO makes it possible to define the basic notions like self, sub-self, BSFR and SSFR at the level of WCW. Also the WCW correlates for various aspects of consciousness like attention, volition, memory, memory recall, anticipation are proposed. Attention is the basic process: attention creates sub-CD and subself by a localization in WCW and projects WCW spinor field to a subset of WCW. This process is completely analogous to position measurement at the level of H. At the level of M^8 it is analogous to momentum measurement.

One can distinguish between the Boolean aspects of cognition assignable to WCW spinors as fermionic Fock states (WCW spinor field restricted to given 3-surface). Fermionic consciousness is present even in absence of non-determinism. The non-determinism makes possible sensory perceptions and spatial consciousness.

A precise definition of sub-CD as a correlate of perceptive field at WCW level implies that the space-time surfaces associated with sub-CDs continue outside it. This gives powerful boundary conditions on the dynamics. For the largest CD in the hierarchy of CDs of a given self, this constraint is absent, and it is a God-like entity in ZEO. This leads to a connection between the western and eastern views about consciousness.

A connection with the minimal surface dynamics emerges [L132]. The sub-CDs to which mental image as subselves are assigned would be naturally associated with portions of dynamically generated frames as loci of non-determinism. If one identifies partonic 2-surfaces as vertices, one can interpret the collection of possible space-time surfaces for a fixed 3-surface at PB as a tree. All paths along the tree are possible time-evolutions of subself. The dynamics of consciousness for fixed 3-surface at PB becomes discrete and provides discrete correlate for a volitional action as selection of a path or a subset of paths in the tree. The reduction of dynamics of mental imagines to discrete dynamics would mean a huge simplification and conforms with the discreteness of cognitive representations.

Challenges

There are many challenges to be faced. The discrete dynamics of sub-self consciousness certainly correlates with the notion of cognitive representation based on adelic physics [L50, L51] and implying a discretization at both space-time level and WCW level. The Galois group for the extension of rationals acting on the roots of the polynomial plays a key role in this dynamics [L110, L117].

One teaser question remains. Localization requires energy quite generally and this conforms with the fact that mental images demand metabolic energy feed. It is possible to redirect attention and it remains unclear whether the mental image disappears totally or suffers BSFR.

This relates directly to the question whether consciousness continues after the physical death. If mental images (and corresponding sub-CDs) can disappear, the same can happen to us since we are mental images of some higher level self. If this cannot happen, BSFR means death and

reincarnation with an opposite arrow of time in a completely universal sense. For instance, sleep period could correspond to a kind of death at some level of the personal self hierarchy generalizing the Id-ego-superego hierarchy of Freud. This would explain why we have no memories of the sleep period.

12.4.6 Appendix: M^8- and H views about classical non-determinism and particle reactions

M^8 picture and $M^8 - H$ duality

In M^8 picture, space-time surfaces correspond to real projections of 4-D complex "roots" of octonionic polynomials obtained from real polynomials with rational coefficients by algebraic continuation, i.e. by replacing real coordinate by complexified octonion coordinate [L44, L45, L46] [L101, L102]. The interested reader finds a rather detailed summary of M^8-H duality in Appendix 12.4.6.

$M^8 - H$ duality maps the point of $M^4 \times E^4$ to a point of $M^4 \times CP_2$ such that the point of $M^4 \subset M^4 \times E^4$ is mapped to some point of $M^4 \subset M^4 \times CP_2$. $M^8 - H$ duality is not a local map. Rather, the normal space of a $x \in X^4 \subset M^8$ goes to a point of CP_2 characterizing its quaternionic normal space.

1. To be a 4-D "root" in the complex sense means that the real part of a complexified octonionic polynomial determining the space-time surfaces vanishes. The number theoretic content of this condition is that the normal space of the space-time surface is quaternionic and therefore associative. The second option would be that the tangent space is associative but this gives only M^4 as a solution.

2. At a given point there are n roots and some of them can coincide in some regions of the space-time surface. These regions correspond to the branchings of the space-time surface at which particle-like entities identified as space-time surfaces meet and interact.

   The quaternionic normal plane at this intersection is not unique so that several CP_2 points of $X^4 \subset H$ correspond to a single point of $X^4 \subset M^8$. The extreme situation is encountered in a point-like singularity when the normal plane at a given point of M^4 is a sub-manifold of CP_2.

   The interpretation is as particle vertices. The intuitive expectation is that they correspond to partonic 2-surfaces and perhaps also string world sheets. These surfaces are mapped to those in $M^4 \times CP_2$ by $M^8 - H$ correspondence.

3. Also 6-D brane like entities are predicted as universal "roots" they correspond to 6-spheres in M^8 with M^4 projection which is a 3-ball with constant value $E = E_n$ of energy as counterpart of the Minkowski time coordinate such that E_n is the root of the real polynomial defining the octonionic polynomial. The momenta $(E_n, p = 0)$ are mapped to points $t_n = (\hbar_{eff}/E_n, 0)$ and define "very special moments of time in the life of self".

   The points with $p \neq 0$, in particular the points corresponding to quark momentum, however correspond to $t < t_n$ at the boundary of cd with size $L(p) = \hbar_{ef}/\sqrt{E_n^2 - p^2}$. To these moments the failure of classical determinism giving rise to one particular kind of quantum non-determinism is concentrated. Note that points of double hyperboloid of M^4 with opposite energies are mapped to opposite boundaries of cd.

4. The intersections of 4-D "roots" with 6-D brane-like entities are 2-D and it might be possible to interpret them as analogs of either partonic 2-surfaces or string world sheets at which several roots become degenerate of octonionic polynomial coincide. Outside the singularity, the roots do not coincide and define separate space-time sheets and it is natural to interpret them as external particles of a particle reaction.

5. At the light-like orbits of partonic 2-surfaces the induced metric for the H-image of the space-time surface becomes degenerate since its signature changes. Could one say that the Minkowskian and Euclidean roots coincide at the partonic orbits?

One can also wonder what the M^8 interpretation of wormhole contacts having two throats could be. Do the two throats correspond to two coincing roots at the level of M^8 having different normal spaces and mapped to separate 2-surfaces in H?

Catastrophe theoretic analogy

Consider the analogy with the catastrophe theory of Thom [A42] in more detail.

1. Catastrophe map is the graph of solutions for the vanishing of the gradient of a potential function as a function of control parameters. One considers only real roots as function of variable control parameters and the number of real roots varies as a function of parameters and one obtains lower-dimensional regions at which the number of roots to catastrophe polynomial changes as roots become degenerate [A42, A27]. Cusp catastrophe serves as the school example.

2. In the recent case, space-time surfaces correspond to roots of complexified octonionic polynomials and the coefficients of the polynomial appear as control parameters. Also complex roots are allowed and real 4-D space-time surface is obtained as a real projection and mapped to H by $M^8 - H$ duality and conjectured to correspond to a preferred extremal of an action determined by the twistor lift of TGD.

3. The basic motivations for this assumption are quantum criticality requiring preferred extremal property, which requires at the level of H the independence of the dynamics on coupling parameters of the twistor lift of Kähler action outside the loci of non-determinism demanded by M^8 level.

Connection between singularities and preferred extremals of various types

The above picture suggests the characterization of the space-time surfaces in terms of their singularities as surfaces of M^8.

At the level of H one can consider 4 kinds of very simple preferred extremals, which give rise to prototype singularities.

1. Einsteinian spacetime $X^4 \subset M^8$ with a 4-D M^4 projection and a unique normal space as a point of CP_2. $X^4 = M^4$ defines a prototype.

2. Cosmic string extremal $X^2 \times Y^2$ with Y^2 a complex surface in CP_2 and defining a set of normal spaces assignable to a point of X^2. $M^2 \times S^2$, S^2 a geodesic sphere defines a proto type. S^2 can be either homological trivial or non-trivial.

3. $X^3 \times S^1 \subset M^4 \times CP_2$, where S^1 is a geodesic circle of CP_2, is a candidate for a preferred extremal and singular surface. Both $M^3 \times S^1$ and $E^3 \times S^1$ are minimal surfaces and vacuum extremals of Kähler action.

   For the Euclidean signature, X^3 could be space-like and define a 3-ball compactifying to S^3 as a sub-manifold of the S^6 brane. The very special moments t_n would be singular in the sense that the normal space at a given point of $X^3 \subset M^4 \subset M^8$ would not be unique and would give rise S^1 singularity.

4. CP_2 type extremal with light-like geodesic as $M^4 \subset H$ projection and corresponding to a light-like geodesic in M^8 with normal spaces forming a 3-D surface in CP_2. Also $M^1 \times Y^3 \subset M^4 \times CP_2$ can be considered but is probably not a preferred extremal.

The intuitive picture is that these 4 types of preferred extremals correspond to singularities of the normal space of $X^4 \subset M^8$ of dimension $d = 0, 1, 2, 4$ and codimension $d_c = 4 - d$.

Analogy with knot theory

In knot theory a knot in 3-D space is projected to 2-plane where one obtains a diagram containing crossings. Knot invariants can be constructed in terms of this diagram. A knot theory inspired intuition is that space-time surfaces near to these special cases are projected to these special surfaces to get the toy model.

1. Canonically embedded $M^4 \subset M^8$ (or $M^4 \subset M^4 \times CP_2$) is an analog of the plane to which the knot is projected. One can project the space-time regions with 4-D $M4$ projection to M^4. In particular, those with a Minkowskian signature of the induced metric.

2. The M^4 projection of CP_2 type extremal is 1-D light-like geodesic. One must project the deformations of CP_2 type extermals to CP_2 type extremal at the level of H. At the level of H, CP_2 type extremal could correspond to a light-like geodesic of M^8 such that each point of the geodesic is singular point such that the union of quaternionic normal spaces defines a 3-D quaternionic surface in CP_2.

   A puncture in E^3 as an infinitesimal hole serves as an analogy. At the puncture, one can say that all normal spaces labelled by points of S^2 are realized.

   At the given point of the light-like geodesic, the quaternionic normal space of point is not unique but a 3-D union of normal spaces and defines a 3-D subset CP_2.

3. For the $X^2 \times Y^2 \subset M^4 \times CP_2$ type cosmic string extremals and their small deformations, one must project to $M^2 \times S^2 \subset CP_2$. For a point of X^2 the normal spaces define $Y^2 \subset CP_2$ so that the singularity is milder.

   For $X^3 \times S^1 \subset M^4 \times CP_2$ the normal spaces at a point of X^3 would define $S^1 \subset CP_2$. If X^3 is Euclidean, these 3-D singularities could correspond to the $t = t_n$ planes associated with the branes. The small deformations of these surfaces would project to $M^3 \times S^1$. This picture would integrate all 3 kinds of singularities and various types of preferred extremals to a single unified picture.

A toy model for the singularities

The following toy model for the singularities in the case of CP_2 type extremals generalizes also to other singularities.

1. A rather general class of CP_2 type extremals can be represented as a map $M^4 \to CP_2$ given by

$$m^k = p^k f(r) \ ,$$

   where p^k is light-like momentum and r is radial $U(2)$ invariant CP_2 coordinate labelling 3-spheres of CP_2 such that $r = \infty$ gives homologically non-trivial geodesic 2-sphere instead of 3-sphere.

   If $f(r)$ approaches constant value for $r \to \infty$, one can say that M^4 time stops at this limit, and one obtains a homologically non-trivial geodesic sphere instead of 3-D surface identifiable as an intersection with 6-D brane. Various external particles of the vertex would correspond to $m^k = p_k f_i(r)$ such that their values at $r = \infty$ coincide.

   It is not possible to obtainh omologically trivial 2-sphere in this manner.

2. Outside the vertex, the CP_2 type space-time sheets have distinct light-like geodesics as M^4 projections and they can be continued to distinct regions of M^4 in the toy model.

   The analog of the knot diagram would be a set of M^4:s with different constant values of CP_2 coordinates. The CP_2 type extremals would be glued along light-like geodesics to various M^4s.

   The CP_2 points of M^4:s meeting at the same geodesic sphere must belong to the same geodesic sphere S^2. The S^2:s associated with different vertices are different. Note that any two geodesic spheres must have common points.

3. In the toy model for the string world sheets $X^2 \times Y^2$ would be projected to a piece of $M^2 \times S^2$ connecting two partonic vertices with the same S^2. S^2:s would be at the ends of the string, whose orbit is a piece of M^2.

   $B^3 \times S^1$ could be interpreted as a subset of 6-D brane with B^3 identified as the $t = t_n$ cross section of M^4 light-cone.

This picture would suggest that the singularities could be indeed located to $t = t_n$ planes and integrated together to form a rough analog of catastrophe map.

Some examples of minimal surfaces with 1-D CP_2 projection

This subsection is not directly relevant to the basic topic and is added to give ideas about the possible role of volume term.

The original proposal was that preferred extremals are extremals of Kähler action but the twistor lift introduced the volume term as an additional term. This removed the huge vacuum degeneracy of Kähler action meaning that any 4-surface for which CP_2 projection was so called Lagrange manifold with the property that induced Kähler form vanishes, was a solution of field equations. For these surface induced Kähler potential is pure gauge.

The addition of the volume term removes this degeneracy and only minimal surfaces of this kind are possible as extremals. It is however not clear whether they are preferred extremals (are they analogs of complex surfaces?).

These solutions have not been studied previously [K9]. Space-time surfaces representing a warped embedding of M^4 with a flat metric represent the simplest example.

1. Denoting the angle coordinate of the geodesic sphere S^1 byΦ and the metric of S^1 by $ds^2 = -R^2 d\Phi^2$ the ansatz reads in linear Minkowski coordinates as $\Phi = k \cdot m$, where k is analog of four-momentum. The induced metric is flat and the second fundamental form vanishes by the linearity of Φ in m so that the field equations are satisfied.

   Boundary conditions require the vanishing of the normal components of momentum currents and give $(\eta^{\alpha\beta} - R^2 p^\alpha p^\beta) n_\beta = 0$ .This condition cannot be satisfied so that these solutions should have infinite size, which looks unphysical.

   The presence of the volume term in the action implies that the induced metric appears in the boundary conditions and this represents a problem quite generally. The only way to overcome the problem is that there are no boundaries. The many-sheetedness indeed makes this possible.

   The warped extremals could represent a reasonable approximation of the space-time surface in the regions which are almost empty.

2. The light velocity defined in terms of time taken to get from the M^4 position A to B, is reduced to $c_1 = \sqrt{1 - |k \cdot k|}$. If k is light-like this does not happen.

   Although the analog of gravitational force is vanishing in warped metric, the deviation the flat metric from M^4 metric given by $|k \cdot k|$ in flat case could it be interpreted as gravitational potential and the gravitational potential energy of test mass would be given by by $E_{gr} = -m|k \cdot k|$.

   Could Nature provide a kind of cognitive representation or toy model of a gravitational field as a piecewise constant function in terms of CDs with which warped vacuum extremals would be associated? The representation would contain length scale dependent Λ as second parameter assigning momentum 4-momentum proportional to $\Lambda\, p^k$ to the CD. The volume energy would include its gravitational potential energy represented in terms of warping?

   For warped solutions the space-time light cone - to be distinguished from its embedding space counterpart - would be defined by $c_1^2 t^2 - r^2 = 0$ and space-time CD would be modified accordingly.

Only single extremal - canonically embedded M^4 - remains from the spectrum of cosmological vacuum extremals for Kähler action having 1-D CP_2 projection and defined by $\Phi = f(a)$, where f is an arbitrary function of light-cone proper time coordinate $a = \sqrt{t^2 - r_M^2}$.

At QFT-GRT limit, the many-sheeted space-time is approximated with Einsteinian cosmology with the deviation of the induced metric from M^4 metric defined by the sum of the corresponding deviations for the sheets. Since the value of Λ becomes large in short p-adic length scales, a cosmology resembling GRT type cosmology could emerge and Einstein's equations would be a remnant of Poincare symmetry.

The induced metric for the solutions has very little to do with the metric appearing at the Einsteininian limit. The models of cosmology as space-time surfaces based on Kähler action with vanishing Λ could however make sense in very long scales for which Λ approaches zero.

For string dominated cosmology, the comoving mass is proportional to a [K76, K9, K48]. One has a silent whisper amplified to a Big bang in GRT sense. Also critical cosmology [K9] as an analog of inflationary cosmology for which curvature scalar as dimensional quantity vanishes can be regarded as a silent whisper amplified to a Big Bang and also it becomes Euclidean for a critical value $a = a_0$ of cosmic time.

12.5 What could 2-D minimal surfaces teach about TGD?

In the quantum TGD based on zero energy ontology (ZEO) space-time surfaces within causal diamonds (CDs) are fundamental objects [L92, L126]. $M^8 - H$ duality plays a central role: the earlier views can be found in [L44, L45, L46] and the recent view in [L101, L102, L123] differing in some aspects from the earlier view. $M^8 - H$ duality means that one can interpret the space-time surfaces in two ways: either as an algebraic surfaces in complexified M^8 or as minimal surfaces in $H = M^4 \times CP_2$ [L126]. $M^8 - H$ duality maps these surfaces to each other.

The twistor lift of TGD is another key element [L52, L72]. It replaces space-time surfaces with their 6-D twistor spaces represented as 6-D surfaces in the product of twistor spaces assignable to M^4 and CP_2 and having an induced twistor structure. This implies dimensional reduction of a 6-D Kähler action to a sum of a 4-D Kähler action and volume term having interpretation in terms of cosmological constant Λ. Kähler structure exists only for the twistor spaces of M^4 and CP_2 [A33] so that the theory is unique.

Each extension of rationals (EQ) corresponds to a different value $\Lambda > 0$. For $\Lambda = 0$, the finite-D extension of rationals determined by real polynomials would be replaced with real analytic functions or subset of them.

Whether $\Lambda = 0$ can be accepted physically, will be one of the key topics of this article. At the level of adelic theory of cognition [L50, L49] this question boils down to the question whether cognition is always finite and related to finite-D extensions of rationals of whether also infinite-D extensions and transcendence can be allowed.

12.5.1 Basic notions

$M^8 - H$ duality and twistor lift of TGD are the basic notions relevant for what follows and its is appropriate to discuss them briefly.

Space-time surfaces at the level of M^8

The recent view of $M^8 - H$ duality [L101, L102, L123] deserves a brief summary.

At M^8 level, space-time surfaces can be regarded as algebraic 4-surfaces in complexified M^8 having interpretation as complexified octonions. The dynamical principle states that the normal space of the space-time surface at each point is associative and therefore quaternionic. The space-time surfaces are determined by the condition that the real part of an octonionic polynomial obtained as an algebraic continuation of a real polynomial with rational coefficients vanishes.

This gives a complex surface which is minimal surface from which one takes a real part by projecting to real part of complexified M^8: it is not clear whether it is minimal surface of M^8. Minimal surface property is the geometric analog of a massless d'Alembert equation [L26, L85].

Also real analytic functions can be considered [L101, L102] but this leads to infinite-D extensions of rationals in the adelization requiring that also the p-adic counterparts of the space-time surfaces exist. Whether this phase which would correspond to $\Lambda = 0$, can be accepted physically, will be one of the key topics in the sequel.

The conditions defining the space-time surfaces are exactly solvable and the conjecture is that these surfaces are minimal surfaces by their holomorphy (the induced metric of the space-time surface does not however play any role and its role is taken by the complexification number theoretic octonion norm which is real valued for the real projections) [L101, L102, L123].

Space-time surfaces at the level of $H = M^4 \times CP_2$

At the level of $H = M^4 \times CP_2$, space-time surfaces are preferred extremals (PEs) of a 6-D Kähler action fixed by the twistor lift of TGD [L72]. The existence of the twistor lift makes TGD unique since only the twistor spaces of $T(M^4)$ and $T(CP_2)$ have the needed Kähler structure [A33]. The 6-D twistor space $T(X^4)$ of the space-time surface X^4 is represented as a 6-surface X^6 in $T(M^4) \times T(CP_2)$. $T(X^4)$ has S^2 as fiber and X^4 as base. The twistor structure of $T(X^4)$ is induced from the product of twistor structures of $T(M^4)$ and $T(CP_2)$. The S^2 bundle structure of X^6 requires dimensional reduction and dimensionally reduced 6-D Kähler action consists of a volume term having an interpretation in terms of length scale dependent cosmological constant Λ and 4-D Kähler action.

Physically "preferred" means holography: to a given 3-surface at the either boundary of CD one can assign a unique space-time surface as an analog of Bohr orbit. This assumption is very probably too strong: the number of Bohr orbits is finite and the dynamically determined frames of the space-time surface would characterize the non-determinism [L126]. "Preferred" has several mathematical meanings, which are conjectured to be equivalent.

One of those meanings is that space-time surfaces simultaneous extremals of both volume term and Kähler action and field equations reduce almost everywhere to the analogs of the conditions satisfied by complex surfaces of complex manifolds. Note that the field equations express local conservation laws for the isometries of $H = M^4 \times CP_2$ and are in this sense hydrodynamic.

The field equations for preferred extremals do not depend on coupling parameters. This expresses quantum criticality and reduces the number of solutions dramatically as required by the fact that at the level the field equations are algebraic rather than differential equations.

Space-time surfaces are therefore minimal surfaces everywhere except at singularities, which are lower-dimensional surfaces. At singularities they are satisfied only for the entire action. The divergences of the isometry currents for the volume term and Kähler action would have delta function singularities, which must cancel each other to guarantee conservation laws.

The singular surfaces can be wormhole throats as boundaries of CP_2 type extremals at which the signature of the induced metric changes, partonic 2-surfaces acting as analogs of vertices at which light-like partonic orbits representing the lines of generalized Feynman (or twistor) diagram meet, and string world sheets having light-like boundaries at partonic orbits.

Also 3-D singularities are predicted and could be associated to time= constant hyperplanes of M^4, which in M^8 picture are associated with the roots of the polynomials determining space-time region: I have christened these roots "very special moments in the life of self" [L84]. The roots define 6-spheres as universal special solutions and they intersect future light-cone along $t = r_n$ hyper-plane. It is possible to glue different solutions together along these planes so that they can serve as loci of classical non-determinism.

The singular surfaces are analogous to the frames of soap films [L126]: part of them are fixed and at the boundaries of CD and part of them are dynamically generated. Classical conservation laws for the isometry currents expressing field equations pose strong conditions on what can happen in vertices.

$M^8 - H$ correspondence for the singularities

By $M^8 - H$ correspondence, the singular surfaces of $X^4 \subset H$ correspond to the singularities of the pre-image at the level of M^8. For the singularities $X^4 \subset M^8$ the quaternionic normal space of X^4 is not unique at points of a $d < 4$ dimensional surface but is replaced with a union of quaternionic normal spaces labelled by the points of sub-manifold of CP_2 for which the dimension is $d_c = 4 - d$. At the level of H, the singular points blow-up to d_c-dimensional surfaces. What happens for the normal space at a puncture of 3-space serves as a good analog.

In particular, the deformation of a CP_2 type extremal as a singularity corresponds to an image of a 1-D singularity with $(d = 1, d_c = 3)$ and $d_c = 3$-dimensional blow up. The properties of

CP_2 type extremals suggest the 1-D curve is light-like curve for mere Kähler action and light-like geodesic for the Kähler action plus volume term.

These situations correspond to $\Lambda = 0$ and $\Lambda > 0$, where Λ is length scale dependent cosmological constant as coefficient of the volume term of action.

Membrane like structures as particularly interesting singularities

Membrane-like structures appear in all length scales from soap bubbles to large cosmic voids and it would be nice if they were fundamental objects in the TGD Universe. The Fermi bubble in the galactic center is an especially interesting membrane-like structure also from the TGD point of view as also the membrane- like structure presumably defining the analog of horizon for the TGD counterpart of a blackhole. Cell membrane is an example of a biological structure of this kind. I have however failed to identify candidates for the membrane-like structures.

An especially interesting singularity would be a static 3-D singularity $M^1 \times X^2$ with a geodesic circle $S^1 \subset CP_2$ as a local blow-up.

1. The simplest guess is a bubble-like structure as a product $M^1 \times S^2 \times S^1 \subset M^4 \times CP_2$. The problem is that a soap bubble is not a minimal surface: a pressure difference between interior and exterior of the bubble is required so that the trace of the second fundamental form is constant. Quite generally, closed 2-D surfaces cannot be minimal surfaces in a flat 3-space since the vanishing curvature of the minimal surface forces the local saddle structure.

2. A correlation between M^4 and CP_2 degrees of freedom is required. In order to obtain a minimal surface, one must achieve a situation in which the S^2 part of the second fundamental form contains a contribution from a geodesic circle $S^1 \subset CP_2$ so that its trace vanishes. A simple example would correspond to a soap bubble-like minimal surface with M^4 projection $M^1 \times X^2$, which has having geodesic circle S^1 as a local CP_2 projection, which depends on the point of $M^1 \times X^2$.

3. The simplest candidate for the minimal surface $M^1 \times S^2 \subset M^4$. One could assign a geodesic circle $S^1 \subset CP_2$ to each point of S^2 in such a way that the orientation of $S^1 \subset CP_2$ depends on the point of S^2.

4. A natural simplifying assumption is that one has $S^1 \subset S^2_1 \subset CP_2$, where S^2_1 is a geodesic sphere of CP_2 which can be either homologically trivial or non-trivial. One would have a map $S^2 \to S^2_1$ such that the image point of point of S^2 defines the position of the North pole of S^2_1 defining the corresponding geodesic circle as the equatorial circle.

   The maps $S^2 \to S^2_1$ are characterized by a winding number. The map could also depend on the time coordinate for M^1 so that the circle S^1 associated with a given point of S^1 would rotate in S^2_1. North pole of S^2_1 defining the corresponding geodesic circle as an equatorial circle. These maps are characterized by a winding number. The map could also depend on the time coordinate for M^1 so that the circle S^1 associated with a given point of S^1 would rotate in S^2_1.

   The minimal surface property might be realized for maximally symmetric maps. Isometric identification using map with winding number $n = \pm 1$ is certainly the simplest imaginable possibility.

Large voids of size scale or order 10^8 light years forming honeycomb like structures are rather mysterious objects, or rather non-objects. The GRT based proposal is that the formation of gravitational bound states leads to these kinds of structures in general relativity but I do now know how convincing these arguments really are.

One should answer two questions: what are these voids and why do they form these lattice-like structures?

One explanation of large voids is based on the TGD based view about space-time as a 4-surface in $H = M^4 \times CP_2$.

1. Space-time surfaces have M^4 projection, which is 4-D for what I call Einsteinian space-times. At this limit general relativity is expected to be a good approximation for the field theory limit of TGD.

   However, the M^4 projection can be also 3-D , 2-D or 1-D. In these cases one has what looks like a membrane, string, or point-like particle. All these options are realized. The simplest membranes would look like $M^1 \times S^2 \times S^1$, S^1 a geodesic circle of CP_2, which depends on a point of $M^1 \times S^2$ defining the M^4 projection. Only this assumption allows us to have a minimal surface. Varying S^1 creates the analog of pressure difference making soap films possible. I discovered this quite recently although the existence of membrane like entities was almost obvious from the beginning.

   Small perturbations tend to thicken the dimension of M^4 projection to 4 but the deformed objects are in an excellent approximation still 3-D, 2-D or 1-D.

2. Large voids could be really voids in a good idealization! Even 4-D space-time would be absent! The void would be the true vacuum. It should be noticed that matter as smaller objects, say cosmic strings thickened to flux tubes, would in turn have galaxies as tangles, which in turn would have stars as tangles. The TGD counterparts of blackholes would be dense flux tube spaghettis filling the entire volume.

3. What is remarkable that membranes are everywhere: large voids, blackhole horizons, Fermi bubbles, cell membranes, soap bubbles, bubbles in water, shock wave fronts, etc....

What could then give rise to the lattice like structures formed from voids? Here TGD suggests a rather obvious solution.

1. The lattices could correspond to tessellations of the 3-D hyperbolic space H^3 for which cosmic time coordinate identified as light-cone proper time is constant. H^3 allows an infinite number of tessellations whereas Euclidean 3-space allows a relatively small number of lattices.

   There is even empirical evidence for these tessellations. Along the same line of sight there are several sources of light and the redshifts are quantized. One speaks of God's fingers [E2] [K76]. This is what any tessellation of cosmic voids would predict: cosmic redshift would define effective distance. Of course also tessellations in smaller scales can be considered.

2. Also ordinary atomic lattices could involve this kind of tessellations with atomic nuclei at the centers of the unit cells as voids. The space between nucleus and atom would literally be empty, even 4-D space-time would be absent!

3. Also the TGD inspired model for genetic code [L122] involves a particular tessellation of H^3 realized at the magnetic body (MB) of a biological system and realizing genetic code. This leads to the conjecture that genetic code is universal and does not characterize only living matter. It would be induced to the space-time surface in the sense that part of tessellation would define a tessellation at the space-time surface. At the level of dark matter at MB, 1-D DNA could also have 2-D and even 3-D analogs, even in ordinary living matter!

12.5.2 Key questions

The basic question to be discussed in the following is what the general ideas about 2-D minimal surfaces can teach about minimal surfaces in M^8 and H, and more generally, about quantum TGD.

Uncertainty Principle and $M^8 - H$ duality

The interpretation of M^8 as analog of momentum space [L101, L102] meant a breakthrough in the understanding of $M^8 - H$ duality but created also a problem. How can one guarantee that $M^8 - H$ duality is consistent with Uncertainty Principle (UP)? The surfaces to which one can assign well defined momentum in M^8 should correspond to the analogs of plane waves in H and geometrically to periodic surfaces.

The fact that at the level of M^8 the surfaces are algebraic surfaces defined by polynomials with rational coefficients poses therefore a problem. Periodicity requires trigonometric functions.

The introduction of real anlytic functions with rational Taylor coeffients would force the introduction of infinite-D extensions of rationals and make this possible. This is however in conflict with the idea about the finiteness of cognition forming the basic principle of adelic physics [L50, L51].

Is the category of polymials enough?

Is it possible to have periodic minimal surfaces at the level of H or at the level of both M^8 and H without leaving the category polynomials?

1. Could the non-local character of the $M^8 - H$ duality in CP_2 degrees freedom miraculously give rise to periodic functions at the level of H? Or should one perhaps modify $M^8 - H$ duality itself to achieve this [L123].

2. Periodic frames assignable to light-like curves in M^8 as light-like curves would allow to achieve periodicity in the same manner as for helicoid but this requires the extension of the category of real polynomials to real analytic functions in M^8. One could even give up the assumption about a Taylor expansion with rational coefficients and assume that the coefficients belong to some possibly transcendental extension of rationals. This option would make sense in $\Lambda = 0$ phase.

3. Or could geometry come in rescue of algebra? Could one construct periodic surfaces both at the level of M^8 and H purely geometrically by gluing minimal surfaces together to form repeating patterns as is done for 2-D minimal surfaces? This option could work in $\Lambda > 0$ phases: smoothness at the junctions would be given up but local conservation laws would hold true for the entire action rather than for volume term and Kähler action separately.

If transcendental extensions are allowed, they would naturally contain some maximal root $e^{1/n}$ and its powers. The induced extension of p-adics is finite-D since e^p is an ordinary p-adic number. Logarithms of $log(k)$, $1 \leq k \leq p$, and their powers are needed to define p-adic logarithm for given p. The outcome is an infinite-D extension. Also π and its powers are expected to belong to the minimal transcendental extension.

It came as a surprise to me that is not known whether e and π are algebraically independent over rationals, that is whether a polynomial equation $P(x, y) = 0$ with rational coefficients is true for $(x, y) = (\pi, e)$ (`https://cutt.ly/xmyL23W`.) This would imply that π belongs to the extension defined by the polynomial $P(y, e)$ in an extension of rationals by e. Same would be true in the corresponding finite-D extensions of p-adic numbers. The algebraic independence of π and e would have rather dramatic implications for the TGD view about cognition. That π and e are algebraically independent follows from a more general conjecture by Schanuel and `https://cutt.ly/ImyL1YJ`).

Is also $\Lambda > 0$ phase physically acceptable?

Can one allow also $\Lambda = 0$ phase for the action. In this case the action reduces to mere Kähler action defined by M^4 and CP_2 Kähler forms analogous to self-dual covariantly constant $U(1)$ gauge fields? Could one see $\Lambda = 0$ phase as an analog of Higgs=0 phase?

In this phase the category of rational functions would expand to a category of real analytic functions and infinite extensions of rationals containing transcendental numbers would be unavoidable and allow light-like curves as frames instead of piecewise light-like geodesics.

One could argue that since the evolution of mathematical consciousness has led to the notion transcendentals and transcendental functions, they must be realized also at the level of space-time surfaces.

One can invent objections against the $\Lambda = 0$ phase for which Kähler action has only CP_2 part and serving at the same time as arguments for the necessity of M^4 part.

1. For a mere CP_2 Kähler action, the CP_2 type extremals representing building bricks of elementary particles become vacuum extremals and are lost from the spectrum. However, also the M^4 part of Kähler action predicted by the twistor lift gives rise to Chern-Simons (C-S) term assignable to the light-like 3-surface X^3_L as the orbit of partonic 2-surface and one can assign a momentum to X^3_L. The boundary conditions guaranteeing momentum conservation make possible momentum exchange between interior and X^3_L.

2. CP_2 Kähler action has a huge vacuum degeneracy since space-time surfaces with 2-D Lagrangian manifold as a CP_2 projection are vacuum extremals. $\Lambda > 0$ eliminates most of these extremals. Also the M^4 part of Kähler action, which vanishes for canonically imbedded M^4, implies that most vacuum extremals of CP_2 Kähler action cease to be extremals even for $\Lambda = 0$.

While writing the first version of this article I had not realized that what the correct form for the Kähler property in M^4 case is.

1. Suppose for definiteness the simplest option that the M^4 Kähler form are associated with the decomposition $M^4 = M^2 \times E^2$. A more general decomposition corresponds to Hamilton-Jacobi structure in which the distributions for $M^2(x)$ and $E^2(x)$ orthogonal to each other are integrable and define slicings of M^4 [L128].

2. The naive guess was that $J^2 = -g$ condition must be satisfied. This implies that the M^2 part of Kähler form of $M^4 = M^2 \times E^2$ decomposition has an electric part, which is imaginary so that the energy density is of form $-E^2 + B^2$ ($= 0$ for M^4). For instance, solutions of $M^2 \times Y^2$, where Y^2 is any Lagrangian manifold of CP_2 would have negative energy for $\Lambda = 0$. Even worse, Kähler gauge potential would be imaginary and the modified Dirac equation would be non-hermitian.

3. The problem disappears by noticing that the M^2 by its signature has hypercomplex rather than complex structure, which means that the counterpart of the imaginary unit satisfies $e^2 = 1$ rather than $i^2 = -1$. This allows a real Kähler electric field and the situation is the same as in Maxwell's theory.

12.5.3 About 2-D minimal surfaces

A brief summary about 2-D minimal surfaces and questions raised by them in TGD framework is in order. One can classify minimal surfaces to those without frame and with frame.

Some examples of 2-D minimal surfaces

The following examples about minimal surfaces are collected from the general Wikipedia article about minimal surface `https://cutt.ly/Hn673ry`) and various other Wikipedia articles. This article gives also references to articles (for instance the article "The classical theory of minimal surfaces" of Meeks and Perez [A47]) and textbooks discussing minimal surfaces , see for instance [A41]. Also links to online sources are given. "Touching Soap Films - An introduction to minimal surfaces" `https://cutt.ly/dmwMnJ7`) serves as a general introduction to minimal surfaces). There is also a gallery of periodic minimal surfaces (`https://cutt.ly/RmwMQ49`), which is of special interest from the TGD point of view.

1. Minimal surfaces without frame

In E^3 frameless minimal surfaces have an infinite size and are often glued from pieces, which asymptotically approach a flat plane.

Catenoid (`https://cutt.ly/in675Z6`) is obtained by a rotation of a catenoid, which is the form of the chain spanned between poles of equal height in the gravitational field of Earth. Catenoid has two planes as asymptotics and is obtained from torus by adding two punctures. Costa's minimal surface (`https://cutt.ly/in65wyP`) is obtained from torus by adding a single puncture and its second end looks like a catenoid.

Frameless minimal surfaces in E^3 allow also lattice-like structures. Schwarz minimal surface (`https://cutt.ly/dn65rJm`) is an example about minimal giving rise to 3-D lattice like structure. These surfaces have minimal genus $g = 3$.

In compact spaces closed minimal surfaces are possible and some quite surprising results hold true, see the popular article "*Math Duo Maps the Infinite Terrain of Minimal Surfaces*" (`http://tinyurl.com/yyetb7c7`). These surfaces have area proportional to volume of the embedding space and the explanation is that these surfaces fill the volume densely [A34, A38].

2. Minimal surfaces with lattice like structure

There exists also minimal surfaces with lattice-like structure.

1. Riemann described a one parameter of minimal surfaces with a 1-D lattice structure consisting of shelfs connected by catenoids (https://cutt.ly/Pn65y3f).

2. Scherk surfaces (https://cutt.ly/3n65oeB) are singly or doubly periodic. Scwartz surfaces (https://cutt.ly/un65pCK) are triply periodic structures defining 3-D lattices and have minimal genus $g = 3$. This kind of surfaces have been used to model condensed matter lattices. These surfaces have also hyperbolic counterparts.

3. Minimal surfaces spanned by frames

Minimal surfaces with frames allow to models soap films and are obtained as a solution of the Plateau's problem (https://cutt.ly/7n65fgT).

1. Helicoid (https://cutt.ly/Wn65jgT) represents a basic example of a simply periodic framed surface. Also helicoid involves transcendental functions. A portion of helicoid is locally isometric to catenoid.

2. Arbitrary curves can serve as frames with some mild restrictions. The minimal surface need not be unique. A given 2-D minimal surface is obtained in topological sense from a compact manifold by adding a puncture to represent boundaries defined by frames or the boundaries at infinity.

Some comments on 2-D minimal surfaces in relation to TGD

The study of the general properties of 2-D minimal surfaces from the TGD perspective suggest a generalization to the TGD framework and also makes possible a wider perspective about TGD itself.

1. Frameless minimal surfaces in TGD framework

Frameless minimal surfaces in E^3 have infinite sizes since they are locally saddle like. In TGD framework, the most interesting space-time surface are expected to be framed. Despite this frameless minimal surfaces are of interest.

1. In the TGD framework the minimal surfaces could extend to infinity in time-direction and remain finite in spatial directions. The asymptotically flat 2-plane could in TGD correspond to the simplest extremals of action: M^4 and "massless extremals" (MEs); surfaces $X^2 \times Y^2$ with X^2 a string world sheet and Y^2 complex manifold of CP_2; and CP_2 type extremals with 1-D light-like curve as CP_2 projection.

   Conservation laws do not allow M^4 even in principle unless the total angular momentum and color charges vanish. Various singularities could deform flat M^4 in close analogy with point and line charges.

2. In curved compact spaces also closed minimal surfaces are possible [A34, A38] (http://tinyurl.com/yyetb7c7). One can wonder whether CP_2 as a curved space might allow a volume-filling closed 2-D or 3-D minimal surfaces besides complex surfaces and minimal Lagrangian manifolds [L85]. For $\Lambda > 0$, only complex surfaces defined by polynomials in M^8 appear in PEs. It is difficult to see how this kind of exotic structure could define a physically interesting partonic 2-surface although formally one could consider a product of string world sheet and this kind of 2-surface.

2. Minimal surfaces with lattice structure

2-D minimal surfaces in E^3 allow lattice-like structures with dimensions 1, 2 and even 3. They are are interesting also in TGD framework.

1. Scwartz surface (https://cutt.ly/un65pCK), call it S, allows in the TGD framework a variant of form $M^1 \times S \times S^1$, where S^1 is a geodesic sphere. Same applies to all 2-D minimal

surfaces allowing a lattice structure and could be in a central role in condensed matter physics according to TGD. Also hyperbolic variants of a lattice like structure expected to relate to the tessellations of hyperbolic 3-space can be considered and could play important role at the level of magnetic bodies (MBs) as indeed suggested [L122].

2. If $\Lambda = 0$ phase is physically acceptable, it would make possible light-like curves as frames and also lattice-like minimal surfaces with periodicity forced by that of the light-like curve assignable to to CP_2 type extremal as M^8 pre-image.

   Note that $\Lambda = 0$ phase relates to $\Lambda > 0$ phase by the breaking of conformal symmetry transforming light-like curves to light-like geodesics. The interpretation of $\Lambda = 0$ phase in terms of the emergence of continuous string world sheet degrees of freedom is attractive.

   Another interpretation would be based on the hierarchy of Jones inclusions of hyper-finite factors of type II_1 (HFFs). $\Lambda > 0$ phase would define the reduced configuration space ("world of calassical worlds" (WCW)) in finite measurement resolution defined by the included HFF representing measurement resolution and $\Lambda = 0$ phase as the factor without this reduction. The approximation of real analytic functions by polynomials of a given degree would define the inclusion. This sequence of approximations would be realized as genuine physical systems ,rather than only approximate descriptions of them.

3. For $\Lambda > 0$ allowing only polynomial function, periodic smooth minimal surfaces in M^8. The construction of Schwartz surface suggests how one can circumvent this difficulty.

   Schwartz surface defines a 3-D lattice obtained by gluing together analogs of unit cells. If a region of a minimal surface intersects orthogonally a plane, the gluing of this surface together with its mirror image gives rise to a larger minimal surface and one can construct an entire lattice-like system in this way. These surfaces are not smooth at the junctions.

   In the TGD framework, one would construct lattice in time direction and the gluing would occur at edges defined by 3-D $t = r_n$ planes ("very special moments in the life of self" [L84]). Local conservation laws as limits of field equations are enough and derivatives can be discontinuous at $t = r_n$ planes. The expected non-uniqueness of the gluing procedure would mean a partial failure of the strict classical determinism having a crucial role in the understanding of cognition in ZEO. This is discussed in [L126].

   M^8-picture suggests a very concrete geometric recipe for constructing minimal surfaces periodic in time direction and this would make it possible to realize UP for $M^8 - H$ duality.

The general vision would be that $\Lambda > 0$ phases the periodic minimal surfaces can be constructed as piecewise smooth lattice-like structures in the category of real polynomials by using the gluing procedure whereas in $\Lambda = 0$ phase they correspond to smooth surfaces in the category of real analytic functions.

3. Minimal surfaces spanned by frames

Minimal surfaces spanned by frames are of special interest from TGD point of view.

1. In the TGD framework. Minimal surfaces are spanned by fixed frames at the boundary of CD and by dynamically generated frames in the interior of CD. The dynamically generated frames break strict determinism, which means that space-time surfaces as analogs of Bohr orbits becomes non-unique [L126] and holography (for its various forms see [L101, L102]) forced by the General Coordinate Invariance is not completely unique.

2. CP_2 type extremal in H would correspond to 1-D singularity in M^8 analogous to a frame assigned 2-D minimal surfaces. The physical picture suggests that this curve is a light-like curve for the Kähler action ($\Lambda = 0$) and a light-like geodesic for action involving also volume term ($\Lambda > 0$). In the first case the periodicity of the light-like curve could give rise to periodic minimal surfaces as generalization of helicoid. In the second case discretized variants could replace these curves.

3. For the minimal surfaces discussed above, polynomials are not enough for their construction and the examples involve transcendental functions like trigonometric, exponential and logarithmic functions in their definition.

The same is expected to be true also in TGD. Should one leave the category of polynomials and allow all real analytic functions with rational Taylor coefficients? Or should one assume also the $\Lambda = 0$ phase making possible real analytic functions?

As far as cognitive representations are involved, this would mean that cognition becomes infinite since the extensions of p-adic become infinite. Could $\Lambda = 0$ phase be associated with an expansion of consciousness, kind of enlightment, and relate to mathematical consciousness?

12.5.4 Periodic minimal surfaces with periodicity in time direction

There are several motivations for the periodic minimal surfaces.

Consistency of $M^8 - H$ duality with Uncertainty Principle

Consistency of $M^8 - H$ duality with UP is one motivation.

1. M^8 is interpreted as an analog of momentum space. $M^8 - H$ correspondence must be consistent with UP. If $M^8 - H$ correspondence in M^4 degrees of freedom involves inversion of form $m^k \to \hbar_{eff} m^k/m^2$. [L101, L102, L123]. This solves the problem only partially. $M^8 - H$ correspondence should realize also the idea about plane wave as space-time counterpart of point in momentum space.

   The first guess [L123] would be that the $X^4 \subset CD \subset M^8$ is mapped to a union of translates of images of CD by inverse of P^k, where is the total momentum assignable to CD. What I saw as a problem, was that this gives a lattice-like many-particle state rather than a single particle state as a counterpart of a plane wave.

   If the momentum is space-like, this is indeed the case. Therefore I proposed that the image is a quantum superposition of translates rather than their union and represents an analog of plane wave. I failed to realize that this is not the case for time-like momentum since periodicity in time direction does not mean lattice as many-particle state.

   A geometric correspondence for time-like momenta is possible after all! The problem is a concrete realization of this correspondence and here the geometric construction gluing together the analogs of unit cells to form a periodic structure in time direction suggests itself.

2. Quite concretely, one could take part of $X^4 \subset CD \subset M^8$ defining particle and construct a periodic surface with a period determined by the total time-like momentum assignable to this part of X^4. X^4 has a slicing by planes $e = e_n$ [L84] assignable to 6-branes with topology of S^6 defining universal special solutions of algebraic equations. Here e_n is a root of the real polynomial defining X^4.

   One could take a piece $[e_1, ..., e_k]$ of $X^4 \subset CD$ and glue it to its time reversal in M^8 to get a basic unit cell and fuse these unit cells together to obtain a periodic structure.

   The differences $e_i - e_j$, which for M^8 correspond to energy differences, are mapped by inversion to time differences $t_i - t_j$ in H. The order of magnitude for the p-adic length scale assignable to CD in question is the same as for the largest difference for the roots as conjectured on basis of the conjecture that the p-adic length scale correspond to a ramified prime of the extension dividing $|t_i - t_j|^2$ for some pair (i, j). The p-adic prime for CD need not however be a ramified prime and one can develop an argument for how it emerges [L126].

3. Rather remarkably, one can glue together portions $[t_1, ..t_r]$ and the mirror image of $[t_k, t_r]$, for any k. All possible sequences of this kind are possible! This suggests an analogy to logical reasoning: $[t_n, t_{n+1}]$ would represent a basic step $t_n \to t_{n+1}$ in the reasoning and one could combine these steps. Could this process serve as the geometric correlate for logical thought or as engineeering at the level of fundamenta interactions?

   The physicalists refusing to accept non-determinism at the fundamental level fail to realize that our technology relies on a fusion of deterministic processes and is therefore not consistent with strict determinism. Also computer programs consist of deterministic pieces.

4. There is still one open question. Does the construction of the time lattices occur only at the level of H or both at the level of M^8 and H? One can argue that the realization of the analog of inverse Fourier transform forces the construction at both sides.

Bohr orbitology for particles in terms of minimal surfaces

In TGD, space-time surfaces correspond to analogs of Bohr orbits. One should also have classical space-time analogs for ordinary bound states as Bohr orbits for particles. Atoms represent the basic example. In TGD Universe, Bohr model should be much more than mere semiclassical model. Also the geodesic orbits of particles in gravitational fields should have minimal surface analogs.

The Bohr orbits should be representable as parts of minimal surfaces identifiable as deformed CP_2 type extremals. There are two options to consider corresponding to $\Lambda = 0$ phase and to $\Lambda > 0$ phases.

1. $\Lambda = 0$ *phase*

$\Lambda = 0$ phase corresponds to a long length scale limit but general consideratons encourage its inclusion as a genuine phase. Its relation to $\Lambda > 0$ phases would be like the relation of real numbers to extensions of rationals and transcendental functions to polynomials.

1. For $\Lambda = 0$, CP_2 type extremals are vacuum extremals and correspond to 1-D singularities, which are light-like curves in M^8 blown up to orbits of wormhole contacts in H.

   Light-like curve as an M^4 projection of Bohr orbit of this kind can give rise to "zitterbewegung" as a helical motion with average cm velocity $v < c$. The proposal for the TGD based geometric description of Higgs mechanism realizes this zitterbewegung of CP_2 type extremals for Kähler action. This makes it possible to assign to any particle orbit - be it Bohr orbit in an atom or a geodesic path in a gravitational field, an average of a light-like curve.

2. Light-likeness gives rise to Virasoro conditions emerging in the bosonic string theories. This served as a stimulus leading to the assignment of extended Kac-Moody symmetries to the light-like partonic orbits X^3 . The isometries of H define the extended Kac-Moody group. The generators of the Kac-Moody algebra depend on the complex coordinate z of the partonic 2-surface and on the light-like radial coordinate of X^3. Super-symplectic symmetries assigned to the light-like $\delta M^4_{\pm} \times CP_2$ and identified as isometries of WCW have an analogous structure [K72] [L109].

   The light-like orbits of the partonic 2-surfaces in H are connected by string world sheets. The interpretation could be that in $\Lambda = 0$ phase strings emerge as additional degrees of freedom.

3. For CP_2 part of Kähler action $\Lambda = 0$ CP_2 type extremals are vacua (this need not be the case for the deformations). The C-S term for CP_2 Kähler action carries no momentum and cannot contribute to momentum and cannot realize momentum conservation for deformed CP_2 type extremals.

   However, the C-S term for the M^4 part of Kähler action defines the partonic orbits as dynamical entities. If the projection of the deformation of CP_2 type extremal at the wormhole throat has M^4 projection with dimension $D = 3$, M^4 C-S term gives rise to non-vanishing momentum currents and the smooth light-orbit is consistent with the momentum conservation if boundary conditions are realized. What is remarkable that M^4 C-S term also gives rise to small CP breaking, whose origin is not understood in the standard model. The tiny C-S breaking term would be paramount for the existence of elementary particles!

The implications of this picture are rather profound. It could be possible to assign to any physical system rather detailed view about the minimal surfaces involved both at the level of H and M^8.

Could tachyonic states appear as parts of non-tachyonic states somewhat like tachyonic virtual particles appear in Feynman graphs?

1. The possibly existing periodic minimal surfaces with tachyonic total momenta would have an interpretation as lattice-like many-particle states. This excludes them as unphysical. In fact, one cannot construct tachyonic periodic minimal surfaces in the proposed way since the planes $t = t_n$ have time-like normal.

2. M^8 picture allows to interpret tachyonicity as a trick. In the M^8 picture the choice of $M^4 \subset M^8$ is in principle free. The mass squared of the particle depends on this choice since M^4 momentum is a projection of M^8 momentum to $M^4 \subset M^8$. For eigenstates of M^4 mass, one can rotate $M^4 \subset M^8$ in such a way that the mass squared vanishes. For a superposition of states with different mass squared possible in ZEO this is not possible but one can choose M^4 so that mass squared is minimized. This gives rise to p-adic thermodynamics as a description for the mixing with heavier states.

   One could understand the tachyonic ground state as an effective description for the choice of M^4 in this manner.

2. $\Lambda > 0$ phase

For $\Lambda > 0$ only light-like geodesics are possible and this forces a modification of the above picture by replacing light-like curves with piece-wise light-like geodesics.

1. A discrete variant of zitterbewegung consisting of pieces of light-like geodesics is suggestive. The dynamics in stringy degrees of freedom would be almost frozen and completely dictated by the ends of the string. Discretized version of smooth dynamics would be in question. This kind of phenomenological model for hadronic strings has been proposed.

2. The change of the direction of the partonic orbit takes place in a vertex. In M^8 picture it is associated with a partonic 2-surface associated with a $t = r_n$ hyperplane at which several CP_2 type extremals meet at the level of H. These reactions could be seen as ordinary particle reactions.

3. Another way to change the direction would be based on the interaction of parton with the interior degrees of freedom so that conservation laws are not lost. The interaction between the 3-D orbit of wormhole throat and interior is defined by the condition that normal components of the isometry currents of the total Kähler action are equal to the divergences of C-S currents the partonic orbit. For the M^4 part of C-S action only momentum currents are non-vanishing whereas for CP_2 only color currents are non-vanishing.

   At the turning points the normal current of the entire Kähler action - and the divergence of the isometry current for C-S part CP_2 type extremal must become non-vanishing and divergent but cancel each other. Local conservation laws hold true and one can speak of a momentum exchange between interior and wormhole throat. This picture applies also to color currents.

3. A connection with Higgs mechanism

The fact that zitterbewegung makes the particle effectively massive in long enough scales, suggests an analogy with the massivation by the Higgs mechanism.

1. The interactions between partonic orbits and the interior of the space-time surface are analogous to the interactions of particles with a Higgs field leading to the massivation as the Higgs field develops a vacuum expectation value.

2. M^4 Kähler form represents a constant self-dual Abelian gauge field. Although this field is not a scalar field, it is analogous to the vacuum expectation value of the Higgs field as far as its effects are considered.

4. A connection twistor diagrams and generalization of cognitive representations

Also a connection with twistor diagrams is suggestive. The light-like geodesic lines appearing as 1-D singularities in M^8 would correspond to light-like differences of the time-like momenta assignable to vertices. In H they are assignable with partonic 2-surfaces identifiable as boundaries of 3-D blow ups of 1-D singularities in M^8. In M^8, the graphs containing time-like momenta connected by singular lines would define analogs of twistor diagrams. Also at the level of H the lines connecting partonic 2-surfaces would be light-like as also the distances between them since the inversion map preserves light-likeness of the tangent curves.

This would pose additional conditions on cognitive representations.

1. The original proposal [**?**]as that cognitive representation consists of points of X^4 for which M^8 coordinates belong to the EQ associated with the polynomial considered. The expectation was that one has a generic situation so that this set is automatically finite.

   The explicit solution of the polynomial equations however led to a surprising finding was that the number of these points was a dense set for the space-time surfaces satisfying co-associativity conditions [L101, L102]. The second surprise was that co-associativity (associativity of normal space) is the only possible option.

2. The additional conditions guaranteeing that the cognitive representation consists of a finite number of objects, generalize it from a discrete set of points to a union of singularities with co-dimension $d_c = 4 - d$, $d = 1, 2, 3$.

   The vertices would be connected by $d = 1$ light-like singularities and belong to 2-D partonic 2-surfaces as $d = 2$ singularities at $t = r_n$ surfaces in turn defining $d = 3$ singularities. Also 2-D string world sheets having $d = 1$ singularities as boundaries would be included.

3. This would also generalize twistor diagrams as a frame holographically coding for the space-time surface as an analog of Bohr orbit. At the M^8 level, the definition of the parts of this structure would involve only parameters with values in EQ (say the end points of a light-like geodesic defining it).

Periodic self-organization patterns, minimal surfaces, and time crystals

Periodic self-organization patterns which die and are reborn appear in biology. Even after images, which die and reincarnate, form this kind of periodic pattern. Presumably these patterns would relate to the magnetic body (MB), which carries dark matter in the TGD sense and controls the biological body (BB) consisting of ordinary matter. The periodic patterns of MB represented as minimal surface would induce corresponding biological patterns.

The notion of time crystal [B12] (`https://cutt.ly/2n65x0k`) as a temporal analog of ordinary crystals in the sense that there is temporal periodicity, was proposed by Frank Wilczeck in 2012. Experimental realization was demonstrated in 2016-2017 [D1] but not in the way theorized by Wilczek. Soon also a no-go theorem against the original form of the time crystal emerged [B20] and motivated generalizations of the Wilzeck's proposal.

Temporal lattice-like structures defined by minimal surfaces would be obvious candidates for the space-time correlates of time crystals.

1. One must first specify what one means with time crystals. If the time crystal is a system in thermo-dynamic equilibrium, the basic thermodynamics denies periodic thermal equilibrium. A thermodynamical non-equilibrium state must be in question and for the experimentally realized time crystals periodic energy feed is necessary.

   Electrons constrained on a ring in an external magnetic field with fractional flux posed to an energy feed form a time crystal in the sense that due to the repulsive Coulomb interaction electrons form a crystal-like structure which rotates. This example serves as an illustration of what time crystal is.

2. Breaking of a discrete time translation symmetry of the energy feed takes place and the period of the time crystal is a multiple of the period of the energy feed. The periodic energy feed guarantees that the system never reaches thermal equilibrium. According to the Wikipedia article, there is no energy associated with the oscillation of the system. In rotating coordinates the state becomes time-independent as is clear from the example. What comes to mind is a dynamical generation of Galilean invariance applied to an angle variable instead of linear spatial coordinate.

3. Also the existence of isolated time crystals has been proposed assuming unusual long range interactions but have not been realized in laboratory.

   Time crystals are highly interesting from the TGD perspective.

1. The periodic minimal surfaces constructed by gluing together unit cells would be time crystals in geometric sense (no thermodynamics) and would provide geometric correlates for plane waves as momentum eigenstates and for periodic self-organization patterns induced by the periodic minimal surfaces realized at the level of the magnetic body. It is difficult to avoid the idea that geometric analogs of time crystals are in question.

2. The hierarchy of effective Planck constants $h_{eff} = nh_0$ is realized at the level of MB. To preserve the values of h_{eff} energy feed is needed since h_{eff} tends to be reduced spontaneously. Therefore energy feed would be necessary for this kind of time crystals. In living systems, the energy feed has an interpretation as a metabolic energy feed.

   The breaking of the discrete time translation symmetry could mean that the period at MB becomes a multiple of the period of the energy feed. The periodic minimal surfaces related to ordinary matter and dark matter interact and this requires con-measurability of the periods to achieve resonance.

3. Zero energy ontology (ZEO) predicts that ordinary ("big") state function reduction (BSFR) involves time reversal [L92, L126]. The experiments of Minev *et al* [L79] [L79] give impressive experimental support for the notion in atomic scales, and that SFR looks completely classical deterministic smooth time evolution for the observer with opposite arrow of time. Macroscopic quantum jump can occur in all scales but ZEO together with h_{eff} hierarchy takes care that the world looks classical! The endless debate about the scale in which quantum world becomes classical would be solely due to complete misunderstanding of the notion of time.

4. Time reversed dissipation looks like self-organization from the point of view of the external observer. A sub-system with non-standard arrow of time apparently extracts energy from the environment [L87]. Could this mechanism make possible systems in which periodic oscillations take place almost without external energy feed?

   Could periodic minimal surfaces provide a model for this kind of system?

1. Suppose that one has a basic unit consisting of the piece $[t_1, .., t_k]$ and its time reversal glued together. One can form a sequence of these units.

   Could the members of these pairs be in states, which are time reversals of each other? The first unit would be in a self-organizing phase and the second unit in a dissipative phase. During the self-organizing period the system would extract part of the dissipated energy from the environment. This kind of state would be "breathing" [L162].

   There is certainly a loss of energy from the system so that a metabolic energy feed is required but it could be small. Could living systems be systems of this kind?

2. One can consider also more general non-periodic minimal surfaces constructed from basic building bricks fitting together like legos or pieces of a puzzle. These minimal surfaces could serve as models for thinking and language and behaviors consisting of fixed temporal patterns.

12.6 The dynamics of SSFRs as quantum measurement cascades in the group algebra of Galois group

Adelic physics [L49, L50] is a proposal for the physics of both sensory experience having real physics as correlate and cognition having various p-adic physics as correlates. Adele is a book-like structure formed by real numbers and the extensions of p-adic number fields induced by a given extension of rationals with the pages of the book glued together along its back consisting of numbers belonging to the extension of rationals. This picture generalizes to space-time level. Adelic physics relies on the notion of cognitive representation as unique number theoretic discretization of the space-time surface. This discretization has also fermionic analog in terms of spinor structure associated with the group algebra of the Galois group of extension.

Adelic physics, $M^8 - H$ duality, and zero energy ontology lead (ZEO) to a proposal that the dynamics involved with "small" state function reductions (SSFRs) as counterparts of weak measurements could be basically number theoretical dynamics with SSFRs identified as reduction

cascades leading to completely un-entangled state in the space of wave functions in Galois group of extension of rationals identifiable as wave functions in the space of cognitive representations. As a side product a prime factorization of the order of Galois group is obtained.

The result looks even more fascinating if the cognitive dynamics is a representation for the dynamics in real degrees of freedom in finite resolution characterized by the extension of rationals. If cognitive representations represent reality approximately, this indeed looks very natural and would provide an analog for adele formula expressing the norm of a rational as the inverse of the product of is p-adic norms.

12.6.1 Adelic physics very briefly

Number theoretic vision leading to adelic physics [L49] provides a general formulation of TGD complementary to the vision [K72] (`http://tinyurl.com/sh42dc2`) about physics as geometry of "world of classical words" (WCW).

1. p-Adic number fields and p-adic space-time sheets serve as correlates of cognition. Adele is a Cartesian product of reals and extensions of all p-adic number fields induced by given extension of rationals. Adeles are thus labelled by extensions of rationals, and one has an evolutionary hierarchy labelled by these extensions. The large the extension, the more complex the extension which can be regarded as $n-D$ space in K sense, that is with K-valued coordinates.

2. Evolution is assigned with the increase of algebraic complexity occurring in statistical sense in BSFRs, and possibly also during the time evolution by unitary evolutions and SSFRs following them. Indeed, in [L104] (`http://tinyurl.com/quofttl`) I considered the possibility that the time evolution of self in this manner could be induced by an iteration of polynomials - at least in approximate sense. Iteration is a universal manner to produce fractals as Julia sets and this would lead to the emergence of Mandelbrot and Julia fractals and their 4-D generalizations. In the sequel will represent and argument that the evolution as iterations could hold true in exact sense.

   Cognitive representations are identified as intersection of reality and various p-adicities (cognition). At space-time level they consist of points of embedding space $H = M^4 \times CP_2$ or M^8 ($M^8 - H$ duality [L44, L45, L46] allows to consider both as embedding space) having preferred coordinates - M^8 indeed has almost unique linear M^8 coordinates for a given octonion structure.

3. Given extension of given number field K (rationals or extension of rationals) is characterized by its Galois group leaving K - say rationals - invariant and mapping products to products and sums to sums. Given extension E of rationals decomposes to extension E_N of extension E_{N-1} of ... of extension E_1 - denote it by $E \equiv H_N = E_N \circ E_{N-1} ... \circ E_1$. It is represented at the level of classical space-time dynamics in M^8 (`http://tinyurl.com/quofttl`) by a polynomial P which is functional composite $P = P_N \circ P_{N-1} \circ ... \circ P_1$. with $P_i(0) = 0$. The Galois group of $G(E)$ has the Galois group $H_{N-1} = G(E_{N-1} \circ ... \circ E_1)$ as a normal subgroup so that $G(E)/H_{N-1}$ is group.

   The elements of $G(E)$ allow a decomposition to a product $g = h_{N-1} \times h_{N-1} \times ...$ and the order of $G(E)$ is given as the product of orders of H_k: $n = n_0 \times .. \times n_{N-1}$. This factorization of prime importance also from quantum point of view. Galois groups with prime order do not allow this decomposition and the maximal decomposition and are actually cyclic groups Z_p of prime order so that primes appear also in this manner.

   Second manner for primes to appear is as ramified primes p_{ram} of extension for which the p-adic dynamics is critical in a well-defined sense since the irreducible polynomial with rational coefficients defining the extension becomes reducible (decomposes into a product) in order $O(p) = 0$. The p-adic primes assigned to elementary particles in p-adic calculation have been identified as ramified primes but also the primes labelling prime extensions possess properties making them candidates for p-adic primes.

   Iterations correspond to the sequence $H_k = G_0^{\circ k}$ of powers of generating Galois groups for the extension of K serving as a starting point. The order of H_k is the power n_0^k of integer

$n_0 = \prod p_{0i}^{k_i}$. Now new primes emerges in the decomposition of n_0. Evolution by iteration is analogous to a unitary evolution as ex^{iHt} power of Hamiltonian, where t parameter takes the role of k .

4. The complexity of extension is characterized by the orders n and the orders n_k as also the number N of the factors. In the case of iterations of extension the limit of large N gives fractal.

5. Galois group acts in the space of cognitive representations and for Galois extensions for which Galois group has same order as extensions, it is natural do consider quantum states as wave functions in $G(E)$ forming n-D group algebra. One can assign to the group algebra also spinor structure giving rise to $D = 2^{M/2}$ fermionic states where one has $N = 2M$ or $N = 2M + 1$). One can also consider chirality constraints reducing D by a power of 2. An attractive idea is that this spinor structure represents many-fermion states consisting of $M/2$ fermion modes and providing representation of the fermionic Fock space in finite measurement resolution.

12.6.2 Number theoretical state function reductions as symmetry breaking cascades and prime factorizations

The proposed picture has very important quantal implications and allows to interpret number theoretic quantum measurement as a number theoretic analog for symmetric breaking cascade and also as a factorization of an integer into primes.

1. The wave functions in $G(E)$ - elements of group algebra of $G(E)$ can be decomposed to tensor products of wave functions in $G(E)/H_{N-1}$ and H_{N-1}: these wave functions in general represent entangled states. One can decompose the wave functions in H_{N-1} in similar manner and the process can be continued so that one obtains a maximal decomposition allowing no further decomposition for any factor. These non-decomposable Galois groups have prime order since its group algebra as Hilbert space of prime dimension has no decomposition into tensor product.

2. In state function reduction of wave function $G(E)$ the density matrices associated with pairs $G(E)/H_{N-1}$ and H_{N-1} are measured. The outcome is an eigenstate or eigen-space and gives rise to symmetry breaking from $G(E) \equiv H_N$ to $E_N \times H_{N-1}$. The sequence of state function reductions should lead to a maximal symmetry breaking corresponding to a wave function as a produce of those associaetd with Galois groups of prime order. This define a prime factorization of the dimension n of Galois group/extension to $n = \prod_{i=1}^{N} p_i^k$! The moments of consciousness for self would correspond to prime factorizations! Self would be number theoretician quite universally!

Also also the fermionic cognitive representation based on finite-D Fock states defined by spinor components of $G(E)$ is involved. The interpretation of Fock state basis as a a basis of Boolean algebra in TGD: the spinor structure of WCW could be representation for Boolean logic as a "square root" of Kähler geometry of WCW. Cognition indeed involves also Boolean logic.

12.6.3 SSFR as number theoretic state function reduction cascade and factorization of integer

A highly interesting unanswered question is following. "Small" state function reductions (SSFRs) define the life cycle of self as their sequence. What are the degrees of freedom where SSFRs occur?

1. SSFRs take place at the active boundary of CD which shifts in statistical sense towards future in the sequence of state function reductions. State at the passive boundary is not changed.

2. The idea that quantum randomness could correspond to classical chaos (or complexity) associated with the iteration of polynomials (Mandelbrot and Julia fractals) [L104] led to reconsider the hypothesis that the polynomial representing space-time decomposes to a product $P = P_2(T - r) \times P_1(r)$. T corresponds to the distance between the tips of CD and $r = t$

to the radial coordinate of M^4 assignable to the passive boundary of CD and equal to time coordinate t. $P_i(0) = 0$ is assumed to hold true.

P_2 would change in SSFRs whereas P_1 and state at passive boundary would not. SSFRs (analogous to so called weak measurements) at active boundary would give rise to sensory input and various associations - Maya in Eastern terminology. P_1 would correspond to the unchanging part of self - "soul" or real self as one might say.

I was also led to consider a simplified hypothesis that P_2 is obtained as iteration $P_2 = Q_1^{\circ n}$ in n:th n unitary evolution preceding SSFR. One would start from some iterate $Q_1^{\circ k}$. This would reduce quantum dynamics to iteration of polynomials and to a deep connection with Mandelbrot and Julia fractals but it was quite clear why this would be true.

3. The mere factorization $P = P_2 \times P_1$ implies that the Galois groups associated with active and passive boundary of CD commute and number theoretic state function reduction cascade for the wave functions in $G(E)$ for the extension determined by P_2 at active boundary could correspond to SSFR. Or course, also other commuting degrees of freedom are possible but number theoretic degrees of freedom could be the most important degrees of freedom involved with SSFRs.

12.6.4 The quantum dynamics of dark genes as factorization of primes

Gene level provides a fascinating application of this picture.

Thiscontribution was inspired by discussion with Bruno Marchal about his with title "Do the laws of physics apply to the mind?" (`https://tinyurl.com/ycls2bpt`). Bruno Marchal is a representative of computationalism, which might be called idealistic and Bruno believes that physics follows from computationalism. The somewhat mystical notion of self-reference is believed to lead to consciousness . I do not share this view. The gist of the posting comes towards end where I describe how computationalism generalizes to quantum computationalism in TGD generalizing also the notion of quantum computation. What conscious problem solving is? This is the question to be discussed.

1. As found, dark photons and dark protons forming DNA codons as triplets could correspond to triplet representations for prime factor Z_3 of Galois group of Z_6. Codon and conjugate codon could in turn correspond to the prime factor Z_2 of Galois group Z_6 so that double strand would correspond to Z_6 suggested by findings of Mills [L31] and TGD inspired model color vision [L63].

2. DNA codons could correspond to extension with Galois group Z_3, and one can consider an entire hierarchy of extensions of extensions of .. .extensions with dimensions n_i satisfying thus $n = \prod_{i=1}^{N} n_i$ and having Z_6 as subgroup at the lowest level of the hierarchy. The number N of factors would be the number of polynomials in the functional composition and thus define a kind of abstraction levels (abstractions are thoughts about thoughts about..., maps of maps of ...). N is expected to increase in evolution.

3. Could this abstraction hierarchy be realized at gene level? Genes decompose into transcribed regions - exons - and introns. Could different decomposition of genes to exons and introns correspond to different values of N and n_i and to different Galois groups. Could genes themselves form larger composites?

   Could genomes form even large structures such as chromosomes with larger Galois groups. Years ago I considered the possibility of a collective gene expression based on the collective MB of organelle, organ, or even population: could this correspond to an extension associated with several genomes?

4. Could SSFR correspond to a sequence of symmetry breakings for the Galois groups of these structures decomposing them to sub-groups? Number theoretic interpretation would in terms of decompositions of integers to primes! Genome would be a quantum computer performing number theory!

5. Metabolic energy feed would increasing h_{eff} would also increase the orders $n_i = h_{eff}/h_0$ of the extensions appearing in the composition of extensions and thus the orders of polynomial factors P_i in the functional composite defining the extensions. Therefore the decompositions would be dynamical.

   Metabolic energy feed requires BSFR changing the arrow of time if metabolic energy feed is actually feed of negative energy to environment. The emergence of a new prime factorization would require BSFR. That the time evolution by iterations would not require BSFR would support the proposal that time evolution by BSFRs could be induced by iteration dynamics for the polynomial P_2 assignable to the active boundary of CD.

12.6.5 The relationship of TGD view about consciousness to computationalism

This text was inspired by discussion with Bruno Marchal about his with title "Do the laws of physics apply to the mind?" (`https://tinyurl.com/ycls2bpt`). Bruno Marchal is a representative of computationalism, which might be called idealistic and Bruno believes that physics follows from computationalism. The somewhat mystical notion of self-reference is believed to lead to consciousness.

I do not share this view. The gist of the posting comes towards end where I describe how computationalism generalizes to quantum computationalism in TGD generalizing also the notion of quantum computation. What conscious problem solving is? This is the question to be discussed.

To my view computationalism is one of the failed approaches to consciousness - it cannot cope with free will for instance. It however contains an essential aspect which is correct: the idea of deterministic program leading from A to B. Problem solving be can regarded as attempt to find this program. You fix A as initial data and try to find a program leading from A to a final state characterized by data B. The program has duration T and can be very long and it is not clear whether it exists at all. You try again and again and eventually you might find it. In the real conscious problem solving this process means making guesses so that the process cannot be deterministic.

What does this view about problem solving correspond to in ZEO? We have states A and B represented as quantum states and we try to find quantum analog of classical program leading from A to B in some time T which can be varied.

1. A and B are realized as superpositions of 3-surfaces and fermionic states at them - located at time values t=0 and t=T. T can vary. Can we find by varying T a (superposition of) deterministic time evolution(s) - preferred extremal(s) (PE) - connecting A and B?

   In ZEO and for fixed A and T PE in general does not exist. In ideal situation (infinite measurement resolution) and for given A and T, B is unique if it exists at all. One has analog of Bohr orbit and the quantum analog of classical program as the superposition of Bohr orbits starting from A and hopefully leading to B as a solution of the problem.

   Remark: These superpositions can be regarded as counterparts of functions in biology and behaviors in neuroscience. The big difference to standard physics is that time=constant snapshot in time evolution of say bio-system is replaced with quantum superposition of very special time evolutions - PEs. Darwinian selection of also behaviors in biology correlates strongly with this.

2. So: given A and B, we try to find a value of T for which superposition of PEs from A to B exists. This would be the quantum program leading from A to B, and solving our problem.

   Actually, not only ours, universe is full of conscious entities solving problems at various levels of self hierarchy. This takes place by a sequences of "small" SFRs (SSFRs, weak measurements) increasing T in statistical sense and replacing the state at B with a new one determined by state A for given value of T. At the level of conscious experience this is sensory perception and all that which is associated with it.

   Finding the solution is analogous to the halting of quantum Turing machine by ordinary state function reduction, which corresponds in ZEO to a "big" (ordinary) SFR (BSFR). This

would mean death in universal sense and reincarnation with reversed arrow of time in ZEO? Or is BSFR and death failure to solve the problem? I cannot answer.

Remark: The notion of self-reference is replaced with much more concrete notion of becoming conscious of what one was conscious of before SSFR. SSFR indeed gives rise to conscious eperience and one avoids the infinite regress associated with genuine self-reference. As an additional bonus one obtains evolution since the extension of rationals characterizing space-time surfaces can increase meaning higher level of consciousness. At the limit algebraic numbers the cognitive representation is dense subset of space-time surface.

3. Also finite measurement resolution and discreteness characterizing computation emerge from number theory.

   To be a solution classically means that the 3-surface(s) representing B to have fixed discrete cognitive representation given by finite number of embedding space points in the extension of rationals defining the adele. Quantally, quantum superpositions of these points with fixed quantum numbers represent the desired final state.

   Also Boolean logic emerges at fundamental level as square root of Kähler geometry one might say. Many-fermion state basis defines a Boolean algebra and time evolution for induced spinors is analogous to truth preserving Boolean map in which truths code for infinite number of conservation laws associated with symmetries of WCW.

4. How to find the possibly existing solution at given step (unitary evolution plus SSFR) with t=T? One performs cognitive quantum measurements at each step represented by SSFR. They reduce to cascades of quantum measurements for the states in the group algebra of Galois group - call it Gal - of Galois extension considered.

   Gal has hierarchical decomposition to inclusion hierarchy of normal subgroups implying the representation of states in group algebra of Gal as entangled states in the tensor product of the group algebras of normal sub-groups of Gal. The hope is that this Galois cascade of SFRs produces desired state as an outcome and one can shout "Eureka!".

12.7 DNA and Time Reversal

This section is devoted to the view about DNA inspired by (zero energy ontology) ZEO [L115, L97] forming the basis of the quantum measurement theory of Topological Geometrodynamics (TGD) [K5, K3] and by the notion of dark DNA [L73] inspired by the TGD view about dark matter as phases of the ordinary matter with effective Planck constant $h_{eff} = nh_0 > h$ [L50, **?**, K23, K24, K25, L56] at (magnetic body) MB [L2, L74, L37, L159] - the third key notion distinguishing TGD from standard model.

12.7.1 Basic picture

The basic prediction of ZEO is that "big" (ordinary) state function reduction (BSFR) changes the arrow of time meaning "death" and "reincarnation" with opposite arrow of time. For dark matter at the MB the periods with a given arrow of time would be long and induce the long-lasting effective change of the arrow of time for the ordinary matter.

This leads to a new view about self-organization [L99] involving in an essential manner time reversed dissipation looking like energy feed in the standard direction and quantum coherent MB as a master quantum controlling the ordinary matter. The energy feed is necessary since the increase of h_{eff} requires energy.

Time reversal and the dynamics of DNA

The time reversals of the basic processes like transcription and replication turn out to be possible only for the conjugate strand - this is basically due to the chiral selection and CPT theorem in TGD context. CPT C denotes harge conjugation, P spatial reflection, and T geometric time reflection to be distinguished from thermo-dynamical time reversal and time reversal occurring in BSFR. The triviality of C (matter-antimatter asymmetry) implies that T acts like P mapping

molecules to their mirror images. By chiral selection enzymes can catalyze processes but not their time reversals. For instance, conjugate strand polymerizes in reverse time direction - this looks like depolymerization in standard time direction. Polymerization of the conjugate strand however occurs in standard time direction but in reverse direction along strand.

The recombination of DNA strands during meiosis is poorly understood. This could correspond to reconnections for the magnetic flux tubes associated with the active DNA strands. Time reversal would occur in BSFR and formerly passive conjugate DNA strands would depolymerize to "loose" codons [L111] (not independent letters) by the time reversed polymerization, the flux tubes associated with the formerly active strands would suffer reconnections inducing recombination without assistance of enzymes, second BSFR would occur, and be followed by the replication of recombined active strands.

Does DNA have longitudinal electric field with direction correlating with the arrow of time?

According to the findings of Becker [J4, J27], the direction of the electric along the body axis field determines whether the system is awake or asleep. By the properties of electric field under time reflection, the arrow of time correlates also with the direction of the electric field. TGD predicts that consciousness is possible even at the level of DNA. Could also DNA have a longitudinal electric field with direction correlating with the arrow of time of DNA at the MB of DNA? Could there be a switch changing the direction of this electric field?

There is an inspiring analogy with microtubules, which are highly dynamical and carry a longitudinal electric field, whose strength correlates with the microtubule length [I74, I75]. Could sticky ends generate a longitudinal field along DNA double strand with strength determined by the lengths of the sticky ends?

In the standard picture the flux of the longitudinal electric field would be proportional to the difference of the negative charges associated with the sticky ends. In TGD framework DNA strands are accompanied by the dark analog of DNA with codons realized as 3-proton units neutralizing the negative charge of the ordinary DNA except at sticky ends.

A simple proposal for the time switch based on the analog of Becker's DC currents emerges: proton flow of the dark protons between sticky ends would change the arrow of time. The model could generalize also to proteins known to be ferro-electrets and accompanied also by their dark analogs.

12.7.2 DNA and time reversal

TGD inspired theory of consciousness based on ZEO [L115] predicts that also DNA is a conscious system: actually TGD Universe is in a well-defined sense panpsychic. In a "big" (ordinary) state function (BSFR) system "dies" and "reincarnates" with a reversed arrow of time. The hierarchy of effective Planck constants $h_{eff} = nh_0$ [**?**, K23, K24, K25] having a number theoretical interpretation [L50] labels the phases of the ordinary matter behaving like dark matter and will be referred to as "dark matter" in the sequel. Large values of h_{eff} make quantum coherence possible in arbitrarily long length and time scales.

The dark matter at the layers of the MB of the system (MB means a deviation from Maxwell's electrodynamics) controls the ordinary bio-matter. Dark matter resides at the flux tubes carrying monopole flux not possible in the Maxwellian world. The TGD based model [L20] identiies the negatively charged exclusion zones (EZs) generated in Pollack effect [L15, **?**] as regions from which part of protons transferred to flux tubes as dark protons. Applied to the water environment of DNA this leads to the notion of dark DNA as flux tubes carrying dark proton triplets representing genetic codons [L73]. Also mRNA, aminoacids, and tRNA would have these representations. Dark DNA strands would accompany the ordinary DNA strands. The positive charge of the dark DNA and mRNA would screen the negative charge of ordinary DNA and stabilize it.

The attention is in the recent article in the dynamical processes associated with DNA. Could time reversal play a key role in various processes related to DNA. The basic process considered are DNA transcription and replication and meiosis and it is interesting to view them in ZEO. Could one imagine a switch inducing time reversal of DNA as a "big" (ordinary) state function (BSFR) in the scale of entire DNA double strand + dark DNA double strand accompanying it?

Deassembly as a time reversal of assembly and time reversal switch for DNA?

In ZEO one must seriously consider the possibility of reverse translation, reverse transcription and reverse polymerization. The recombination of DNA strands, which is the least well-understood part of meiosis, might involve time reversal of the polymerization of the passive strand and also DNA repair might involve time reversal. Time reversal might allow the healing of genetic defects.

Time reversed processes might occur at least in DNA scale but it is an open question whether they occur in long time scales. As already found, matter-antimatter asymmetry and chiral selection pose strong constraints on the allowed time reversals: they can occur only for the conjugate DNA strand as catalyzed processes. The time reversal of translation is not possible but time reversal of transcription using the conjugate strand is.

1. Few natural scientists like the branch of philosophy called deconstructionism (in particular, "anything goes" irritates any TOE builder) but it would seem that deconstruction is an excellent characterization of assembly and de-assembly as time reversals of each other.

   Deconstruction would not be actually a new idea. Sustainable development means that nowadays wastes are treated systematically. Various mechanical and electric devices are de-constructed into their basic building bricks to be used again.

   Why not the same in biology? For instance, could protens be deconstructed to tRNA and mRNA, which in turn would be deconstructed to mRNA codon? It turns out that chiral selection prevents time reverse translation.

2. Deconstruction at the level of DNA would naturally involve time reversed DNA + dark DNA and very naturally the passive strand related by a conjugation to active strand would be now active. Deconstruction would be a construction in a reversed time direction. Could this give a reason why for the presence of the passive DNA strand?

   One must clarify how the strands are related? What does time reversal do to the strands?

   (a) Since charge conjugation replacing protons with antiprotons does not occur, C must act trivially. $CPT = 1$ which is identity in quantum field theories but in TGD states that the states at the boundaries of CD are permuted - the corresponding fermionic vacua are analogous to Dirac sea and its conjugate. This impllies that PT acts trivially and T acts as a reflection P changing the chiralities and direction of the strands.

   (b) Time reversal would transform left-handed strand to right-handed vice versa and the 3' and 5' ends would be permuted. The effect would be a permutation of the strands geometrically. DNA strands would become their mirror images geometrically and for the $3' \to 5'$ orientation the order codons would be the same.

   (c) The strands of DNA have opposite chiralities. Chiral selection can explain why only the second DNA strand is active: there are no ezymes catalyzing it transcription. In the time reversal the passive strand would become active and the time reversed DNA transcription would begin from 3' end so that the resulting mRNA would conjugate of the mRNA associated with the active strand. For standard time direction the process would look like conjugate mRNA sequence approaching the usually passive strand and decaying to the "loose" mRNA codons [L111] (nucleotides in standard picture).

   (d) If the processes proceed from $3' \to 5$ direction determined by chemistry, the time reversed transcription would produce the same mRNA. In standard time direction mRNA consistent with conjugate DNA strand would attach to conjugate DNA strand and split to RNA codons (in TGD and to RNA nucleotides in standard picture).

3. How could one achieve the deconstruction of say mRNA as a time reversal at the level of DNA? Could there exist a simple time reversal switch in DNA reversing the electric field of DNA+dark DNA? Could there be an enzyme changing the position of this switch?

   What could be this switch? In next secton it will be proposed that switch would just move the part of the dark proton sequence associated with sticky end nucleotides to the opposite

end of the DNA strand! There would be a proton current flowing along the ordinary DNA strand.

These switching currents could be the counterparts for the direct currents of Becker [J4, J27] and would change the direction of DNA's electric field! This mechanism would change the arrow of time and direction of the electric also at the level of the entire body as it falls in sleep or wakes up! Same applies to the electric field from the frontal lobes to hindbrain.

DNA transcription and replication and their time reversals

Could the time reversals of DNA replication and transcription occur? Is the depolymerization of the DNA strand equivalent to the time reversal or polymerization or are these separate processes? Does the time reversal of the replication make sense?

The basic constraint comes from the discrete symmetries. By matter-antimatter asymmetry charge conjugation is trivial - otherwise also antiprotons would define representation of the dark code. Since the generalization of quantum field theoretic identity $CPT = 1$ holds true one must have that a generalization of $PT = 1$ holds true. Time reversal would change the chirality of DNA strands.

Chirality selection for enzymes in turn poses a second powerful constraint meaning that time reversed processes can occur for the passive conjugate DNA strand only (having opposite chirality as compared to active DNA strand). The implication is that enzyme, which have a fixed chirality, can catalyze in standard time direction only processes for the active DNA strand but not for the passive strand. Enzymes can however catalyze time reversed processes for the conjugate strand. In particular, the degradation of active DNA strand cannot be equivalent with time reversal of polymerization since the latter cannot be catalyzed by enzymes.

Consider first the discrete symmetries in more detail.

1. The key constraints emerge from the ZEO based generalization of the $CPT = 1$ identity of quantum field theories generalized to ZEO. Here C is charge conjugation, P is reflection and T time reflection. In ZEO "1" is replaced by permutation of states at the opposite boundaries of CD defining the zero energy state and the replacement of Dirac vacuum with its conjugate. Call this permutation operation P_{ZEO} so that one has $CPT = P_{ZEO}$.

2. Since antiprotons are not involved in biology by matter-antimatter asymmetry, $C = 1$ is true and one obtains $PT = P_{ZEO}$. Therefore T must act as reflection and map DNA strand to its mirror image. Chirality is changed and the order of codons becomes opposite and 3' and 5' ends are permuted. The DNA strand looks like the original one as far as codons are considered but is its geometric mirror image so it is not expected to be active - unless P permutes 3' and 5'. From Wikipedia [I5] one learns that this is not the case. Hence the conjugate strand would become active in the time reversal.

   In particular, the time reversed catalyzed processes can use only the conjugate strand as a template since only in this case the enzymes satisfy the chirality constraint. In particular, this applies to polymerization and depolymerization, which are not time reversed process as was the first guess. Furthermore, the polymerization for conjugate trand is depolymerization in reversed time direction.

   Matter-antimatter asymmetry and chiral selection therefore imply that catalyzed processes for the active DNA strands are in the standard time direction and for the passive DNA strands in the opposite time direction.

Some examples help to understand what would be involved.

1. Consider first the time reversal of the transcription. If the time reversal occurs it must attach mRNA strand to the time reversed conjugate strand and the time reversed transcription would mean splitting of mRNA to "loose" codons [L111]: this process can be catalyzed by enzymes with standard chirality. If the conjugate of the gene coding for mRNA does not exist as a gene, this process is not possible. Therefore mRNA must allow also the ordinary depolymerization catalyzed by enzymes. Same is expected to apply to the depolymerization of DNA and proteins. Loose codons would be analogous to tRNAs.

This raises a question about how symmetric the spectrum of genes is. How often does the conjugate of gene exist? If there is strong symmetry breaking the reverse transcription rarely occurs.

2. An interesting challenge is to understand the details of DNA replication and its possible time reversal. What constraints does the chiral selection for enzymes pose? The replication of both strands is catalyzed by the same enzyme: DNA polymerase and the processes occur simultaneously. Since enzymes have single chirality only, this leaves only one possibility: the replication of the conjugate strand involves time reversal and is depolymerization in the reversed arrow of time.

   Indeed, the replication of the conjugate strand occurs in a direction opposite to the ordinary ($3' \to 5'$). The replication of the conjugates strand would be the decay to codons but in reversed time direction. Note that the splitting of the DNA double strand to separate strands (unentangled quantum systems) is necessary to change the arrow of time only for the conjugate strand.

Meiosis and time reversal

Meiosis is an especially interesting application since the reshuffling of DNA strands in meiosis is not well-understood in biology-as-nothing-but-chemistry approach. The crucial step is the shuffling of the corresponding pieces of homologous DNA strands. Could the reshuffling involve de-assembly regarded as a time reversal of the assembly followed by re-assembly meaning a return to the original arrow of time: this would be completely analogous to what mechanic does when repairing a machine. Also the DNA repair could rely on this mechanism.

1. The first observation made already earlier is that the formation of several reconnections between - say - active DNA strand involving touching at several points with subsequent reconnection at the level of magnetic flux tubes would give an elegant description for the reconnection at the level of say active strands. Here magnetic flux tubes would demonstrate their explanatory power.

   The problem is that if this occurs for pairs of both active and passive strands, there is no guarantee that the reconnection patterns determining the re-shuffling are consistent. How can one guarantee this?

2. Here time reversal of polymerization for the passive DNA strand comes in rescue. Two BSFRs changing the arrow of time would take place.

   (a) The arrow of time changes for both strands of DNA. At the de-assebly step the passive strand decays to codons. This is just time reversal for polymerization and by the chirality selection for enzymes only the passive strand can de-assemble in this manner. This happens for the conjugate strands of both double DNA strands involved.

   (b) At the shuffling step the two formerly active time reversed DNA strands pair with each other and the repeated reconnections about as a sequence of SSFRs inducing shuffling of the pieces of DNA. This process cannot be catalyzed by enzymes since the required chirality would be wrong. Since the outcome is non-deterministic the situation must be quantum critical in the sense that the classical time evolutions defining the zero energy state are initial value sensitive and state function reduction selects superposition of evolutions corresponding to the same outcome.

   (c) At the re-assembly step the arrow of time changes back to the original for the resulting shuffled active DNA strands replicate.

Whether the translation of mRNA to proteins could have a time reversal was asked in the earlier article [L108]? This does not seem to be possible. Due to the chiral selection proteins do not have double strand structure with strands possessing opposite chiralities. Also mRNA has only one chirality. Therefore the time reversal of translation proceeding from mirror proteins and mirror tRNA to mirror mRNA is not possible.

12.7.3 Could the sticky ends make DNA double strand a conscious ferroelectret?

The basic motivation for this section could be Becker's finding [J4, J27]; its direction determines whether the system is awake or asleep. In ZEO [L115] these states could correspond to opposite arrows of time at some level of the fractal hierarchy of the layers of MB labelled by the values of h_{eff}. The arrow of time would change in BSFR. The sign of the longitudinal electric field correlates with the arrow of time on basic of the basic properties of electromagnetic field tensor so that BSFR should change the direction of electric field: this suggests some kind of switch changing the arrow of time and in standard ontology turning consciousness on/off.

Could the same be true for DNA + dark DNA system as well? In the sequel the idea that sticky ends make the DNA double strand + its dark counterpart with $h_{eff} > h$ a ferro-electret carrying longitudinal electric field is considered. The longitudinal electric field is non-vanishing also in standard framework without dark DNA if the lengths at the ends of the DNA double strand are different. This field would be analogous to the electric field along the body axis.

This model is discussed also in a related article [L161]. As far as contents are considered, the recent discussion is more or less identical except that the main emphasis is on consciousness.

Different ends of DNA double strand

There is a variety of different ends of DNA double strand and of telomere.

1. Blunt ends contain two paired bases so that they do not define a full codon.

$$5' - CTGATCTGACTGATGCGTATGCTAGT - 3'$$
$$3' - GACTAGACTGACTACGCATACGATCA - 5'$$

   Straight cut by exonuclease enzyme produce blunt ends.

2. Overhangs are short, mimally just one nucleotide A in 3' end: one could have for instance following configuration

$$5' - ATCTGACTA - 3'$$
$$3' - TAGACTGA - 5'$$

   Overhangs are most often palindromic.

3. An example of longer sticky end is following:

$$5' - ATCTGACT3' - TAGACTGACTACG$$

   The length of the unpaired portion of sticky end can be hundreds of nucleotides.

4. Frayed ends correspond to sequence of basic pairs breaking the A-T, C-G pairing rules.

$$5' - ATCTGACTAGGCA - 3'$$
$$3' - TAGACTGACTACG - 5'$$

Empirical evidence for the ferroelectret property of DNA

To the best of our knowledge, there is no reported evidence for longitudinal static electric fields in DNA in an extensive Web search. This might be simply because of inability to measure them in past. Indeed, a model for DNA nucleotides A,T,C,G as ferroelectrets based solely on standard chemistry is discussed [I88] and would imply that also DNA can be ferroelectret. This could in a special case give rise to a longitudinal electric field, and if there is an electric field in the absence of external electric field (spontaneous ferroelectricity), it could be also in the direction of DNA strand.

The reported existence of electric currents along DNA perhaps analogous to Becker's DC currents is one indirect evidence for the longitudinal electric field. A very interesting test would be so called DNA crystals [I70, I26] (see also the popular artcle at `https://cutt.ly/Hd3fvMW`)) in electric field, heated, or put under mechanical stress.

DNA is analogous like cell interior being negatively charged with one negative charge per nucleotide assignable to the phosphate. The stability of DNA against Coulomb force is however not well-understood and TGD would solve the problem with a pairing of DNA strand with a parallel helical flux tube carrying 3 dark protons per codon with dark proton triplet realizing genetic codon. Ordinary chemical codons would be a secondary representation of the code. Could this make possible ferroelectret property of DNA?

Could the sticky ends of the telomeres give rise to a longitudinal electric field along DNA?

In the standard picture about DNA different negative charges at the sticky ends could give a longitudinal electric field proportional to the difference of the charges. DNA double strand would however have a net charge now. Second possibility is that the nucleotides behave as dipoles even in the absence of the external electric field. If these dipoles are forced to be parallel to DNA by an external electric field they give rise to a longitudinal electric field.

TGD based view is that DNA is paired with dark analog of DNA. This view leads to the suggestion that sticky ends/overhangs give rise to positive or negative charges at the end of DNA and that opposites at the ends of DNA generate strong longitudinal electric field along DNA. For DNA with blunt ends there would be no electric field.

What would be needed for chromosome as dipole like entity is that the ends of the chromosome carrying the telomeres have charges of opposite sign: in the simplest case they would have the same magnitude so that one would have a dipole.

1. Could telomeres be analogous to microtubules?

Microtubules are highly dynamical having a varying length. They also have a longitudinal electric field [I74, I75]. Likewise, the the ends of chromosomes are dynamical and their length is changing and controlled by the telomerase enzyme [I86, I90]. Could telomeres or entire chromosomes be analogous to microtubules? Could chromosomes (`https://cutt.ly/Ud21bjd`) carry longitudinal electric fields? That would not be surprising since living matters are populated by ferroelectrets [I56].

Remark: The option that only telomeres could carry these fields would require that the joint between the coding portion of DNA and telomere is charged. This does not look natural.

Due to the properties of the electric field under time reversal, the direction of the bio-electric field would in TGD Universe correlate with the arrow of time [L115] changing in "big" (ordinary) state function reductions (BSFRs) meaning "death" or "falling asleep" and re-incarnation with an opposite arrow of time. In particular, sleep could correspond to conscious experience but with a different arrow of time at some level of the hierarchy of layers of MB) [L77] serving as master controlling the biological body (BB).

Remark: The hierarchy of Planck constants $h_{eff} = nh_0$ labelling phases of ordinary matter behaving like ark matter predicts [L50, L77] macroscopic quantum coherence explaining the coherence of biomatter. This allow BSFRs in arbitrarily long length and time scales, for instance, the scales of chromosomes.

The first guess motivated by the findings of Becker about bio-electric fields [J4, J27] is that when the telomere shortens, the electric field associated with DNA weakens, and eventually the organism dies [I29]. Telomere length is controlled by telomerase enzyme and for stem cells, germ cells and cancer cells the shortening does not occur [I58].

Telomeres are dynamical and could somehow provide DNA with a longitudinal electric field closely related to this dynamics. The strength of the electric field associated with the DNA double strand could correlate with the properties of telomeres and in particlar the lengths of their negatively charged sticky ends at the ends of the chromosome.

2. The TGD based model for DNA as ferroelectret

Although most of the telomere has a normal base-pairing, there is an additional unpaired nucleotide sequence - overhang - associated with either strand. In the minimal case it is just one nucleotide A. What could this mean in TGD framework: could it give the desired constant electric field along DNA strand. Is its strength proportional to the length of the overhang determined by the number of its nucleotides? There would be 1 negative charge per nucleotide.

1. Suppose that both strands are accompanied by dark DNA strands parallel to them and having opposite charge neutralizing the DNA in the scale of this pairing. Dark codon would be identified as a 3-proton unit. Dark RNA, tRNA and amino-acids are predicted. Vertebrate genetic code is predicted correctly in the sense that the number of DNA codons corresponding to given dark amino-acid is the same as for vertebrate genetic code [L73, L98].

2. What could be the counterpart of the sticky end for dark DNA sequence? Suppose that the dark DNA strands be equally long so that there would be no symmetry breaking. This leaves two natural options for a given sticky end.

   (a) Both dark DNA strands have portions associated with the sticky end. Since the sticky end/overhang would be neutralized, this would give for the end of the double strand a positive charge $Q = ne$, n the number of nucleotides in the sticky end.

   (b) Both dark DNA strand portions are missing at the sticky end. Now the charge would be negative and equal to the charge $Q = -ne$ of the sticky end.

3. The magnitude of the electric field along DNA flux tube created by a single sticky end would be

$$E = \frac{Q}{S} = \frac{en}{S} \quad ,$$

   where S is the thickness of the system DNA + dark DNA. The fields of the sticky ends sum up and there would be a net electric field along DNA double strand +dark DNA given by

$$E = \frac{Q_1 - Q_2}{S} = \frac{e(n_1 - n_2)}{S} \quad .$$

   One can consider two options.

   Option I: There is dark DNA present (TGD option) and the situation is a) at the first end of the chromosome and b) at the opposite end. One obtains opposite signs of charges $Q_1 = n_1 e$ and $Q_2 = -n_2 e$ and electric field is $E = (n_1 + n_2)e/S$.

   Option II: There is no dark DNA (standard physics option). The charges at the sticky ends are negative and one has $E = e(n_1 - n_2)/S$.

4. The video about telomeres [I77] (`https://cutt.ly/Mfi0Cc1`) suggests that the sticky ends are associated with different DNA strands and are of the same length. For the standard physics option (no dark DNA) charges at the sticky ends have the same sign and one has $E = e(n_1 - n_2)/S$. The field vanishes for Option II and equals to $E = 2n/S$ for Option I.

   This field would be quite strong. The electric fields at opposite ends of the chromosome sum up and cancel each other along DNA if the charges are of the same sign : there is however positive interaction energy causing a repulsive force. For the TGD option the Coulomb energy is negative. For the standard physics option it would be positive and would not favor the stability of DNA.

Quantitative estimates
In the sequel some simple quantitative estimates are performed.

1. Minimization of electrostatic energy taking into account only the nearest neighbor interactions

The system must minimize its electrostatic energy to be stable. Assume that the charges of the overhangs are opposite: $n_1 = -n_2 = n$. For the more general situation with $n_1 \neq n_2$. For the same sign for n_1 and n_2 there would be a repulsion between the ends of DNA.

1. In this case overhangs would give a negative contribution to the electrostatic energy of the system.

$$E_{ends} = -\frac{n^2 e^2 L}{S} \quad ,$$

where L is the length of DNA double strand without overhangs and S is it transversal area. Otherwise the contribution is positive.

2. The negative electrostatic energies between dark strand and ordinary strand with opposite charges. There are two pairs of this kind. In the first approximation one has

$$E_{OD} = -2N\frac{e^2}{R_{OD}} \ .$$

N is the total number of nucleotides in DNA without overhangs and R_{OD} is the distance between dark and ordinary DNA strands. One has $N = (dn/dl)L$, where dn/dl is the number of codons per unit length. One has approximately $dn/dl = 10$ nucleotides per nanometer.

This gives

$$E_{OD} = -2\frac{(dn/dl)e^2L}{R_{OD}} \ .$$

The ratio of the two negative contributions tending to stabilize the system is

$$r = \frac{E_{OD}}{E_{ends}} = 2\frac{(dn/dl)S}{R_{OD}} \simeq \frac{20S}{nm \times R_{OD}} \ .$$

3. There are positive electrostatic interaction energies between dark strands with distance $R = R_{DD}$ and ordinary strands with distance $R = R_{OO}$. The energy is given by

$$E = \frac{Ne^2}{R} = \frac{(dn/dl)e^2L}{R} \ .$$

The total contribution to the electrostatic energy is positive and given by

$$E_{OO} + E_{DD} = (dn/dl)e^2L \times (\frac{1}{R_{OO}} + \frac{1}{R_{DD}}) \ .$$

The total electrostatic energy in this approximation is

$$E = e^2L[-\frac{n^2}{S} - 2(dn/dl)(\frac{1}{R_{OD}} - \frac{1}{R_{OO}} - \frac{1}{R_{DD}}) \ .$$

4. The generalized electrostatic force in the longitudinal direction is given by

$$F = -\frac{dE}{dL} = -e^2[-\frac{n^2}{S} - 2(dn/dl)(\frac{1}{R_{OD}} - \frac{1}{R_{OO}} - \frac{1}{R_{DD}}) \ .$$

For $n > n_{min}$ DNA tends to get longer and for $n < n_{min}$ it tends to get shorter.

5. In equilibrium this force must vanish. $F = 0$ condition fixes the number n of nucleotides in the sticky end:

$$n^2 = n_0^2 = (dn/dl) \times S[-\frac{2}{R_{OD}} + \frac{1}{R_{OO}} + \frac{1}{R_{DD}}] \ ,$$

This gives

$$n = n_{min} = \sqrt{(dn/dl)\frac{S}{R_{DD}}} \times \sqrt{-2\frac{R_{DD}}{R_{OD}} + \frac{R_{DD}}{R_{OO}} + 1} = \sqrt{\frac{10S}{R_{DD}nm}}\sqrt{-2\frac{R_{DD}}{R_{OD}} + \frac{R_{DD}}{R_{OO}} + 1} \ .$$

Note that the condition $n_{min} > 0$ requires that without the overhangs at the end the configuration would be unstable.

$$2\frac{R_{DD}}{R_{OD}} \geq \frac{R_{DD}}{R_{OO}} + 1 \ .$$

must hold true. Since the right-hand side is larger than unity one must have $2R_{DD} > R_{OO}$. As a special case one could have a maximally symmetric DODO type configuration with $R_{OO} = R_{DD} = R_{OD}$ for which the above inequality becomes equality and one has $n = 0$. $n = 1$ is realized rather generally and is maximally near to this situation

6. n would not depend on the length L of the chromosome in the approximation taking into account only the nearest neighbor interactions between various DNA codons. Taking them into account implies that the electrostatic energy is a nonlinear function of L and n_{min} is predicted to depend on L - probably the dependence is weak suggesting that the dependence of $L = L(coding) + L(telomere)$ - or actually the telomere length $L(telomere)$ - on n_{min} is strong so that it would be an ideal control variable.

7. The increase of the length n of the overhang creates a force increasing the length of DNA and its reduction does the opposite. One can say the situation is critical and that $n = n_{min}$ stabilizes the situation. The reduction of the length of overhang below critical value would have disastrous effects.

This model is certainly not the only one that one can imagine and involves drastic approximations since only the nearest neighbour Coulomb interactions has been taken into account. Also the sticky ends of the chromosome could have different lengths and thus charges so that the chromosome would have a net charge and the stable length for DNA would depend on this charge.

Also the distances between various DNA strands serve as parameters and the stable length depends on these parameters: these parameters could depend on chemical parameters like pH and thermo-dynamical parameters. The length of the sticky end is expected to vary also during the life span of the chromosome and also depend on how many DNA replications preceded the generation of the chromosome. The length of the sticky end has spectrum and implies a spectrum for the telomere length since the length $L(coding)$ of the coding part of the chromosome cannot be changed. In the linear approximation all lengths $L = L(coding) + L(telomere)$ are allowed and if the corrections are small, $L(telomere)$ is very sensitive to $L(stickyend)$.

The length of the sticky end rather than the length of the telomere would be the primary controller. The quite high strength of the longitudinal electric field is a surprise. An interesting prediction is that prokaryotes with circular DNA strands would have no wake-up-sleep cycle like eukaryotes. Viruses however have both circular and open strands.

2. Minimization of the electrostatic energy taking into account interaction between non-nearest neighbors

What kind of corrections the inclusion of the Coulomb interactions of charges which are not nearest neighbors couldhave?

1. Nearest neighbors have been identified as neighbors in transversal direction and it has been assumed that only DNA-DNA and DDNA-DDNA, and DNA-DDNA interactions matter. A better approximation takes into account also the repulsive nearest- neighbor interactions of phosphates and those of dark protons along dark DNA. The same story applies to DNA-DDNA interactions.

   All these terms give a contribution proportional to L and mean only a scaling of the parameter n_0, whose order of magnitude remains the same and by the presence of the longitudinal dipole electric field can be positive.

2. Consider the contribution of the interactions of given DNA codon and DDNA codon with the non-nearest neighbors along DNA and dark DNA. These interactions can be regarded as dipole and higher multipole interactions since the total charges of the codon pair DNA + DDNA vanish. In the lowest order approximation dipole-dipole interactions depending on the distance r between dipoles like $1/r^3$.

3. Simple dimensional arguments give the general form of the dipole contributions. By dimensional considerations alone, the sum over dipole interaction energies for a given codon or nucleotide gives a contribution proportional to $1/L^2$. Summing over these contributions gives a total contribution proportional to $1/L$.

   The dipole contribution is proportional to $(dn/dl)^2$, to the square of the dipole moments of a given nucleotide (codon). Since dipole moments are of the order eR, R the transversal scale of DNA+DDNA system, individual dipole-dipole interaction energy is proportional to e^2S

   Therefore the Coulomb interaction energy would be of the general form

   $$E = \frac{e^2L}{S}[-n^2 + n_0^2] + ke^2(dn/dl)^2\frac{S}{L})] \ .$$

   where k is a numerical factor determined by the details of the model. Note that dark protons forming a dark variant of ordinary nucleus are expected to have also counterparts of strong interactions expected to be short ranged.

4. The minimization of energy would give

   $$F = -\frac{dE}{DL} = \frac{e^2L}{S}[-n^2 + n_0^2] + ke^2(dn/dl)^2\frac{S}{L})] = 0 \ .$$

   This gives for $L(n)$

   $$L(n) = \frac{dn}{dl}S\sqrt{\frac{k}{-n^2 + n_0^2}} \ .$$

   The condition that the argument of square root in non-negative, implies that one must have either $(k > 0, n < n_0)$ or $(k < 0, n > n_0)$. $n < n_0$ option seems to be the physical one.

5. $n < n_0$ requires $k > 0$ so that the dipole interaction energy is positive. For $n \to 0$ L approaches to

   $$L(0) = \frac{dn}{dl}S\sqrt{\frac{k}{n_0^2}} \ .$$

   $L(0)$ could correspond to the length for the coding part of DNA (no telomere is allowed). At the limit $n \to \infty$ $L(n)$ approaches infinite value and the length of the telomere becomes extremely sensitive to the value of n and n becomes an ideal control variable.

   For $n > n_0$ one must have $k < 0$ meaning that the contribution of the dipole-dipole interactions to the total energy is negative. The stable DNA length shortens roughly like $L \propto 1/n$ as n increases: this does not conform with the intuitive picture.

Relation to TGD inspired theory of consciousness

Two remarks from the point of view of TGD inspired theory of consciousness based on ZEO are in order.

1. The proposal motivated by the properties of electromagnetic field tensor under time reflectin T is that the direction of electric field flux should correlate with the arrow of time. One would expect that the change of the arrow of time requires the change of the direction of the electric field. Somehow the length of dark DNA should be reduced at the first end and increased at the opposite end.

   Could the dark protons be added to or removed from the flux tube defining dark DNA to achieve this. Pollack effect [L15, I76] is in TGD framework indeed explained in terms of the transfer of ordinary protons to dark protons (with $h_{eff} = nh_0 > h$) at the dark magnetic flux tubes [L20] and has become basic element of the TGD inspired quantum biology.

The roles of DNA strands are expected to change in time reversal so that the active strand (the transcribed one) would become passive and *vice versa*. The gene expression would come however its time reversal: mRNA would be un-transcribed to mRNA codons by the formerly passive strand.

2. If one could change the roles of active and passive strands by changing the arrow of time - that is the direction of the longitudinal electric field of DNA - by changing the numbers of dark protons at the ends of DNA, one could have a dramatic demonstration for the key idea. An external electric field with direction opposite to that of DNA might allow achieving this. This would be like changing the direction of spontaneous magnetization by using an external magnetic field.

12.7.4 Tests for the TGD based model of DNA as ferroelectret

The standard physics view is that the possible ferroelectricity for DNA is due to the instantaneous polarization of codons A,T,C,G in external field which is proportional to electric field E if the polarization vanishes for $E = 0$. Ferroelectriy is analogous to spontaneous magnetism that there is electric field also for $E = 0$: this requires permanent electric dipole moments generated by small external field an left when the field is taken to zero.

In [I51] a model for the polarizability of nucleotides A,T,C, G is developed based on standard physics so that the external electric field would generate dipole moment for given nucleotide. What one hopes is model producing ferro-electric behavior. The model calculations give ferroelectric behavior and a square shaped hysteresis curve. In case of entire DNA each nucleotide would behave independently in inhomogenous electric field with varying direction.

Also in [I88] the dipole moments are estimated for both bases and nucleotides, and the esimated dipole moments are in the range of 2-6 Debyes ($D = .02$ enm) that is $.04 - .12$ enm . TGD estimate for the electric field is about ne/S, $S = \pi R^2$ the effective area of the flux tube assignable to DNA + dark DNA.

The first thing to notice is that the flux would be along entire DNA, not only the telomere and the overhangs portions carry the charges creating the electric field along DNA. Electric flux flows along DNA. Telomere would be a kind of buffer against the evil world. Overhang/sticky ends could play a key role in control of the arrow of time for DNA. Similar mechanism would be at work at the level of entire body changing the direction of endogenous electric field and leading to wake-up to sleep or vice versa [J4, J27].

Suppose that the charges at the opposite ends of DNA are of opposite sign. An un-necessary strong assumption is that they are of the same magnitude. The dipole moment would be roughly given by the difference $Q_1 - Q_2$ of the charges multiplied by the distance L between ends of the chromosome along the DNA strand. Note that the channeling of electric flux along DNA would be rely on TGD view about space allowing monopole flux tubes whose deformations carry also electric field.

The static electric field would be realized as a conserved electric flux flux along the entire DNA, not only telomere. The order of magnitude is 10 GV/m for $R = 1$ nm so that it would be rather strong. The strength of electric field is proportional to $1/R^2$ and R is expected to vary in the range $1 - 10$ nm. Note that $L(151) = 10$ nm corresponds to the p-adic length scaled the thickness of the DNA coil and chromosome thickness.

The effective dipole moment per nucleotide would be $p \simeq ned \simeq n \times .3$ enm and quantized as multiples of n. The estimate is at most by a factor $2.2 - 7.5$ larger than the estimates from the atomic contributions and would allow to select between the standard model and TGD based model.

Nanoscopic implications

What could be possible experimental consequences of the proposed electric field? Consider first the situation at the level of single DNA double strand.

1. The accelerated motion of a test charge along DNA could serve as a test for this option. One can consider both quantum motion without dissipation - perhaps along the dark DNA - and

Ohmic current along the ordinary DNA. They would runs also in absence of external electric field unlike ordinary Ohmic currents.

These currents could be nanoscopic analogs of the DC currents observed by Becker in body scale and brain scale. If they are steady currents the current is conserved and must return so that a closed current loop is formed. The currents could be also pulselike taking surplus dark protons between ends of the chromosomes and changing the their roles. This would be quantum event associated with BSFR and could mean time reversal.

Electronic (not protonic) currents along DNA [I32] have been observed for single DNA strands in an external electric and it is found that the conductivity is surprisingly high. In the recent case conduction double strand property and sticky ends would be essential.

2. How could the current return in steady situation? This question must be answered also for Becker's current. Does the current flow as ohmic current along ordinary DNA and return back along the dark DNA as non-dissipative current? The proton current along DNA along electric field to negatively charged and dark protons would be accelerating: the quantum description would correspond to a particle in linear potential, which is standard quantum mechanical problem.

   The larger the charge (the length of the sticky end), the stronger the current. Its magnitude would be quantized being proportional to the length and charge ne of the sticky end. The variation of sticky end length would vary the strength of the current.

   The is evidence for proton AC current conduction in the DNA double strand-imidazole composite material under anhydrous conditions (no water) in the freqency range 4 Hz - 1 MHz [I69]. If the mechanism is the proposed one - probably not - the oscillatory current could correspond to occurrence of BSFRs changing the arrow of time with 2 BSFRs *per* each period of $T = 1/f$. This would predict the current to be $I = 2nef$, where $\pm ne$ are the charges at the ends of the double DNA strand.

How to test whether DNA double strand is ferroelectret?

Possible tests of the model are considered in the sequel.

1. How to test whether DNA double strand is ferroelectret?

1. The measurement of the possible longitudinal electric field of DNA and its correlation with the length of the telomer or of the sticky end would be an interesting expermental project. DNA exconuclease restriction enzyme allowing to cut pieces from the end of either DNA strand could allow creation of desired length of unpaired portion of DNA. Also blunt ends could be created and the prediction is that there is no electric field in this case.

2. The telomere or the entire DNA would be like a dipole and would interact with external electric fields. One should be able to prepare a DNA sample as an electret so that DNAs would have the same dipole direction and this structure could be put in an electric field allowing to measure the dipole moment of DNA as a macroscopic motion in the field.

   The external electric field would give rise to a torque acting on the entire DNA double strand. If nucleotides behave as independent dipoles as the standard physics based model suggests, this would not be the case and the dipole moments of the nucleotides would only turn in the direction of the external field.

3. One could also study whether and how the possible DNA dipole moment making sense for short enough DNA double strands is affected by the telomerase affecting the length of telomere. The first guess would be that is the length of the sticky end which is affected and that the length of the telomere correlates with this by stability conditions. Pyroelectricity and piezoelectricity and the use of external electric field produce ferroelectrets from various biological tissues [I56]. These methods applied to DNA crystals [I70, I26] could allow to test the hypothesis.

The measurement of the possible longitudinal electric field of chromosome or DNA double strand and its correlation with its length could serve as a futuristic bioelectric marker: this could be an experimental project. Currently, the measurement of telomere length by quantitative PCR is quite common and for a summary of critical factors and recommendations for assay design, interested readers may see [I66]. Also, a full description and protocol for examination of the telomere G-overhang structure in different plant, human and vertebrate models are available [I31, I57, I80, I82].

Could pyroelectricity, piezoelectricity, or the behavior in external electric fields be used to demonstrate that DNA has a longitudinal internal electric field

One can consider also the consequences at condensed matter level. Athensteadt has found [I56] that it is possible to make various tissues of vertebrates piezoelectric or pyroelectric.

Pyroelectric materials (see `https://cutt.ly/5d3gT8r`) are crystals in which the change of the temperature involving thermal energy flow induces a macroscopic electric polarization and therefore electric field making the material ferroelectric. In piezo-electric materials (`https://cutt.ly/cd3gJ4v`) mechanical stress induces a generation of polarization and macroscopic electric field. Also an external electric field can induce polarization producing a ferroelectret.

One can visualize the situation using a triangle having kinetic, electric, and thermal energies as corners. For piezoelectric materials the motion occurs along the edge connecting electric and mechanical energy. For pyroelectric materials the motion occurs along the edge connecting electric and thermal energy.

The proposal is that DNA double strand + dark DNA strand carries internal electric field is 1-D ferroelectric aperiodic crystal due to its inherent polarization. One cannot exclude the possibility that also single DNA strand + dark strand has this property. DNA should be *n vivo* state. DNA crystals [I70, I26] might allow to test the phenomenon. For instance, it is known that DNA suspended in liquid which is evaporated forms crystal (`https://cutt.ly/Hd3fvMW`). Could DNA crystals become ferroelectrets by heating or cooling or by applying a mechanical stress or an external electric field?

If this would occur, the interpretation would be that DNA strands become parallel and have parallel electric fields giving rise to ferroelectricity. In the positive case, one could test the hypothesis by using DNA preparations with different values of n for the number of overhang nucleotides: electric field in the ideal situation would be proportional to n if the area density of the parallel DNA strands is the same.

12.8 Mysteries related to gene expression and meiosis

The selection of the allele in gene expression and meiosis still involves mysteries.

1. In mitosis (`https://cutt.ly/3HZfSps`) the chromosome pair of DNA consisting of the chromosomes of parents of cell replicates. Each cell has both mother's and father's genes, which are homologous but not identical. Allele dominance means that in a given cell only either allele tends to be expressed (`https://cutt.ly/ZHJicsQ`). Whether mother's or father's allele dominates, depends on the cell. The origin of this dominance is not understood.

2. In meiosis (`https://cutt.ly/zHZfJVl`) occurring in the formation of gametes the chromosome pair is replaced with a single chromosome and the DNA strands effectively reconnect so that the new strand contains alleles from either parent, which seems to be selected randomly. If the random recombination occurs for both strand pairs, it is difficult to understand how the combination processes can be identical. The recombination process however take in a similar way for both DNA strands. Most naturally, the reconnection would occur only for the other pair of strands from parents. These strands could be the strands which are active in transcription. After this, this strand could serve as a template in DNA replication to form a DNA double strand.

Condensed matter physicists are discovering that the world of electrons at atomic level is govering by knotting and linking (`https://cutt.ly/mHVCrPC`). This picture is just what TGD

predicts but applies to all systems, not only electrons, and in all scales from hadron physics to cosmology. Besides particle like entities there would be magnetic flux tubes connecting them to networks. This is completely new from the perspective of quantum field theory based description based on point-like particles.

Since 3-space is a surface in $M^4 \times CP_2$ is 3-D, flux tubes and string world sheets accompanying them are necessarily linked and knotted: this distinguishes TGD from string models. This implies braiding and makes possible topological quantum computation (TQC) like activities at fundamental level, in particular in living matter and especially at the DNA level.

Furthermore, since spacetime is a 4-D, string world sheets and flux tubes can reconnect in a topologically stable manner (in superstring models this is not possible). Reconnection becomes a fundamental aspect of the TGD inspired quantum biology. For instance, reconnection plays a central role in the TGD inspired view of a living system as a topological quantum computer [L140].

Reconnection also plays a key role in the recombination of DNA strands of father and mother chromosomes leading to the formation of gametes. In TGD it would be preceded by a reconnection at the level of dark DNA associated with magnetic flux tubes and occurring in cell divisions. The reconnected flux tubes representing gametes would serve as templates for the recombination of the ordinary DNA strands. This picture leads to surprisingly strong predictions concerning natural selection at cell level and the notion of sex.

12.8.1 Are DNA expression and the formation of gametes induced by dark gametes?

TGD suggests that the recombination of DNA is induced by a reconnection process at the level of dark DNA [L161]. The reconnection process for dark DNA strands of father and mother at the level of MB would induce the recombination process at the level of ordinary DNA strands. Second suggestion is that dark gametes formed in the replication of cells control the gene expression and induce allele dominance depending on cells. Futher implication would be that cells have a well-defined sex. Perhaps even organelles and organs could have such.

1. The recombination process for DNA would be guided by a reconnection process for dark DNA at the magnetic flux tubes. Suppose that the pairs of dark DNA strands at the magnetic flux tubes reconnect to form a pair of strands in which the pieces of strands are mixed just like they are thought to do for ordinary DNA. One obtains for a given strand two outcomes with father $\leftrightarrow$ mother symmetry realized for the corresponding pieces of the strands. The symmetry related pairs correspond to different sexes and if only the other strand is selected, the sex of the descendant is fixed.

2. Dark meiosis as a reconnection process at the level of dark DNA would occur before meiosis, naturally in the previous DNA replication since otherwise the cells would MBs with both sexes. This dark DNA would select from the paternal and material ordinary DNA strands ordinary codons and fuse them to the ordinary DNA strand of the gamete. The process would rely on resonance mechanism [L78, L107, L122, L142]. This process could occur for both DNA strands or a single strand. It might be possible to test, which option is realized. The ordinary model has problems in understanding why the both strands suffer the same recombination: now this problem would not be encountered.

TGD view about genes involves the notion of dark DNA realized at the level of magnetic body (MB) and suggests a solution to the mystery of allele dominance.

1. The process leading to the DNA of gamete occurs at the level of dark DNA as reconnection. Two strands are formed by reconnection and yield two different gametes with opposite sex and related by father father $\leftrightarrow$ mother symmetry.

2. Could dark gametes at the level of MB form already in fertilization or considerably before the generation of gametes, say in previous cell replication? If dark gametes form in the fertilization, the ordinary gametes would be copies of these two dark gametes and there would be only two kinds of gametes and only two kinds of children, males and females. This is not certainly true.

If the dark gametes are formed later in the daughter cell, most naturally in cell replication, daughter cells can have different dark DNA producing different gametes as their copies. The members of dark gamete pair related by father $\leftrightarrow$ mother symmetry would produce male and female kind gene expressions.

3. Only single gamete DNA can appear in a given gamete, which could be understood if only the second dark gamete DNA can be associated with a given cell. A pair of gametes could form in the cell replication and the members of the pair go to different daughter cells. Allele dominance would emerge after the first replication in which dark meiosis would occur for the first time.

   One could say that ordinary mitosis involves dark meiosis leading to allele dominance in a given cell and ordinary meiosis takes place only later. There would male and female cells and one could say that fertilization occurs repeatedly in dark meiosis.

4. The resonance mechanism [L142] allows us to understand the allele dominance quantum mechanically. The dark DNA controls gene expression and is in energy resonance with ordinary DNA. Depending on the dark gene, the resonance selects either the allele of mother or of father.

5. If new dark gametes emerge at each cell division, there is a large number of descendants at the cell level. The survival of a cell with a given dark gamete implies that the ordinary gametes associated with it have a higher chance to participate in sexual reproduction. Only those dark gametes, for which the cells controlled by them survive and have produced ordinary gametes as their images, have a change to participate in sexual production, which is like the finals in Olympics. Evolution would be survival of the fittest already at the level of cells and selection would occur already at the level of cells.

6. The two dark gametes produced in the dark meiosis in cell replication and going to different cells in cell division are related by father $\leftrightarrow$ mother symmetry and since XX chromosome pair characterizes female and XY chromosome pair male, sister and brother cells, which are mirror images of each other emerge and are associated with different cells. Therefore cells would have a well-defined sex!

   This raises interesting questions. Could organelles and even organs tend to have same cellular sex so that also these could be said to have a well-defined sex? Could the battle between sexes start already at the cell level and possibly lead to extinction of the other sex? Could cells have sexual relationships like us and tend to pair? Could possible multi-cellular structures with a well-defined sex have this kind of relationships? What comes into mind are epithelial layers consisting of two cell layers and various binary structures in the body and brain.

12.8.2 Summary of the TGD based view of mitosis and meiosis

The above considerations boil down to the following overall view of mitosis and meiosis in the TGD framework.

Consider first ordinary mitosis and meiosis.

1. In the ordinary mitosis two copies of chromosomes are formed. After this cell divides. The same could happen for the dark chromosomes. But this would leave allele dominance a mystery.

2. Ordinary meiosis involves replication of chromosomes of soma cells with chromosomes of father and mother. This is followed by recombination of the chromosomes followed by cell division so that two germ cells are obtained. After that both daughter cells with recombinant genomes split to germ cells giving four germ cells.

The TGD view of meiosis would be different. Dark meiosis and ordinary meiosis need not occur simultaneously and dark meiosis could occur before the ordinary one in some earlier mitosis.

1. Dark DNA can suffer at some cell replication dark meiosis involving recombination of dark DNAs for both chromosomes. The resulting dark DNA strands go to separate cells. The dark parts of the DNA would be analogous to that of gametes which would be different for the two daughter cells.

   Since dark DNA controls ordinary DNA, the dark gamete would by resonance mechanism select which allele dominates. One would have two kinds of cells with different allele dominances. One could say that the cells have different sex. This is a testable prediction.

2. If this replication occurs after some replication after the first replication, the dark gametes formed in the dark meiosis of different cells are different, and one can obtain a large number of different dark gametes. This number is not so large as for the ordinary meiosis since dark gametes do not change in the cell replications.

3. The dark gametes, which have formed by dark meiosis already in an earlier cell replication preceding meiosis, would determine the outcome of the recombination of ordinary DNA in the ordinary meiosis following dark meiosis after some cell replications. After this the dark gametes pair with ordinary DNA and give rise to an ordinary gamete.

12.8.3 Bioharmony, resonance mechanism, and emotions

TGD assigns to the genetic code a bioharmony [L78, L107, L122, L142] bas a correlate for emotional states of moods.

1. The working hypothesis is that bioharmony dictates the frequency ratios of genes represent as triplets of dadrk photons exactly and that the sfrequency cale does not matter. Codons and genes would play the role of addresses in communications using dark 3N-photons as analogs of Bose-Einstein condensates. One would have 3N-resonance instead of ordinary (1-)resonance. For instance, gene expression would be guided by dark gametes and the dark gene would select by resonance mechanism the allele of either mother or father.

2. Just as the chords code for musical harmony and emotions, dark codons would code for bioharmony and serve as correlates for emotions at the molecular level. This gene expression would be responsible for emotional intelligence.

3. The 3-chords associated with the genetic code would correspond to a combination of a unique tetrahedral harmony and icosahedral harmony realized as Hamiltonian cycles.

   There is a considerable number of icosahedral harmonies, which appear in 3 basic classes. Bioharmony is a fusion of tetrahedral harmony with 3 icosahedral harmonies of type Z_6, Z_4 and Z_2. The icosahedral harmony with Z_6 symmetry is unique and corresponds to 3 amino acids (AAs) coded by 6 codons and one AA coded by 2 codons. The two harmonies with Z_4 symmetry correspond to 5 AAs coded by 4 codons. Z_2 can correspond to π rotation or reflection and are coded by 10 codons in absence of symmetry breaking. The number of harmonies with Z_2 symmetry is considerably higher.

   There are many open questions.

1. Could the possibly stable molecular bioharmonies correlate or even characterize the dark gametes and correlate with the sex of the cell. Could the molecular bioharmonies characterize genes or cells? Could the two Z_4 harmonies distinguish between the two sexes?

2. If bioharmonies correlate with emotions, one would expect that they can change. I have proposed a model [L64] explaining the strange finding that the RNA from conditioned neurons of a snail induce conditioning in the unconditioned neurons of second snail (`http://tinyurl.com/y92w39gs`). The molecular emotions crucial for the conditions would correlate with the bioharmony assignable to RNA.

3. How stable are the bioharmonies? How long lasting bioharmonies could be? Could they define cellular moods lasting for the entire life and basically determine the personality?

4. Could the change of bioharmony correlate with epigenetic change as suggested by resonance mechanism. A correlation between bioharmony and gene expression controlled by mechanisms like methylation is suggestive.

12.8.4 About the notion of sex?

Sex is determined by X and Y chromosomes. The females gametes have two X chromosomes and male gametes have both X and Y chromosome. The mixing of sex chromosomes would give two XX and two YX chromosomes and the selection would be determined the sex.

The ordinary cells have both mother and father chromosomes and allele dominance decides about the gene expression. If the proposed picture holds true, each cell division would generate new kinds of dark gametes dictating the gene expression. As far as gene expression is considered there would be a large collection of different descendants, which can have both sexes.

If only the second variant of the dark gamete appears in a given cell, each cell would have a well-defined sex. If organelle or even organ consist dominantly of cells of either kind, it could be said to have a well defined sex. The notion of sex would not boil down to a single bit. We would be composites of cell structures with different sexes and a collective of a large number of descendants. This would force us to give up the naive genetic determinism.

Chapter 13

TGD View about Language

13.1 Introduction

This chapter has been written together with Reza Rastmanesh, who proposed the topics of the article leading to this chapter. Human languages differ dramatically from their analogs for animals. Animal languages consist mainly of simple signals, warnings and threats for instance; emotional expression dominates and grammar is lacking. Birds can have impressive repertoire of different song patterns and monkeys have gesture language.

There is a huge variety of human languages: speech and written language, sign languages based on gestures, the language of mathematics and computer languages in which emotional expression is absent. One can also regard music as a kind language expressing emotions and creating them. Also pictures define linguistic representations. Children and animals learn language by mimicry and also learn the grammar and syntax without conscious efforts. Adults can learn a foreign language by learning the vocabulary and the rules of grammar. Human language is also special in that it involves conceptualization, metaphors, and analogies representing abstract concepts in terms of objects and actions of the external world.

One might understand the semantic aspect of language in terms of association and conditioning. Language acquisition involves showing the object and saying the word describing it. This suggests that conditioning and association happens so that mere word generates an imagined percept of the object. Conditioning and formation of associations is a very general form of learning assumed to relate to the increase of synaptic strengths leading to a generation of association pathways. In computer science pattern recognition and completion models it mathematically. One one can ask whether the learning of language and language understanding is something more than this.

For more detailed approaches of language theories, interested readers may be referred to references [J22, J25, J24, J30]. The article of Kempe and Brooks [J29] and the review article "From Molecule to Metaphor: A neural theory of language" about the language theory of Jerome A. Feldman by Stefan Frank [J28] gives a deeper perspective to language theories. The notion of embodiment is in key role in these theories and will be in a key role also in the proposal to be discussed.

13.1.1 About language genes

Forkhead box protein P2 (FOXP2) encodes a transcription factor involved in language acquisition and speech [J9]. In addition to FOXP2 a limited number of genes are involved in speaking [J13]. All vertebrates possess FOXP2, however it is estimated that some 120,000-200,000 thousand years ago, some mutations occurred only in humans which aided humans to start initial forms of speaking [J22]. Animals have their own primitive language; both voices and gestures with meaning make communications possible. They mainly recognize each other and communicate with pheromones. As for vocabulary, a short review of the Old Testament, cuneiform writings, glossary of old books, and hieroglyphs clearly shows that the number of entries was quite limited in the past. Therefore, a further progression of language could be almost a matter of cultural communications and technological advances.

However, today it is clear that crucial mutations occurred in the non-coding part of the genome controlling the expression of genes coding for proteins [J13] which lead to language evolution. Therefore, the evolutionary step was associated with control of existing genes. Humans are also distinguished from animals by their learning abilities.

Language acquisition must rely on conditioning/associations between language expressions and experiences. It seems that embodiment is the mechanism, which associates to a linguistic expression an imagined sensory perceipt and/or motor action making the emergence of meaning. What is needed is long term memory and also some kind of standardization of percepts so that they consist of standardized mental images. Pattern recognition and completion could give this standardization.

Since sensory and motor imagination could be seen as almost sensory experiences and almost motor actions, this suggests that new communications between auditory organs and sensory and motor areas emerged. Even more generally, this kind of communication could have emerged quite generally. This would be essentially a new form of conditioning and the same mechanism could apply to all kinds of conditionings.

13.1.2 How the mutation of only a few genes led to cultural evolution?

Amazingly, only a few mutations for relatively few genes seems so have led to human languages. Why few point mutations of relatively few genes could have transformed biological evolution to cultural evolution? What happened for these genes? In the biochemistry framework it is difficult to imagine an answer to this question. Here TGD could come in rescue.

Number theoretic physics is part of quantum TGD and essential for understanding evolution as an increase of algebraic complexity. Evolutionary hierarchies would correspond to hierarchies of algebraic extensions of rationals. The dimension n of extension defines effective Planck constant $h_{eff}/h_0 = n$, the larger the dimension, the larger the scale of quantum coherence at corresponding level of magnetic body (MB) associated with the system. One can also say that n is analog of IQ. One can assign a value of h_{eff} characterizing their evolutionary level also to genes. The genes with larger h_{eff} would serve as control genes. The increase of h_{eff} for genes would mean an evolutionary step. Perhaps a dramatic increase of h_{eff} occurred to FOXP2 and some other genes as human language emerged.

Second mechanism could be energy resonance in the coupling of the analogs of DNA, RNA, tRNA, and amino acids consisting of dark proton triplet with their chemical counterparts. The coupling would be between the entire gene and its dark analog and codon sequence would play a role of address. In both cases small changes of the gene could spoil or produce an energy resonance. This sensitivity would make genes an ideal control tool but would also serve as a general mechanism also for genetic diseases. The increase of h_{eff} accompanied by a small mutation to guarantee energy resonance could be the mechanism explaining the importance of FOXP2 and similar control genes.

Note: This chapter was prepared in collaboration with Dr Reza Rastmanesh who provided a lot of biological and neurosscientific knowhow and made inspiring questions.

13.2 Number theoretical aspects of quantum biology

The basic ideas about consciousness and life are discussed in Appendix. Here the aspects relevant for the recent work are discussed.

Fig. 13.1 summarises the role of number theory in the TGD inspired vision concerning consciousness, cognition, and quantum biology and **Fig. 13.2** the role of dark matter in TGD inspired quantum biology.

13.2.1 Dark proton representation of genetic code

Fig. 13.3 summarizes the TGD based vision about genetic codes.

Codons as dark nucleons?

The model for codons of genetic code emerged from the attempts to understand water memory [**?**] The outcome was a totally unexpected finding [**?**] the states of dark nucleons formed from three

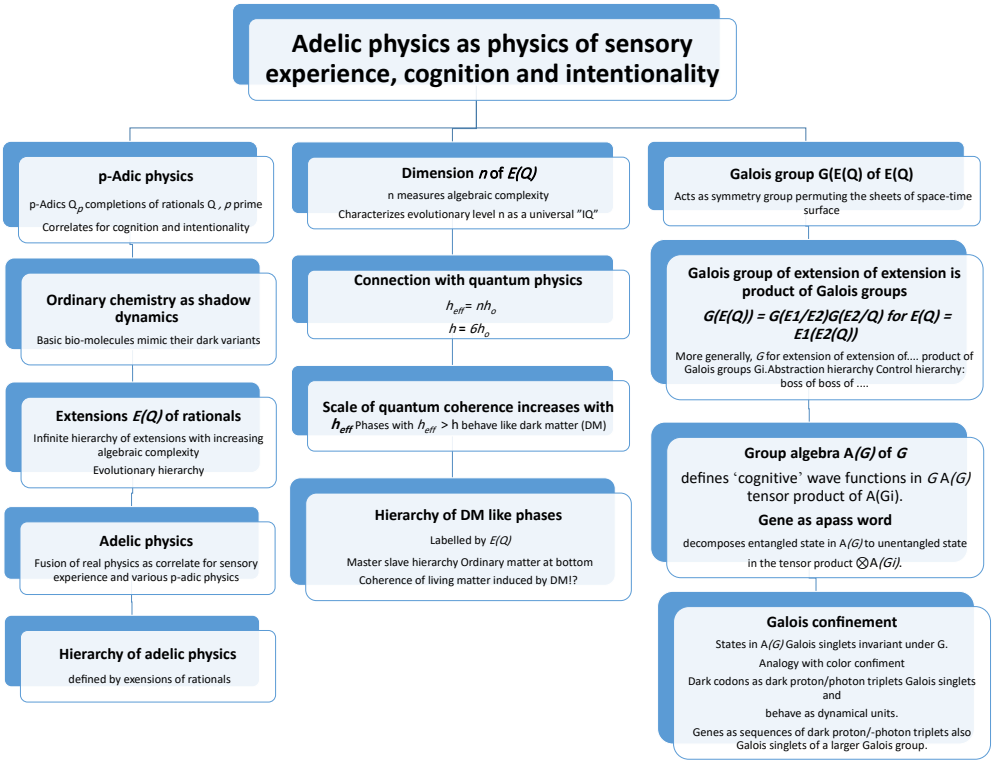

Figure 13.1: Adelic physics as physics of sensory experience, cognition and intentionality

quarks connected by color bonds can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAs, 20 amino acids, and tRNA and there is natural mapping of DNA and RNA type states to amino acid type states such that the numbers of DNAs/RNAs mapped to given amino acid are same as for the vertebrate genetic code.

The basic idea is simple. The basic difference from the model of free nucleon is that the nucleons in question - maybe also nuclear nucleons - consist of 3 linearly ordered quarks - just as DNA codons consist of three nucleotides. One might therefore ask whether codons could correspond to dark nucleons obtained as open strings with 3 quarks connected by two color flux tubes or as closed triangles connected by 3 color flux tubes. Only the first option works without additional assumptions. The codons in turn would be connected by color flux tubes having quantum numbers of pion or η.

This representation of the genetic would be based on entanglement rather than letter sequences. Could dark nucleons constructed as a string of 3 quarks using color flux tubes realize 64 DNA codons? Could 20 amino acids be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner? The codons would not be separable to letters but entangled states of 3 quarks anymore.

Genetic code would be defined by projecting DNA codons with the same total quark and color bond spin projections to the amino acid with the same (or opposite) spin projections. The attractive force between parallel vortices rotating in opposite directions serves as a metaphor for the idea. This hypothesis allows immediately the calculation of the degeneracies of various spin states. The code projects the states in $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ to the states of 4×5 with the same or opposite spin projection. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1, 2, 3, 2\}$ and $D_b \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of amino acids coded by D codons would be

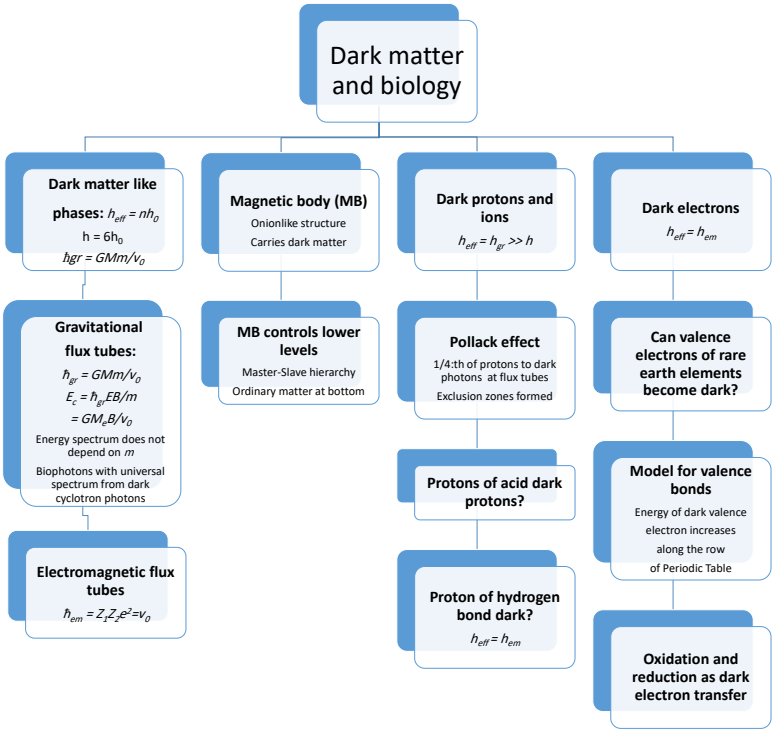

Figure 13.2: Dark matter in TGD inspired quantum biology

$$[N(1), N(2), N(3), N(4), N(6)] = [2, 7, 2, 6, 3] \quad .$$

The correct numbers for vertebrate nuclear code are $(N(1), N(2), N(3), N(4), N(6)) = (2, 9, 1, 5, 3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in the second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2, 9, 1, 5, 3)$!

Codons as dark proton triplets?

The model of codon as dark nucleon predicts analogs Δ resonances whose masses differ from those of nucleons.

The hint comes from the fact that DNA nucleotides have a negative charge, which is problematic from the point of view of DNA stability. This suggests that dark codons should have a charge of 3 units screenng the charge of the ordinary DNA codon. Pollack effect [**?**]eans formation of negatively charged exclusion zones as protons are transferred to dark protons at magnetic flux tubes. Could DNA be formed by Pollack effect? Could codons be represented as dark proton triplets?

The problem is that protons however have only 2 spin states: 4 states would be needed as in the case of quarks having also color. Where could the counterparts of spin and color come from?

One could consider adding a neural pion-like and/or ρ_0 meson-like bond connecting neighboring protons. Since ρ_0 has spin 1, this would give 1+3=4 states per bond. However, 2 states are enough and one must get rid of 2 states. The string-like structure of the proton triplet

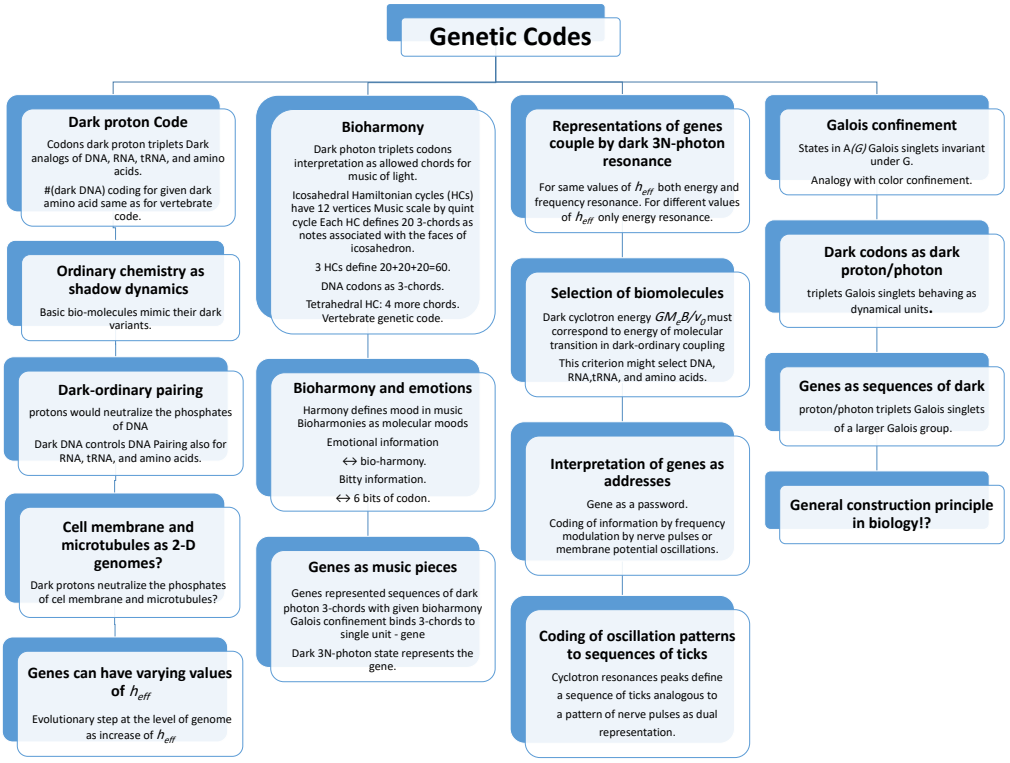

Figure 13.3: Genetic codes in TGD framework

suggests that the rotation group reduces to $SO(2) \subset SO(3)$ so that ρ meson states split into singlets with helicities 0,1,-1. The doublet (-1,1) would serve as the analog of the isospin doublet (u,d) for baryons and enough to achieve a correct effective number $N = 4$ of states per single DNA codon. Helicity would replace isospin and the tensor product states could be constructed effectively as tensor products of 3 representations $2 \otimes 2$.

There is also an issue related to the fermionic statistics. Protons are fermions and the total wave function for them must be antisymmetric. For baryons color singlet property allows this. Can one require statistics in the ordinary sense also now? Or could the effective 1-dimensionality of the magnetic flux tube allow braid statistics?

The following variant gives good hopes about the ordinary statistics.

1. Adelic physics [**?**]rings in additional discrete degrees of freedom assignable to the group algebra of Galois group of extension of rationals inducing the extensions of p-adic number fields appearing in the adele [**?**]

2. Galois group acts on the space of space-time surfaces, and one can say that one has wave function at the orbit of the Galois group consisting of space-time sheets. At quantum level quantum states correspond to wave functions in the group algebra of Galois group of extension.

3. The role of color degrees of freedom in helping to achieve correct statistics in the case of baryon could be taken by Galois degrees of freedom. One can even consider the notion of Galois confinement as a generalization of color confinement [**?**]inding codons as dark proton triplets to dynamical units. Codons should be antisymmetric under exchange of dark

protons in Galois degrees of freedom. Also genes as sequences of codons could be bound to dynamical units as Galois singlets. Could this allow ordinary statistics.

If this picture is correct, genetic code would be realized already at the level of dark nuclear physics or even at the level of ordinary nuclear physics if the nuclei of ordinary nuclear physics are nuclear strings. Chemical realization of genetic code would be induced from the fundamental realization in terms of dark nucleon sequences and vertebrate code would be the most perfect one. Chemistry would be a kind of shadow of the dynamics of positively charged dark nucleon strings accompanying the DNA strands and this could explain the stability of the DNA strand having 2 units of negative charge per nucleotide. Biochemistry might be controlled by the dark matter at flux tubes.

13.2.2 Bio-harmony as a realization of genetic code

TGD leads to a notion of bio-harmony in terms of icosahedral and tetrahedral geometries and 3-chords made of light assigned to the triangular faces of icosahedron and tetrahedron [L18, L19, L98]. The surprise was that vertebrate genetic code emerged as a prediction: the numbers of DNA codons coding for a given amino acid are predicted correctly. DNA codons correspond to triangular faces and the orbit of a given triangle under the symmetries of the bio-harmony in question corresponds to DNA codons coding for the amino acid assigned with the orbit.

Codon corresponds to 6 bits: this is information in the usual computational sense. Bio-harmony codes for mood: emotional information related to emotional intelligence as ability to get to the same mood allowing to receive this information. Bio-harmony would be a fundamental representation of information realized already at molecular level and speech, hearing and other expressions of information would be based on it. For emotional expression at RNA level possibly involved with conditioning at synaptic level see [L62].

Does the generation of nerve pulse patterns by a gene mean at the cell membrane from dark DNA to dark protein map to dark protein (it could be also dark RNA or dark DNA even) associated with the cell membrane. What about communications with RNA and enzymes involved with transcription and translation. Do all basic biocatalytic processes involve them.

What about a generalization of Josephson currents? Dark ions certainly define them but could also dark proton triplets and their sequences associated with proteins give rise to oscillating Josephson currents through cell membrane and therefore to dark Josephson radiation with 3N dark photon units! Proteins themselves need not move much!

The universal language could be restricted to the genetic code which would be realized by dark proton triplets. The 64 codons are formed from 3 20-chord harmonies associated with icosahedron and the unique 4-chord harmony associated with tetrahedron. Bio-harmonies are associated with the so-called Hamiltonian cycles ,which go through every vertex of Platonic solid once. For icosahedron the number of vertices is 12, the number of notes in 12-note scale.

Also tetrahedron, cube, octahedron and dodecahedron are possible and one can consider the possibility that they also define harmonies in terms of Hamiltonian cycles. Dodecahedron would have 5-chords (pentagons as faces) as basic chords and there is only single harmony. Same mood always, very eastern and enlightened as also the fact that scale would have 20 notes.

Also octahedron gives 3-chords (triangular faces) whereas cube gives 4-chords (squares as faces). One can of course speculate with the idea that DNA could also represent this kind of harmonies: sometimes the 3N rule is indeed broken, for instance for introns.

Galois confinement [L110] allows the possibility to interpret dark genes as sequences of N dark proton triplets as higher level structures behaving like a single quantal unit. This would be true also for the corresponding dark photon sequences consisting of 3N dark photons representing the gene in bio-harmony as an analog of a music piece consisting of 3-chords and played by transcribing it to mRNA.

The picture can be viewed even more generally. Any discrete structure, defining graph, in particular cognitive representation providing a unique finite discretization of space-time surface as points with the coordinates of the 8-D embedding space coordinates in the extension of rationals, defines harmonies in terms of Hamiltonian cycles. Could also these harmonies make sense? The restrictions of the cognitive representations to 2-D partonic 2-surfaces would define something

analogous to bio-harmony as Hamiltonian cycle of 2-D graph (Platonic surfaces solids can be regarded as 2-D graphs). The interpretation as representations of Galois groups and the notion of Galois confinement is possible although one loses the symmetries of the Platonic solids allowing to identify genetic code.

About the details of the genetic code based on bio-harmony

TGD suggests several realizations of music harmonies in terms of Hamiltonian cycles representing the notes of music scale, most naturally 12-note scale represented as vertices of the graph used. The most plausible realization of the harmony is as icosahedral harmony [L11] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/yyjpm25r`).

1. Icosahedron (see `http://tinyurl.com/l5sphzz`) has 12 vertices and Hamiltonian cycle as a representation of 12-note scale would go through all vertices such that two nearest vertices along the cycle would differ by quint (frequency scaling by factor 3/2 modulo octave equivalence). Icosahedron allows a large number of inequivalent Hamiltonian cycles and thus harmonies characterized by the subgroup of the icosahedral group leaving the cycle invariant. This group can be Z_6, Z_4, or Z_2 which acts either as a reflection group or corresponds to a rotation by π.

2. The fusion of 3 icosahedral harmonies with symmetry groups Z_6, Z_4 and Z_2 gives 20+20+20=60 3-chords and 3+1 + 5 + 10 =19 orbits of these under symmetry group and almost vertebrate genetic code when 3-chords are identified as analogs of DNA codons and their orbits as amino acids. One obtains counterparts of 60 DNA codons and 3+1 + 5 + 10 =19 amino acids so that 4 DNA codons and 1 amino acid are missing.

3. The problem disappears if one adds tetrahedral harmony with 4 codons as faces of tetrahedron and 1 amino acid as the orbit of the face of tetrahedron. One obtains 64 analogs of DNA codons and 20 analogs of amino acids: this harmony was coined as bio-harmony in [L18, L19]. The predicted number of DNA codons coding for given amino acid is the number of triangles at the orbit of a given triangle and the numbers are those for genetic code.

4. How to realize the fusion of harmonies? Perhaps the simplest realization found hitherto is based on the union of a tetrahedron of 3 icosahedrons obtained by gluing tetrahedron to icosahedron along its face which is a triangle. The precise geometric interpretation of this realization has been however missing and some possibilities have been considered. The model could explain the two additional amino acids Pyl and Sec appearing in Nature [L18, L19] as being related to different variant for the chemical counterparts of the bio-harmony.

   There is also a slight breaking of symmetries: ile 4-plet breaks into ile triplet and met singlet and trp double breaks into stop and trp also leu 4-plet can break in leu triplet and ser singlet (see `http://tinyurl.com/puw82x8`). This symmetry breaking should be understood.

Cell membrane and microtubules as a higher level representation of genetic code?

Also the representation of genetic code at the level of cell membrane can be considered [L73]. This kind of proposal have been made with different motivations by Okecukwu Nwamba [I71]. The motivation for the current proposal is that the lipids have at their ends negatively charged phosphates just as DNA nucleotides have. The generalization of DNA as a 1-D lattice like structure to a 2-D cylindrical lattice containing nucleotide like units - letters - possibly assignable to lipids and realized as dark protons. Single lipid could be in the role of ribose+nucleotide unit and accompanied by a neutralizing and stabilizing dark proton. For axons one would have cylindrical lattice dark DNA lattice. The two lipid layers could correspond to two DNA strands: the analogs of the passive and active strand.

The finding is that membrane affects protein's behavior. This would be understandable in the proposed pictures 2-D analog of 1-D nucleotides sequences with codons replaced with counterparts of genes as basic units. That lipids are accompanied by phosphates with charge -1 gives the hint. Phosphate charge is neutralized by a dark proton as an analog of a nucleotide.

The notion of Galois confinement identifying genes as units consisting of N dark proton triplets representing genetic codons suggests that genes possibly assignable to the lipid layers of

the cell membrane could communicate using dark $3N$-photon sequences with the proteins, genome, RNA and DNA. Dark variants of the control genes could initiate a nerve pulse pattern. An interesting possibility is that ganglions, nucleus like structures assignable to sensory organs and appearing as basal ganglia in brain [I49] (`https://cutt.ly/zfWoBFt`) could communicate with genes.

Also microtubules have GTPs with charge -3 bound to tubulins. In dynamical instability known as treadmilling the transformation of GTP$\rightarrow GDP$ bound to β tubulin by hydrolysis induces the shortening of the microtubule at minus end whereas the addition of tubulins bound to GTP induces the growth at plus end. Also actin molecules bound to ATP show a similar behavior. Could they be accompanied by dark DNA codons? Are all codons allowed or does the absence of XTP, X= T,C,G mean that only codons of type GGG would be present?

For the dark codons for the cell membrane the p-adic length scale $L(151) \simeq 10^{-8}$ m would correspond to the lipid's transversal size scale and would be the distance between the dark protons. The scale of dark nuclear energy would be proportional to $1/L(151)$ and scaled down by factor $\sim 10^{-3}$ from that for DNA. The energy scale should be above the thermal energy at room temperature about .025 eV. If the energy scale is 2.5 eV (energy of visible photon) for DNA, the condition is satisfied. Note that 2.5 eV is in the bio-photon energy range. For p-adic large scales longer than $L(151)$ thermal instability becomes a problem.

It is interesting to compare the number of codons per unit length for ordinary genetic code (and its dark variant) and for various membranes and microtubules.

- For the ordinary genetic code there are 10 codons per 10 nm defining p-adic length scale $L(151)$. This gives a codon density $dn/dl = 10^3/\mu m$ in absence of coiling. The total number of codons in human DNA with a total length $L \sim 1$ meter is of order $N \sim 10^9$ codons. The packing fraction of DNA due to coiling is therefore huge: of order 10^6.

- If each lipid phosphate is accompanied by a dark proton and if lipid correspond to square at axonal cylinder with side of length $d = L(151)$ and the radius R of axon corresponds to the p-adic length scale $L(167) = 2.5\mu$ m (also of the same order as nucleus size), there are about $dn/dl = 2\pi(R/d)^2 \sim (2\pi/3) \times 10^4 \sim 1.3 \times 10^5/\mu m$. Axon should have length $L \sim 1$ cm to contain the entire genome.

  The same rough estimate applies to microtubules except that there would be one codon per GTP so that the estimate would be 3 times higher if GTP corresponds to length scale $L(151)$ of tubulin molecule. It has been proposed that genetic code is realized at the microtubular level.

- The nuclear membrane assumed to have a radius about $L(167) = 2.5\mu$m could represent $N \sim (4/3)R^2/d^2 \sim .8 \times 10^5$ codons. This is a fraction 10^{-5} about the total number of codons. For a neuronal membrane with radius $R \sim 10^{-4}$ meters assignable to a large neuron the fraction would be roughly 10^{-1}. The fraction of dark codons associated with membranes could correspond to genes involved with the control and communication with genome and other cell membranes. Note that the non-coding intronic portion dominates in the genome of higher vertebrates. One can ask whether the chromosome structure is somehow visible in the membrane genome and microtubular genome.

13.2.3 Galois group of space-time surface as new discrete degrees of freedom

Galois confinemenent

The problem is to understand how dark photon triplets occur as asymptotic states - one would expect many-photon states with a single photon as a basic unit. The explanation would be completely analogous to that for the appearance of 3-quark states as asymptotic states in hadron physics - the analog of color confinement [L111]. Dark photons would form Z_3 triplets under the Z_3 subgroup of the Galois group associated with corresponding space-time surface, and only Z_3 singlets realized as 3-photon states would be possible.

The invariance under $Gal(F)$ would correspond to a special case of Galois confinement, a notion introduced in [L108] with physical motivations coming partially from the TGD based model of genetic code based on dark photon triplets.

Cognitive measurement cascades

Quantum states form Galois group algebra - wave functions in Galois group of extension E. E has in general decomposition of extension E_1 as extension of E_2 as extension of ... to a series . Galois group of E has decomposition to product of $Gal(E) = Gal(E/E_1)Gal(E_1)$ and same decomposition holds true for $Gal(E_1)$ so that one has hierarchy of normal subgroups corresponding extension of extension of...hierarchy defined by a composite polynomial $P(x) == P_1(P_2(x))$ with P_2 having similar representation. P defines in M^8 picture the space-time surface. This maps a tensor product composition for group algebra and the factors of group algebra entangle. SSFR corresponds to a quantum measurement cascade: SSFR in $Gal(E/E_1)$, SSFR in $Gal(E_1/E_2)$ etc.

Could this cascade relate to the parsing of a linguistic expression? It would certainly correspond to a sentence S_1 about a sentence S_2 about ... such that one substitutes a concrete sentence for S_1 first, then to S_2, etc.... The sentences in the sequence indeed have h_{eff} which decreases. This is the case in the cascade of SSFRs since $h_{eff}/h_0 = n$ is the dimension of E_n.

I also mentioned the number theoretic measurement cascades for purely number theoretic Galois degrees of freedom. `http://tgdtheory.fi/public_html/articles/SSFRGalois.pdf`.

Could cascade of flux tubes decaying to smaller flux tubes with smaller value of h_{eff} should correspond to this hierarchy. Certainly this is linguistics but the sentence as argument could correspond to several sub-sentences - different flux tubes. Could a neural pathway defined by the branching axon correspond to a concretization of this kind statement about statement (or multistatement, perhaps nerve pulse pattern generated by nerve pulse patterns arriving to a given neuron) about...

13.2.4 Energy and frequency resonance as basic elements of dark photon communications

Dark photon realization of genetic code leads to a view about fundamental linguistic communication based on resonance and we will write a separate paper connecting TGD with language soon. Two systems can be in communication when there is resonance. $E = h_{eff}f$ and energy conservation implies

$$h_{eff,1}f_1 = h_{eff,2}f_2 \quad .$$

For $h_{eff,1} = h_{eff,2}$, energy conservation implies that both energies and frequencies are identical:$E_1 = E_2$ and $f_2 = f_2$. Both energy and frequency resonances in question.

In the general case one has $f_1/f_2 = h_{eff,2}/h_{eff,1}$ and frequency scaling takes place. The studies of water memory lead to the observation that this kind of phenomenon indeed occurs [I28]. The communications of dark matter with ordinary matter and those between different values of h_{eff} involve only energy resonance. Frequency and wavelength scaling makes it possible for long scales to control short scales. Dark photons with EEG frequencies associated with the big part of MB transform to bio photons with a wavelength of say cell size scale and control dynamics in these short scales: for instance, induce molecular transitions. This is impossible in standard physics.

The resonance condition becomes even stronger if it is required there is a large number of biomolecules in resonance with dark matter realized as dark variants of biomolecules and dark ions. Cyclotron resonance energies are proportional to $\hbar_{eff}$ characterizing magnetic flux tubes and to the valued of the magnetic field strength dictated by the quantization of the monopole flux quantization by the thickness of the flux tube which can be do some degree varied by varying the thickness of the flux tube giving rise to frequency modulation.

The findings of Blackman *et al* [J6] suggest that $B_{end} = 0.2$ Gauss defines an important value in the spectrum of B_{end} values. It could correspond to the field strength for the monopole flux part of the Earth's magnetic field: besides this there would be a non-monopole flux part allowed also in the Maxwellian theory.

There are however indications that the value B_{end} is quantized and is proportional to the inverse of a biologically important p-adic length scale and thus would be quantized in octaves.

This could relate directly to the octave equivalence phenomenon in music experience. The model of bio-harmony [L18, L19, L98] suggests a further quantization of the octave to Pythagorean 12-note scale of music. This would not be only essential for the music experience but communications of emotions and molecular level using the music of light.

Selection of basic biomolecules by energy resonance

The dark particles must have energy resonance with bio-molecules in order to induce their transitions. This seems to pose extremely strong conditions possibly selecting the bio-molecules able to form interacting networks with dark matter and with each other. One expects that only some amino acids and DNA type molecules survive.

Nottale's hypothesis provides a partial solution to these conditions. Nottale proposed the notion of gravitational Planck constant

$$\hbar_{gr} = GMm/v_0$$

assignable in TGD to gravitational flux tubes connecting large mass M and small mass m and v_0 is velocity parameter. The gravitational flux tube presumably carries no monopole flux. The TGD based additional hypothesis that one has equals to

$$hbar_{gr} = h_{eff} = nh_0 \quad .$$

This implies that the cyclotron energy spectrum

$$E_c = n\hbar_{gr}\frac{eB}{m} = n\frac{GM}{v_0}eB$$

of the charged particle does not depend at all on its m. Therefore in a given magnetic field, say B_{end}, the cyclotron resonance spectrum is independent of the particle.

The energy resonance condition reduces to the condition that the charged ion or molecule has some cyclotron energy coming as a multiple of fundamental in its spectrum in the spectrum of its transition energies. Even this condition is very strong since the energy scale for cyclotron energy in B_{end} is in the bio-photon energy range containing energies in visible and UV. The fact that bio-photons have a quasi-continuous spectrum strongly suggests that B_{end} has a spectrum. The model of bio-harmony [L11, L78] suggests that the values of B_{end} correspond to Pythagorean scaling constructible by quint cycle.

The above simplified picture is formulated for single dark photon communications. The dark proton and dark photon realizations of the genetic code requires 3-resonance that is a simultaneous energy resonance for the 3 members of dark photon triplet. In dark-dark pairing also frequency resonance is possible. In dark-ordinary pairing frequency increases and couples long scales with short scales. Also resonant communications between genes with N codons involving $3N$ dark photon frequencies must be possible. This requires new physics provided by number theoretical vision.

What happens in the cyclotron resonance?

3 cyclotron energies for flux tubes characterize dark 3-proton triplet and Nottale's hypothesis predicts that they depend on the values of B_{end} for the flux tubes only. Bio-harmony suggests that the spectrum of frequencies and thus B_{end} corresponds to Pythagorean 12-note scale for a given octave. The allowed chords of bioharmy would characterize the emotional state at the molecular level and correspond to the holistic emotional aspects of the communication beside the binary information.

The resonance would require that the dark cyclotron energy changes are equal to corresponding energies in molecular transitions. Galois confinement [L108] makes possible also 3-N resonance. The resonance condition would select basic biomolecules and the ability of dark analogs of biomolecules to simultaneously resonate with several biomolecules would give additional conditions. In particular this would select DNAs and amino acids.

An open question is whether the coupling to ordinary biomolecules involves a transformation of a dark photon triplet or an N-plet to a single ordinary photon. For instance, does the sum of

the 3 cyclotron excitation energies appear in the coupling of dark 3-proton state to amino acid in protein? This would have an analog as 4-wave coupling in laser physics allowing in biology the transformation of dark photon triplet to single biophoton/or 3 bio-photons or vice versa. 6-wave coupling of laser physics would be analogous to the coupling of ordinary 3-photon state to dark 3-photon and back to ordinary 3-photon state.

The resonance itself would mean a process in which dark 3-proton cyclotron excitation returns to the ground state and generates dark 3-photon transforming transforming to ordinary photon (or 3-photon) and absorbed by the ordinary codon or amino acid excitation to hither energy state. This state would in turn emit an ordinary photon transforming to dark 3-photon absorbed by dark codon. This mechanism generalizes to 3N-proton states representing genes or dark proteins.

13.3 TGD based view about brain

13.3.1 A new view about the role of nerve pulses in sensory perception

Sensory perception would in TGD generate sensory mental images at sensory organs: this would solve a basic problem of neuroscience due to the similarity of neural tissue in various sensory areas. The new view about time and memory implied by ZEO solves the problem caused by the phantom limb. The pain in the phantom limb is a sensory memory of pain.

The stimulation of temporal lobes indeed generates sensory memories, and people with a cognitive impairment are known for memory feats such as being able to draw a building seen in the past with every detail or to learn music pieces with single listening. These feats can be understood if the memories correspond to "seeing" in time direction with a beam of dark photons travelling to the past reflected back. ZEO allows this.

Since perception involves a lot of processing this would require forth-and back signaling between brain and sensory organs. There would be virtual sensory input from the brain or via the brain. Sensory percept would be an artwork, standardized mental image, resulting as pattern recognition assigning to sensory input standardized mental image nearest to the input.

1. Nerve pulses would not mediate information inside the brain. They would only build short connections between existing flux tube connections parallel to axons. Same happens in an old fashioned telephone network by relays: it would be energy consuming to keep the connections on all the time.

   The velocity of nerve pulse conduction is quite too slow to realize the iteration leading to a standardized sensory mental image. If the signal velocity is light velocity, duration of order 1 ms for nerve pulse also for 10 cm neural pathway about 10^6 forth and back travels between sensory cortex and retina.

   Communications would occur by dark photons signals with $h_{eff}/h = n$ and with maximal signal velocity allowing for an iteration leading to standardized perceptions as near as possible to the sensory input and representing only the essential features. Dark photons could transform in an energy conserving manner to biophotons with energies in visible and UV range (at least) and thus above thermal energy and therefore having effects not masked by thermal radiation. Brain is known to emit biophotons and they are also associated with axons [K18, K13].

2. All information molecules (neural transmitters, hormones, messengers) would be connection builders so that the view of neuroscience would be badly wrong here. I have discussed this idea earlier but in a slightly different form: the proposal was that information molecules are attached to the end of a flux tube getting longer as the molecule travels to its target. This is possible but unnecessary since it is enough to build just the bridge between existing connections. **Remark:** The view of neuroscience might be very different if information technologies would have been known for a century ago. Same applies to homeopathy and water memory [K41], which still remains curse words in mainstream science, although a lot about the mechanisms involved is known.

   The standard view about learning as strengthening of synaptic connections would translate to a gradual build-up of permanent flux tube connections so that communications with dark

photon signals would be possible all the time. This would lead to fusion of sender and receiver to a single quantum entangled system.

If the meridians of acupuncture network correspond to this kind of permanent network, they would not require nerve pulses, transmitters, nor information molecules.

3. Nerve pulse patterns would however generate Josephson radiation at EEG frequencies propagating from the brain to its MB from axonal membranes serving as Josephson junctions. EEG would code the nerve pulse patterns as frequency modulated Josephson radiation [K29].

The view about sensory perception and function of nerve pulse transmission differs from the standard view. Nerve pulse transition would not be communication between parts of CNS but building of the communication line for dark photons making possible communications with maximal signal velocity [L42] [K68].

1. This would allow generation of sensory mental images at sensory organs by an iteration involving virtual sensory input from brain to sensory organs. Pattern recognition would be realized as a build-up of an artwork representing standardized mental image as near as possible to the original sensory input.

2. Neurotransmitters and all information molecules would be bridges needed to construct connected communication lines. Learning as formation of permanent synaptic connections would be generation of permanent bridges of this kind.

3. Cell membrane and perhaps also other structures serve as generalized Josephson junctions [K29]. The (generalized) Josephson radiation generated by nerve pulses would give rise to EEG (and perhaps also to its fractal counterparts) as communication of neural information from brain to MB via Josephson frequency modulation. The size scale of the layer of MB would be rather large, of the order $1/f_c$, of the order Earth size in alpha band ($f_c \simeq 10$ Hz).

This view allows to understand imagination as virtual sensory inputs *resp.* motor actions from MB via brain which do not reach actual sensory organs *resp.* muscles but virtual sensory organs inside brain for which a good candidates are basal ganglia - ganglions are also associated a with sensory receptors. Dreams (REM), hallucinations, and psychedelic experiences (motor activities during sleep) could be understood as virtual sensory input reaching the sensory organs (muscles).

Also memory recall could involve virtual (real in the case of sensory memories) sensory input from MB at which memory mental images are realized [L115] [L84].

13.3.2 Binaural beat as a support for TGD view about brain

The phenomenon known as binaural beat [J12] provides support for the TGD view about the brain. Binaural beat occurs when sound waves with slightly different frequencies arrive in both ears. The beat can be understood as interference due to the time-varying phase difference of the waves. What is heard is the difference frequency, even when it is below 20 Hz - for instance 10 Hz-, and therefore not audible. The amplitude modulation with 10 Hz would be perceived, not the 10 Hz frequency. Strangely, the binaural beat occurs also when the signals arrive only to separated ears so that interference is not possible.

The TGD based explanation could be that the sound waves generate dark photon signals propagating along flux tubes and having classical em waves as correlates. The waves from different ears would interfere if the flux tubes meet at some point in the brain located at auditory areas perhaps. The first option is that this interference gives rise to the experience of the binaural beat and superposes with the sensory input assigned to ears (one cannot exclude the possibility that the sensory qualia are assigned to virtual sensory organs in the brain). Second option is that the virtual sensory input as feedback sent back to ears as dark photons superpose to the sensory input from ears.

13.3.3 The roles of nerve pulses and oscillations of neuronal membrane in the TGD picture

1. Nerve pulses - or more precisely, the transmitters emitted at synaptics contacts - connect flux tubes to longer pathways along which dark photons signals travel. Biophotons are dark photons transformed to ordinary so that there is empirical basis for this. Dark photons are an optimal tool for communications: light velocity and coherence.

   This allows the build of percepts as standardized sensory mental images by feedback. Nanosecond is the time scale for a single feedback loop so that there is a lot of time for this. This also explains dreams as virtual sensory input from the brain of MB to sensory organs in particular eyes (REM).

   Imagination can be understood as virtual sensory input which does not reach sensory organs or muscles but stops before it. Imagination is almost sensory experience with input from MB or brain. The notion of virtual sensory input is central for understanding speech comprehension and also inner speech.

2. Nerve pulses patterns modulate generalized Josephson frequencies for the membrane proteins (ion channels and pumps, etc...) and Josephson radiation to big bart of MB codes for the sensory input.

   Motor output is from MB in reverse time direction induced by BSFRs. A good guess is that it is via genes and induces gene expression by producing proteins but possible are also other forms of gene expression such as as dark photon signals to cell/neuronal membrane inducing nerve pulse patterns building connected wave guides for motor output as dark photons signals to propagate

13.3.4 Memories

To understand what memories and memory recall could be in ZEO one must specify what the geometrical correlate of subjective "Now" have?

1. The first proposal was that it corresponds to the active boundary of causal diamond (CD). It however turned out that the subjective "Now" could more naturally correspond to the $t = T$ slice of CD with maximal size located in the middle of the CD. Here t corresponds to a linear Minkowski time axis connecting the tips of the CD. If one accepts $M^8 - H$ duality [L100], this picture can be made precise.

   The moments "Now" would correspond to "special moments in the life of self" [L100, L114] identifiable as intersections of 6-spheres, which are brane-like entities (branes are encountered in M-theory) appearing as universal special solutions of algebraic equations determining the space-time surfaces in M^8_c. The values of T correspond to the roots of the real polynomial defining the space-time surface so that the values of "Now" are quantized.

2. During the sequence of state function reductions the active boundary of CD would shift towards the geometric future and the size of CD would increase (in statistical sense). The sub-CDs accompanying sensory and other mental images would shift to the direction of geometric future as CD increases and become potential memory mental images suffering BSFRs in a shorter time scale.

   The self would experience a memory mental image as a sub-self in memory recall to be discussed below. The time=constant snap-shots at the upper half of CD assignable to the memory mental images are ordered with respect to the Minkowski time t but the order is opposite to that for the subjective experiences. This was a great surprise to me. They would correspond to subselves to which memory recall builds a connection by entanglement quantally or by sending a signal, which is reflected back in BSFR for the memory mental images.

   What about recall of episodic memories in ZEO?

1. Spontaneous memory recall could correspond to a death of a memory mental image with an opposite arrow of time and re-incarnation with the same arrow of time as self. This could be accompanied by emission of a past directed "negative energy" signal received by self associated with the moment "Now". The interpretation would be in terms of extraction of metabolic energy: memory recall indeed requires metabolic energy. Active memory recall could correspond to a receival of future directed "positive energy" signal coming from "Now" having interpretation as metabolic energy feed. Energy conservation would force the memory mental image to change the arrow of time.

2. The prediction would be that in active memory recall by a "positive energy" signal received by the memory sub-CDs, the order of recalled memories is opposite to that for the real experiences. There is evidence for this kind of change [J21] (see also the popular article "*The human brain works backwards to retrieve memories*" at `http://tinyurl.com/y7hbqmug`).

13.3.5 Associations at quantum level

How associations could be formed at quantum level? Certainly memories and memory recall are involved and ZEO provides a universal model of memories.

1. In contrast to the naïve expectations, in ZEO the memory mental images would be sub-selves and would comove with the active boundary of causal diamond (CD identified as an intersection of future and past directed light-cones) and shift to the direction of the geometric future after their creation at $t = T$ hyper-plane of CD at which upper and lower light-cones of CD are glued to together. This is the largest time slice of CD and assumed to define the geometric correlate for the subjective moment "Now".

   Memory mental image (associated with sub-CD) continues its Karma's cycle having as basic unit a birth in BSFR, a life consisting of a sequence of analogs of unitary time evolutions followed by SSFRs, death in BSFR and living a life with opposite arrow of time. Memory mental images can live in the brain of the geometry future being connected to the brain "Now" by long flux tubes.

2. Memory recall wakes up the memory mental images by sending a message using dark photons received by the memory mental image. The universal model of language suggests that the signal is biological system coded genes serving also as addresses.

3. Conditioning in its simplest form should associate two mental images. The classical example about conditioning is a dog, which learns to expect food after it hears the sound of a bell. The primary experience involves both the sound of the bell and getting the food. After the conditioning the mere sound of the bell stimulates activities like salivation. Positive or negative emotions facilitate conditioning. In ZEO framework the learning of the conditioned response would involve two mental images: imagined experience about obtaining the food and the sound of a bell.

   They should fuse to a composite mental image, perhaps by entanglement. These primary memory mental images and their almost copies produced later and involving only the bell and the imagined food would form a population of memory mental images in the geometric future shifting farther away. As the dog hears the sound of the bell, a message to the memory mental images in the geometric future is sent. It is realized as frequency modulated dark Josephson radiation from say basal ganglia of sensory organs.

4. A naïve guess is that the modulated Josephson frequencies correspond to a period larger than the temporal distance of the memory mental image from "Now" and defining its age. Rather low frequencies are involved for long term memories and the values of h_{eff} must be scaled correspondingly. The longer the time span of the memory, the larger the value of h_{eff}. The emergence of language is therefore accompanied by the emergence of long term memory. The memory mental images about expectation of food +sound of bell have however a shorter time span. These signals wake-up the memory mental images but they are however not conscious to self - and as they die they send a signal back to the brain inducing an imagined mental image involving also the promise of food.

5. In some cases the signal can reach the sensory organs and a sensory memory mental image is generated. This picture applies also to the acquisition of the language. The larger value of h_{eff} associated with language genes (the value of h_{eff} could vary for a given language gene) meaning larger layers of MBs and a possible fusion of MBs of he communicators, and therefore the ability to remember the associations of the words to sensory mental images for a long time. Hearing of the linguistic expression would also generate internal speech as a particular virtual motor action.

13.4 A TGD inspired vision about language

13.4.1 The role of MB

The proposal is that new layer of MB assignable to larger part of MB outside body was involved with the emergence of language. There are several arguments in favor of this proposal.

1. The model for how mutation of few genes like FOXP2 lead the evolution of human languages to be discussed relies on the idea that the value of h_{eff} assignable to dark variants of language genes increases. This means the emergence of new layer of MB having onion-like structure. What emerged was grammatics and syntax as hierarchical structures represented as many-sheeted space-time structures distinguishing humans from other animals could have emerged: these tructures can be assigned to MB and they have also interpretaton in terms of extension of rationals leading to n-sheeted structures. The new level of hierarchy would have emerged at the level of the MB including also dark gene first: flux tubes inside flux tubes inside labelled by values of h_{eff}.

2. The development of language led to a cultural evolution and could have been a quantum leap in the evolution of collective levels of consciousness: emergence of new levels in the hierarchy of extensions of rationals. Maybe the emergence of gene with large h_{eff} meant that it receives control commands from this collective level of consciousness possibly assgnable to communications, social group, or even larger structure. Recall that the size scale of MB assignable to EEG frequencies is of order Earth size. The basic structure of language are indeed very "social". Subjects, objects, verbs expressing what they do to each other, relations between these entities, attributes (adjectives) characterizing their states. Also the notions of plural and singular.

3. One can also ask how it is possible to distinguish between sensory input created by living beings and having meaning from that produced to dead matter. Also humans give emotional meaning to bird's song and vocal signals and gestures of animals but not to the sounds of dead Nature. For autists this ability might be very weakly developed. The natural answer to the queston is that all communications are also communications between magnetic bodies, quite concrete touching, makes it possible to distinguish natural sounds from speech and signals with represent communications. Communications require attention and the flux tube connections between communicators would be correlates for the attention.

   Mere mimicry does not require interpretation of the signal as communications. Some birds can mimic the sound of even a car. I remember my astonishment when finnish bird "talitiainen" mimicked the fate motif of Beethoven's symphony No. 5. My neighbours listened to classical music!

   There should be also a fundamental difference between the communications of ordinary sounds and speech to brain. The communications of speech could be via the large part of MB outside body whereas ordinary sensory data would be communicated via small part of MB to brain.

4. In language acquisition the role of parents, in particular mother, is crucial. One might of course argue that just mimicry and rewards are enough. But how the child knows that mother is trying to teach her that the word "apple" corresponds to the object that the mother is holding at ther hand. Is the fusion and entanglement of MBs needed?

The acquisition of language by child might also involve the MBs of child and Mother at least fusing to a larger structure. This might help the child to understand that the purpose is to learn to reproduce the word associated with the object that word describes. It could also make possible to learn the grammatics and syntax by becoming a part of larger self already learned these notions.

5. Speech communications happen magically in a good company when people are friendly and benevolent. As a young man I was extremely shy in a company of people who were not my friends. When I had intention to say something, I tried to form sentences in my mind as internal speech before possibly getting courage to talk but found it extremely difficult and I remained usually silent. In a company of good friends I realized that it was not so difficult at all: someone talked through me using me as an instrument.

13.4.2 Genes and language

What is the role of FOXP2 and other control genes?

The question that led to the writing of this article was whether the mutation of the genome leading to FOXP2 gene and other similar genes responsible for control of the genome did lead to the evolution of human language. How? The above mechanism does not distinguish in no manner between linguistic and ordinary associations. What happened?

Evolution in TGD framework means the increase of number the increase of the complexity of extension of rationals and thus increase of its dimension $h_{eff}/h_0 = n$ defining a universal measure of intelligence and also a measure for the temporal and spatial scale of quantum coherence. A possibly dramatic increase of h_{eff} for FOXP2 gene and other key genes is a natural hypothesis explaining why the complexity of the language evolved and led from signals to sentences requiring longer time scale of quantum coherence and also the emergence of complex hierarchical structures naturally assignable to the new extension as extension of the original one.

The larger the value of h_{eff}, the larger the scale of the layer of MB. This suggests that a new level of collective consciousness essential for communications emerged. This layer would be associated with the system formed by the systems communicating using language. This would explain the ability to distinguish between sounds produced by inanimate systems and sounds produced by living systems and having meaning.

The emergence of this new level would have meant emergence of many new things: of speech, of longer time scales of memory and planned action, of a new level of cognition, of imagination in longer time scales, and of cultural evolution.

Second mechanism related to the emergence of FOXP2 and other similar control genes could be energy resonance in the coupling of the analogs of DNA, RNA, tRNA, and amino acids. The coupling would be between the entire gene and its dark analog. Whether the energy resonance occurs for all cyclotron energies of codons separately or for their sum remains an open question. For both scenarios small changes of the gene can spoil or produce an energy resonance. This sensitivity would make genes an ideal control tool but would also serve as a general mechanism also for genetic diseases. The increase of h_{eff} accompanied by a small mutation to guarantee energy resonance could be the mechanism explaining the importance of FOXP2 and similar genes.

What about the development of speech organs and brain areas related to speech?

The development of speech required development of speech organs and brain areas for understanding of language and language production. How important was their role or was the mutation of certain genes responsible for language control enough to initiate the evolution leading to the development of speech organs and needed brain areas?

One can consider the emerge of a layer of MB with a considerably longer scale perhaps assignable to some collective level of consciousness - perhaps even the entire species. MB as a TGD counterpart for magnetic fields in Maxwellian theory indeed has layers or order of Earth size and even much larger. The proposed emergence of a big layer of MB with a large value of h_{eff} could relate closely to Sheldrake's proposal [I79] about learning at the level of species. How this new layer could have affected the evolution of speech organs and new brain regions.

1. MB is the key player in TGD. The TGD Universe allows conscious entities and they tend to have ideas as we know. Did MB at some level of hierarchy get an idea about expression of information using temporal sound patterns coupling to dark photons with specific frequencies? That would be a representation of bio-harmony in a new much longer spatial and time scale: did this evolutionary step correspond to the emergence of a new even larger value of h_{eff} to the dark matter hierarchy. Maybe the realization of this new faculty would have been a fractally scaled up variant of earlier realizations making this easier. Did MB make a plan which was eventually realized after a lot of trials and errors?

2. What this plan could correspond to? Here p-adic physics enters into the game. p-Adic dynamics for p-adic variants of space-time sheets obeys the same field equations as real space-time sheets. It however allows breaking of a strict determinism of real number based field equations: this non-determinism would correspond to the freedom of imagination.

   p-Adic data could give rise to full space-time surface as dynamical patterns but they could correspond only to a piece of its real counterpart. Imagination would be non-realistic. Imagined motor actions and sensory inputs would correspond to this kind of partially fulfilled entions: signals would not reach sensory organs or muscles.

3. How this would apply to MB's plan to create sound producing organs? This plan could proceed by trial and error to become more realistic and gradually find a complete realization. The reduction of the planning to trial and error at dark gene level - would be an enormous simplification and could have meant mutations increasing the value of h_{eff} bringing in larger layers of MB related to the brain areas and speech organs.

13.4.3 Meaning from embodiment in the TGD framework

The notion of embodiment is central for the understanding of how speech gets its meaning. The simplest sentences represent sensory inputs or motor actions. But also very abstract expressions have metaphoric representations in terms of subject and objects and verbs representing actions. Embodiment means that language expressions are transformed to virtual sensory inputs and virtual motor actions creating imaginations of the real ones. This requires formation of associations as generation of sensory and motor mental images.

For instance, the sentence "A does something to B" creates virtual sensory and motor mental images in which A indeed does something to B. Mental images representing A and B and "does something" are generated and could correspond to interaction between two mental images. Basically remembering sensory percept in which A does something to B is enough to provide the meaning and the linguistic decomposition is a model. For instance, the heard speech generates internal speech helping in understanding.

The experience or imagined experience as virtual almost experience with input from MB rather than environment is associated with the expression of language. When the language has been learned, a mere language expression generates memory mental images about the experience associated with the expression. The mechanism is naturally pattern recognition and completion as a general mechanism of association and conditioning also in neuroscience and artificial pattern recognition.

Questions

In the TGD framework the questions are the following ones.

1. How memories are represented and how they give rise to conscious memory mental images? ZEO leads to a general proposal for how memory mental images are represented. First communication of sensory input to the part of MB containing a subself representing memory mental image, call it M. M receives the signals and experiences BSFR analogous to motor action involving a signal to the direction of geometric past to subself representing "Me Now". This signal is transformed to a nerve pulse pattern generating a virtual almost sensory mental image.

The general proposal is that in biology at cellular level motor actions are generated as time reversed signals from MB to dark genome inducing neural activity by a signal to cell membrane. The signal from MB to genome would take place by dark photon representation of genetic code and induce BSFR. This mechanism would be quite general.

Genes with N codons must be represented as a dark 3N-photon signal behaving like a single particle like entity. This is not possible in standard physics but adelic physics relying on number theory makes this possible. The notion of Galois confinement [L111] allows dark photon 3N-plets representing genes as sequences of N 3-chords of bio-harmony - kind of music pieces - serving as dynamical units analogous to baryons as color confined units formed from 3 quarks and thus behaving as dynamical units.

The signal would generate a sequence cyclotron resonance peaks at the genome giving rise to a sequence of ticks at dark genome. They must in turn generate a signal to the cell membrane received as a sequence of ticks inducing the sequence of nerve pulses. This seems to require realization of genetic code at the level of the cell membrane level proposed [L58]. The general principle would be the same as in computer language LISP manipulating lists: only identical genes serving as addresses can be in communications by cyclotron resonance. Not only the notion of cyclotrotron radiation but also the notion of generalized Josephson radiation [L17] must be further generalized: dark Josephson photons are replaced with dark 3N-photons.

2. Where the sensory signal to MB is generated? Its generation at neuronal or cell membranes as generalized Josephson radiation is not plausible since the time scales do not fit together. The modulation of Josephson radiation by nerve pulses patterns produces ripples rather than slow frequency modulation. A more plausible proposal is that the sensory signal to MB is generated at the basal ganglia of sensory organs as a generalized Josephson radiation with frequency modulation generated by the sensory input.

3. What is the basic quantum mechanism of association of the memory mental image B to a sensory input A? In the neuroscience framework it would happen in the associative regions of the brain by new pulse patterns and by learning based on changes in synaptic contacts. Now this would take place at analogous regions of MB to which sensory input is sent as a signal and induced cyclotron resonance for 3N-chords.

   A pattern recognition at the level of MB would be in question. This involves a completion of the sinput pattern - sensory mental image - to a pattern representing memory mental image associated with it. This requires a generalization of the existing view about pattern recognition to quantum level. Also this step could involve resonance leading to a fusion of the associated mental images by entanglement. This fused pair of mental images would generate a dark 3N-photon signal propagating to the brain as a generalized cyclotron radiation.

Association to memory mental images gives meaning to linguistic expressions

Association of the auditory input to memory mental images would provide linguistic expressions with meaning.

1. Association is a way to assign meaning to linguistic expressions by embodiment. Language expression is associated with an imagined sensory experience or motor activity. Also internal speech is imagined speech as imagined motor activity and generated by written text.

   Association requires wake-up of memory mental image by the speech signal, which in turn generates a virtual sensory brain or lower level of layers of MB . In ZEO memory mental images are in the geometric future of "me Now" so that BSFR must take place: the memory self "dies" when it sends the message as a dark photon signal. The signal eventually arrives in the brain and generates a nerve pulse pattern needed by dark photon communications generating the virtual sensory to virtual sensory organs.

   Memory mental images at MB are woken up in ordinary memory recall presumably taking place at the hippocampus [J7]. The frequencies involved are theta frequencies suggesting that the layers involved of MB have the size scale of Earth. In the case of speech the frequencies are in the range 150-300 Hz which suggests that layers corresponding to these frequencies

are involved. Also longer time scales such as minute time scale are involved and much bigger layers of MB could be involved.

2. The signals could be sent to the MB from sensory organs:

   (a) Ganglions associated with sensory organs are analogous to brain nuclei and would be the primary receivers of the sensory input. Nerve pulses are generated by neurons above then. Ganglions must play an important role in the generation of sensory experience and motor activities. Ganglions in the brain are called basal ganglia. They could serve as receivers of virtual sensory input and motor output from the brain.

   The neuron structures above ganglions also generate nerve pulses and these give rise to communications to the brain along flux tubes associated with neural pathways by dark photons signals. These communications would represent ordinary sensory communications, in particular sounds as mere sounds without meaning. They would also give rise to language acquisition via association.

   (b) The view about communications to MB as Josephson radiation modulated by membrane voltage variations suggests that the frequency modulations of membrane potential at frequencies of speech are involved. The earlier proposal that nerve pulse patterns could induce this modulation. They however would correspond to ripples of long wavelength waves. Of course, also axonal membranes involve oscillations of the membrane potential inducing the modulation but this modulation of generalized Josephson energy involving also difference of cyclotron energies is much smaller than that caused by nerve pulses.

   The oscillations ganglion membrane potential induced by sound waves could be involved. Frequency modulated Josephson radiation modulated by sounds would propagate to some part of MB. One can consider even the possibility that dark genes such as FOXP2 generate dark 3N-photon radiation. These dark genes could be also realized at the level of cell membrane.

   What could be the radiation in the case of dark genes. Could it be generalized Josephson radiation assignable to an array of Josephson junctions defined by dark genes and their conjugates. Sound waves could induce frequency modulations of oscillations of the voltage between the dark genes just by putting them into motion. Does the distance matter.

   (c) The signals would be received by frequency resonance by some layer of MB responsible for memories representing word-sensory/motor associations. What this layer of MB is and where it is located? The flux tubes should allow 3-N dark photon sequences. Their realization outside the biological body does not look realistic. This suggests that the part of MB can be assigned with the brain of the geometric future. Magnetic loops would return back to the brain of the geometric future. The longer the time scale of the memory, the longer the loop. The realization of sensory or in part of MB analogous to associative cortex. What happens in the part of the MB of the future brain representing the memory about association. The analogy of pattern completion of incoming sound signal to sensory input should take place and generate a virtual sensory input to the geometric past as a response along flux loops arriving at the virtual basal ganglia defining virtual sensory organs. Two long loops would be involved. From sensory basal ganglia to the highest motor and sensory areas? And from these to virtual sensory and motor organs.

   (d) The branching of axons suggests a branching of corresponding flux tubes. What could happen in this process? In branching the value of h_{eff} could be reduced for dark photons - for instance by frequency doubling. Frequency doubling would transform audible frequencies to patterns of nerve pulses with much higher frequencies. From long to short scales. h_{eff} hierarchy would be essential.

   A possible interpretation as a cognitive quantum measurement is possible. Cognitive quantum measurement as a cascade of measurements in the group algebra of the Galois

group of extension would give rise to a gradual reduction of effective Planck constants for the factors of the tensor product.

This cascade could correspond to the branching of axons leading to the reduction of biophoton energy in visible or UV to energy above thermal energy and assignable to cell membrane. What happens in branching of the flux tube? Is energy shared to that of n dark photons with the same frequency and smaller h_{eff}. Or does a localization to a single branch occur. h_{eff} would be reduced and f would increase. E would be conserved. Also both processes can occur. Division into n dark photons with $h_{eff} --> h_{eff}/n$ with f preserved plus a reduction $h_{eff}/n \to h_{eff}/nm$ and increase $f \to mf$ increasing by factor m.

(e) The communication via long flux loops to the small part of MB at the brain cannot correspond to this kind of process since the value of h_{eff} assignable to FOXP2 genes should be preserved. The communication could be to dark control genes such as dark FOXP2 generating signal to neuronal membrane - perhaps dark control gene also there - giving rise to nerve pulse pattern generating virtual almost sensory experience at the virtual sensory organs defined by basal ganglia.

This feedback should have been present already before the emergence of language but in shorter scales and leading to lower layers in the hierarchical structure of the brain ordered by evolution. They would correspond to a hierarchy of increasing values of h_{eff} realized at the level of genome.

These long feedback loops could end also at lower layers inside the brain and also the hierarchy of cortical layers could relate to this kind of feedback hierarchy. The virtual sensory input to the basal ganglia inside the brain would give rise to imagined sensory perceptions and motor actions.

(f) The interpretation as analog of Fourier transform [A4] is suggestive. The cyclotron resonance peaks would generate a sequence of ticks analogous to a Fourier transform of the incoming waves. Music-speech dichotomy suggests itself strongly. Speech could be analogous to a sequence of SFRs - ticks - and singing to superpositions of classical time evolutions connecting them. It is said that the right brain sings and the left brain talks. Could some brain regions sing in the sense that they receive or send the signal as dark cyclotron radiation and could some brain regions talk in the sense that this radiation would induce or be induced by internal speech as virtual motor action.

A holistic representation in terms of frequencies would be transformed to "reductionistic" representation as time series. The correlation function for ticks would have the frequencies in its Fourier transform: stochastic resonance or its analog. Eventually this association to a sequence of ticks could generate a nerve pulse pattern creating a neural pathway making possible virtual sensory input in various sensory areas.

Given language expression corresponds to a huge number sensory percepts and one could argue that this requires a huge number of associations. In the computationalistic framework this would mean a huge amount of computer storage. The model for the generation of mental images predicts that the sensory mental images are standardized mental images generated by a feedback loop giving rise to a pattern recognition. Standard mental images allow also abstraction and conceptualization. One can even consider a quantum counterpart of the classical notion of concept. Concept as the set of its instances would be replaced by wave function in the set of instances giving a large number of different views about the concept.

13.4.4 Bio-harmony as a universal language

Bio-harmony [L11, L78] realizing genetic code for communications is an ideal candidate for a universal language: codon would represent 6 bits and the allowed 64 chords would represent mood at molecular level. There is quite a large number of fundamental moods. Both dark codons and 3-chords bound to units by Galois confinement [L108] can be combined to dark genes by Galois confinement. This language would be minimal. The contents of the message would be minimal - the

address of the receiver same as that of sender - so that LISP like language would be in question. The communications would be based on 3N-resonance. U-shaped flux tubes from receiver and sender forming bridges by reconnection would be the topological aspect of the communications.

The space-time surface associated with n:th order polynomial in M^8 defining the extension of rationals has n sheets corresponding to the roots of the polynomial [L86, L84]. These many-sheeted structures would give rise to a geometric representation of hierarchical linguistic structures.

There is also an abstraction hierarchy defined by the functional composition of polynomials giving rise to representation of the Galois group of extension in terms of inclusion hierarchy of normal subgroups. Flux tubes within flux tubes within.... are possible. For extension of extension of ... with extensions having dimensions $n_1, n_2, ...$ one would have n_1-sheeted structure with sheets replaced with n_2 sheeted structures replaced with..... Substitution of x in $P_{n_1}(x)$ with $P_{n_2}(x)$ with x replaced with....would correspond to this replacement.

Cascades of quantum measurements for the states of the Galois group algebra to a product state in the tensor product of Galois group algebras of the hierarchy of normal subgroups would define cognitive measurements which could be crucial for understanding of language by analysis [L110].

Speech is only one form of communication of binary and emotional information

Concerning production and understanding of speech, one must see the situation more generally in TGD framework.

1. Speech is only one form to communicate information and emotions. Also gestures define a language being based on motor expression. An interesting test is how complex gestures developed before speech and whether FoxP2 has anything to do with sign language. Does sign language have grammatics and syntax characterizing formal languages?

2. Music and singing is the second form of language and expresses emotions rather than bits. Here harmony is an essential notion. Some basic chords define the harmony expressing the mood. Bits/words do not matter, only the chords used.

   This leads in TGD to the model of bioharmony in terms of icosahedral and tetrahedral geometries and 3-chords made of light assigned to the triangular faces of icosahedron and tetrahedron. The surprise was that vertebrate genetic code emerged as a prediction: the numbers of DNA codons coding for a given amino-acid is predicted correctly. DNA codons correspond to triangular faces and the orbit of a given triangle under the symmetries of the bioharmony in question corresponds to DNA codons coding for the amino-acid assigned with the orbit.

   Codon corresponds to 6 bits: this is information in the usual computational sense. Bioharmony codes for mood: emotional information related to emotional intelligence as ability to get to the same mood allowing to receive this information. Bioharmony would be a fundamental representation of information realized already at molecular level and speech, hearing and other expressions of information would be based on it.

   The surprising findings that RNA is central in conditioning [**?**]uggest that RNA somehow represents emotions crucial for conditioning [**?**] Dark DNA and bioharmony for which emotions would be realized at molecular level would make it possible.

What does Universality mean?

There are two views about language: Universality (or computationalism involving only grammar and syntax) concentrates on the formal aspects whereas connectionism concentrates language as a conditioning. For the first option one speaks of language learning as learning of formal rules and this applies to written language and language of mathematics. For the latter option one speaks of language acquisition as an almost unconscious process of imitation. These two views would be fused together in TGD view.

1. There would be only one universal language at the fundamental level. For communications it would be defined by genetic code realized as 3-chords of dark photons forming in turn

3N-frequency composites serving also as units. This code has both the bitty aspect: codon corresponds to 6 bits and the emotional aspect defined by given bio-harmony characterizing that is by the 3-chords defining the bio-harmony and in this manner mood. Genome would define genotype of language and specific languages would be phenotypes.

This code is used in communications between various levels of the hierarchy. At least in control commands arriving from MB to genome. The analog of Josephson radiation from cell membrane mediating sensory data to MB would consist of a sequence of notes but if cell membrane realizes genetic code, also Josephson radiation could consist of 3N-frequency dark photon composites representing genes. Note that the notion of tick makes sense also for 3N-chords. The message would be sent as Josephson radiation or cyclotron radiation and received as ticks corresponding to state function reductions.

Of course, one cannot exclude the single note option - mere temporal pattern of ticks with varying time separations - for the messages to the genome could be the case of speech having constant pitch. For singing and speech mediating emotions the situation melody or sequence of 3-chords would be needed.

Since the language would be realized at DNA level, even plants could communicate using it. Plants are known to communicate and there is evidence that plants can cognize and even count [I33](`https://cutt.ly/ffRYXH8`). In TGD framework also hormonal communications thought to be chemical would take place by biophotons: the hormones connected by flux tube to molecule in say hypothalamus would build the waveguides to second molecule in body for dark photons to propagate.

The basic new physics building bricks in this picture would be 3N-frequency cyclotron resonance transforming the oscillating signal from basal ganglia membranes to a sequence of ticks in turn inducing a sequence of nerve pulses generating the virtual sensory experience using stochastic resonance coding the frequencies of original signal to peaks in the frequency spectrum of the correlation function for the sequences of nerve pulses. Also dark 3N-photon Josephson radiation assignable to genes represented also at cell membrane level would emerge as a new concept.

2. The universal aspects of the language would be realized as a basic expression of dark genes realized in terms of 3N dark photon composites propagating along flux tubes. The content of the packet is the address to which it sent! This would be just like in computer language LISP. This would be the genotype of language, the universal language based on 3N-frequency-resonance between sender and receiver genes.

   This would completely separate the meaning of language expressions from the basic communication mechanism. This is of course true also for kinds of communications. The sender and receiver provide the meaning for language expressions by sensory perceiving them. Understanding of how the meaning is generated is the key problem. This requires theory of consciousness and a new view about the conscious brain.

3. TGD view is based on dark 3N-photon resonance communications between genomes and possibly also the genomes associated with the cell membranes and microtubules realizing the genetic code. The sensory input together with the language expression would provide the primary sensory percept - just as in learning by example. When communicated to the brain and even MB a secondary virtual almost sensory percept and virtual almost motor action would be generated as imagined sensory inputs.

   This would be the fundamental association giving meaning to the language. Conditioning would occur and when the mere linguistic input is received, the virtual sensory precept and motor output are generated. Does this require anything new: for instance, does it require that the associations are remembered in some sense or are the associations realized as in neuroscience in terms of synaptic strengths? One would have memory as a learned behavior.

   First the sensory input generated by linguistic expression is communicated from the basal ganglia of sensory organ or virtual sensory organ to the sensory and motor cortices by using dark 3N-photon resonance. After this the virtual sensory input and almost imagined) perception is generated. How?: as dark 3N-photon signals propagating in opposite spatial

direction to sensory organs. The fact that nerve pulse conduction is in a single direction only suggests that also time reversal occurs in BSFR.

4. This general picture applies to the formation of associations and conditioning quite generally. This would be also the mechanism of imagination, which also sharply distinguishes humans from animals. The special ability of the humans to imagine would have emerged at the same time as the complex language. This could be due to the mutations of certain language genes like FOXP2 acting as genes for which the 3N-photon resonance is realized and one must understand how this could be the case.

The proposed notion of universality is not in conflict with the fact there exist large number of languages. The development of different languages is actually easy to understand as reflecting the fact that there is underlying universal language which is minimal in the sense that the content of the message is the address of the receiver. Language acquisition is a conditioning process associating sensory inputs and motor outputs to language expressions at a more fundamental level and the words are just labels for them. This is like general coordinate invariance in general relativity. Points of space-time can have infinite manner of different labelings in terms of numbers (now words).

13.4.5 Geometrization and topologization of the grammar and syntax in terms of many-sheeted space-time

These aspects of speech make understanding of speech acquisition possible but what about intentional learning of speech involving learning of grammar and syntax, which have nothing to do with contents of speech? In computer languages and mathematics as language this aspect would dominate.

Fractal flux tubes networks and structures of language

The TGD proposal is that magnetic flux tube networks - possibly trees in case of speech and associated with nerve pulse patterns are in an essential role. Flux tubes are effectively 1-D and have orientation which corresponds to temporal direction of speech and spatial direction of written language. There are flux tubes inside flux tubes flux tubes giving rise to hierarchical structures corresponding to the parsing of language expressions. MB would as many-sheeted structure would geometrize/topologize grammar and syntax.

There are aso 2-D and even 3-D flux tube networks but not accompanied by neural networks. These would be essential for the geometric and holistic aspects of cognition: visual cognition in particular. The meridian system of Eastern medicine could be associated with the MB. These flux tube networks would have been present before the emergence of the neural system and would be possessed even by plants. TGD could reduce the structures of language to purely geometric structures. Sentences would correspond to many-sheeted space-time surfaces with their topology representing the parsing structure. Basic space-time sheets would represent words, and the gluing of them to larger space-time sheets by topological sum operation would build sentences. Topological sum of surfaces A and A_0 essentially means that A is inside A_0. Also the ordering of the words matters: AB and BA are not the same thing. When A and B are inside an effectively 1-D magnetic flux tube A_0, the ordering of the positions inside the flux tube makes it possible to tell whether A is before B or vice versa.

Non-associativity forcing use of brackets in mathematical expressions would be also important ($(A+B)C \neq A+BC$). For instance, $(AB)C$ would correspond to the structure formed from a pair A_0C of flux tubes by putting AB inside flux tube A_0. $A(BC)$ would be obtained from the AA_0 by putting BC inside A_0. Putting inside brackets means gluing at a larger space-time sheet. The reader is encouraged to imagine what these examples look like when represented in terms of flux tubes within flux tubes.

The hierarchy of extensions of rationals realized in terms of functional composition of polynomials defining space-time surfaces in M^8 as n-sheeted structures provides a number theoretical view about linguistic structures [L100]. The functional decomposition $P_1 \to P_1 \circ P_2(x)$ replaces each space-time sheet of the n_1-sheeted structure with an n_2-sheeted structure associated with P_2. This is like fractal zoom each sheet to n_2 sheets.

This is due to the fundamental theorem of algebra stating that a polynomial P_n of complex argument with degree n obtains all its values n times. The argument $y = P_{n_2}(x)$ of $z = P_{n_1}(y)$ has the same value for n_2 points x_k. This gives n_2 sheets at y. The value z in turned obtained for n_1 points. Therefore n_1 sheets decompose to n_2 sheets.

How the structural elements of language can be understood?

One must understand what is behind the notions of subject, object, verb. How tense, case, singular and plural , pronouns, adverbs, etc. are expressed: at the level of genetic code or of conscious experience as contents of imagined sensory experience and motor activity associated with the experience? Are they coded already by the oscillation pattern of the basal ganglia membrane giving rise to imagined experience beside genuine sensory experience? This would be the most elegant option.

The same FoxP2 gene or its analogs could be involved. Consider tense as an example. How the tense would be coded to the oscillations of the ganglia membrane or to the position of these membranes in the brain - to what subself they represent. Who is talking and about what and when!

- "I see" would correspond to a real sensory perception.
- "I saw" corresponds to immediate personal memory: could this be a virtual almost percept produced by a memory and realized at different places as virtual sensory percept. Basal ganglia associated with a level higher than sensory organs responsible for imaginations and inner speech..
- "I will see" would correspond to sensory percept, precognitions in reversed arrow of time.
- "I have done" seems to refer to a remote past: different time scale and perhaps different value of h_{eff}.
- "I had done" is talk of another self above or parallel me in self hierarchy about me as sub-self as an outsider. Now the basal ganglia would be at some part of the brain containing mental images representing some outsiders, say community as sub-self.

One should also understand what makes the sentence a question or command. In written language formal tools to express whether the sentence represents a question, command or something else have emerged. The many-sheeted structure of space-time should express these aspects of language using fixed words as vocabulary at the basic level. For instance, the building bricks for "Did you do this?" and "Do this!" should have the same "genotype" but different "phenotypes" if the reduction to dark genetic code makes sense. The context represented by a mental image containing the standard mental images representing the words of the sentence would determine "phenotype" allowing to differentiate between the two cases. The geometric representation would be based on flux tubes. Context - the larger flux tube - would be associated with the mental image "I do not know" for "Did you do this?" and "I am the boss" for "Do this!": this context would determine the phenotype just like the environment affects the phenotype in ordinary genetics.

13.5 Appendix: Living matter, biochemistry, and consciousness

The model for living matter relies heavily on the notions of MB carrying $h_{eff} > h$ phases behaving like dark matter and ZEO.

13.5.1 ZEO based quantum measurement theory extends to a theory of consciousness

ZEO based quantum measurement theory [L115] leads to a quantum theory of consciousness (see **Fig. 13.4**)by lifting the observer from an outsider to part of physical system. In particular, the theory predicts that the arrow of time changes in "big" (ordinary) state function reductions

(BSFRs) as opposed to "small" SFRs (SSFRs) as the counterparts of weak measurements (see **Fig. 13.5**).

This suggests that self-organization in all scales reduces to dissipation with reversed arrow of time. The energies of states increase with h_{eff} and h_{eff} tends to be reduced spontaneously. This means that energy feed is needed to preserved the distribution for h_{eff}: in biology this corresponds to metabolic energy feed. The energy feed necessary for self-organization would reduce to dissipation of self-organizing system in reversed time direction. Dark matter at MB of the system would serve as a master controlling the ordinary matter serving in the role of slave. Note that there would be master-slave hierarchy of MBs ordered by h_{eff}.

This would happen at magnetic and have dramatic implications. Time reversed dissipation looks like energy feed from the environment to system. Self-organization involves always energy feed and generation of structures rather than their disappearance in apparent conflict with second law. Self-organization would correspond to dissipation in reversed time direction implied by generalized second law. No specific mechanisms would be required and only metabolic energy storages- systems able to receive the energy dissipated in reversed time direction - are enough. Obviously this provides a totally new vision about energy technology.

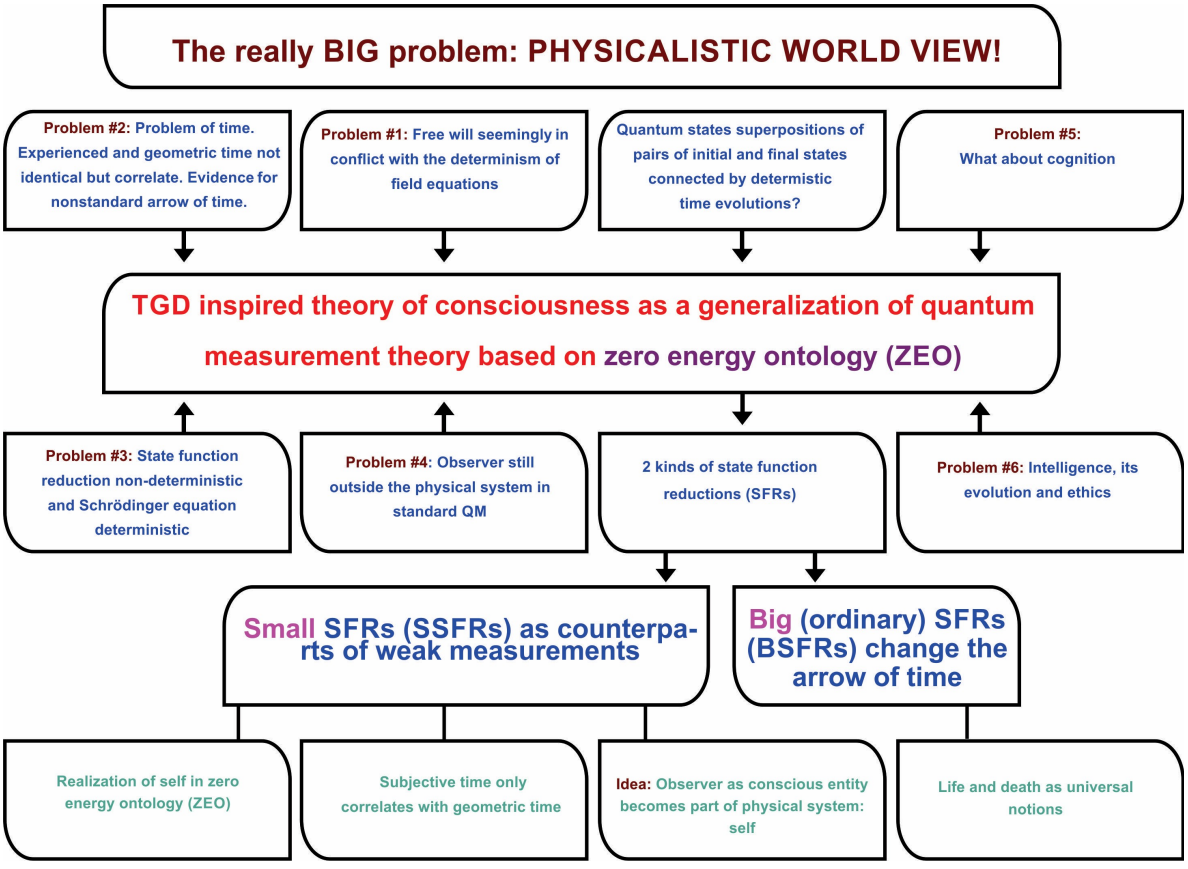

Figure 13.4: Consciousness theory from quantum measurement theory

13.5.2 p-Adic physics as a correlate of intention and cognition

One of the earlier ideas about the arrow of subjective time was that it corresponds to a phase transition front representing a transformation of intentions to actions and propagating towards the geometric future quantum jump by quantum jump. The assumption about this front is unnecessary in the recent view inspired by ZEO. Intentions should relate to active aspects of conscious

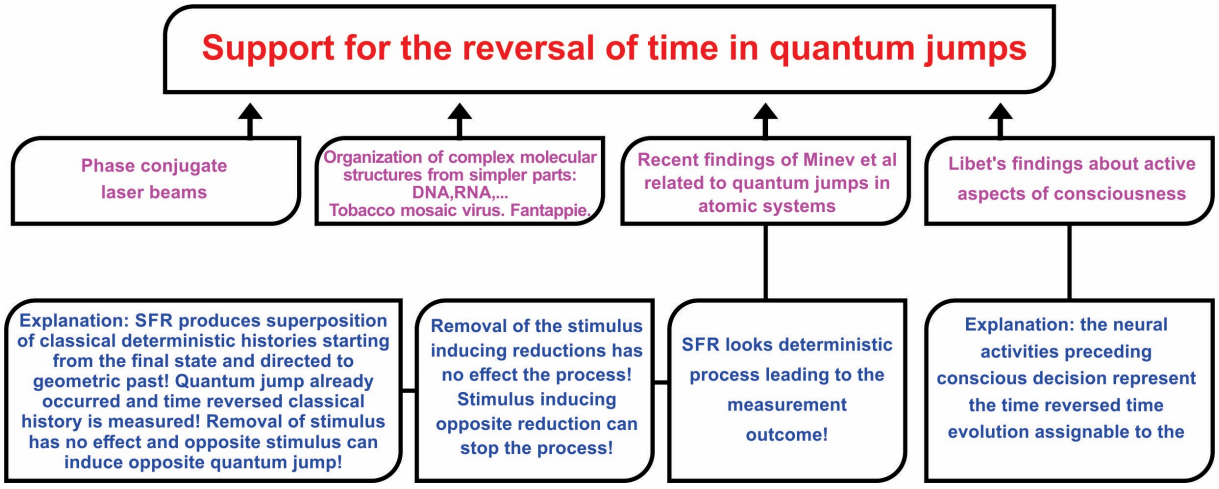

Figure 13.5: Time reversal occurs in BSFR

experience. The question is what the quantum physical correlates of intentions are and what happens in the transformation of intention to action.

1. The old proposal is that p-adic-to-real transition could correspond to a realization of intention as action. One can even consider the possibility that the sequence of state function reductions decomposes to pairs real-to-padic and p-adic-to-real transitions. This picture does not explain why and how intention gradually evolves increasingly stronger, and is finally realized. The identification of p-adic space-time sheets as correlates of cognition is however natural.

2. The newer proposal, which might be called adelic, is that real and p-adic space-time sheets form a larger sensory-cognitive structure: cognitive and sensory aspects would be simultaneously present. Real and p-adic space- time surfaces would form a single coherent whole which could be called adelic space-time. All p-adic manifolds could be present and define kind of chart maps about real preferred extremals so that they would not be independent entities as for the first option. The first objection is that the separate assignment of fermions to every Cartesian factor of the adelic space-time does not make sense. This objection is circumvented if fermions belong to the intersection of realities and p-adicities.

   This makes sense if string world sheets carrying the induced spinor fields- define seats of cognitive representations in the intersection of reality and p-adicities. Cognition would be still associated with the p-adic space- time sheets and sensory experience with real ones. What can be sensed and cognized would be represented by the intersection.

   Intention would be however something different for the adelic option. The intention to perform quantum jump at the opposite boundary would develop during the sequence of state

function reductions at fixed boundary and eventually Negentropy Maximization Principle (NMP) [K50] [L39] (stating that in given state function reduction negentropy gain is in some sense maximized) would force the transformation of intention to action as first state function reduction at opposite boundary. NMP would guarantee that the urge to do something develops so strong that eventually something is done.

Intention involves two aspects: The plan for achieving something which corresponds to cognition and the will to achieve something which corresponds to emotional state. These aspects could correspond to p-adic andreal aspects of intentionality.

The recent view relying strongly on $M^8 - H$ duality lead to ask whether the picture could be made more precise.This picture forces also to challenge the above picture.

1. The basic idea is that p-adic integration constants of the differential equation are pseudo-constants having a vanishing derivative but depending on finite number of pinary digits-rational numbers satisfy this condition. In M^8 picture a real polynomial with rational (or possibly algebraic) coefficients determines the space-time surface. The roots of this polynomial as a function of radial light-coordinate r at light-like boundary of CD determine this polynomial. When pseudo constant are allowed, the coefficients become pseudo constants, which are constants at the interval $[0;T]$ divided to sub-intervals $I_1 = [0;t_1]$, $I_2 = [t_1;t_2]$, ...,$I_N = [t_{N-1};t_N]$ by the division $0 < t_1 < t_2 < ...t_N = T$.

2. Could the division to the intervals be unique by some argument? The roots of P are identified as moments for which SSFRs occur. Could tk correspond to a root of the polynomial P_k defined in the interva lI_k. Could the "very special moments in the life of self" as roots of a polynomial correspond to introduction of new pseudo constants as a p-adic correlate for the state function reduction? Each interval has it own polynomial P_k and the allowed roots r_{k_i} become to the interval $[t_k;t_{k+1}]$ and their number is usually smaller than the degree n of the polynomial. Assume that each polynomial restricted to its own range defines a 4-surface inside the same CD. One would have m separate p-adic space-time surfaces. These surfaces would serve as correlates for intentions or dreams.

How could the real space-time surface as a realized intention relate to these surfaces?

1. Each of the 4-surfaces with genuinely constant coefficients of P_k has its own cognitive representation as points common to real and all p-adic variants. If the number of points t_k is finite one indeed has p-adic pseudo-constants for any prime p.

2. The realization of intention should be a quantum jump, state function reduction, or action of free will. Does this state function reduction have the selection of one of the polynomials P_k as a real polynomial defining the real space-time surface as a geometric correlate.

3. Could one generalize this to fermionic degrees of freedom. In [L93] its is proposed that one could super-symmetrize TGD and quark spinors as embedding space spinors by replacing embedding space coordinates with super fields with components expressible as hermitian composites of second quantized quark and antiquark oscillator operators. Analogous generalization would be made for the second quantized quark field.

   In the M^8 picture the real polynomial would be replaced with a polynomial of super coordinate algebraically continued to super-octonionic coordinate. Solutions of the algebraic equations defining space-time surface would be now super-space-time surfaces which are unions of components assignable with the fermionic super coefficients of the super-polynomial.

   The rational coefficients of this polynomial could be replaced with pseudo- constants and the above picture seems to generalize. The spinor super-field would be a restriction of the M^8 spinor super-field to the p-adic branches of the p-adic space-time surface. Could the above picture about intentional act as a choice of the real branch generalize.

The next important step is to understand intentional action at quantum level.

1. The most general vision is that intention corresponds to a superposition of p-adic spacetime surfaces with coefficients of polynomials which are genuine pseudo constants and by number theoretic universality same in all p-adic sectors. These superpositions would represent intentions and dreams. One could also speak of a dreamy CD containing a dreamy quantum Universe. Since cognitive representations are considered, everything would reduce to an extension of rationals, and the quantum dynamics by SSFRs and BSFRs would not formally differ from that for the real space-time surface and one could speak about transition amplitudes between dreams.

2. The realization of an intentional action would correspond to an SFR in which the pseudo constants become genuine constants. The simplest model is that one of the polynomials P_k is selected and be extended to a polynomial in the entire CD associated with P. The origin of CD is in a unique role in M^8 picture and $P(0) = 0$ makes possible hierarchies of extensions and conservation of number theoretical data as roots of P in the composition of polynomials realized for space-time surfaces.

   If $P_k(0)$ is required also for $k > 1$, any P_k can be selected. One can however challenge the idea that intentional action involves a selection. If $P_k(0) = 0$ for $k > 1$ is not assumed, P_1 associated with the interval $[0, t_1]$ must be chosen and CD corresponds to its size cale. One can talk about a partial realization of the intention in accordance with the intuitive expectations. For instance, imagined sensory percepts and motor actions could correspond to this kind of partial realizations.

3. If motor action corresponds to BSFR, intentional action can be realized only for BSFR. SSFR could not allow a realization of intention if the sequence of SSFRs corresponds to a functional composition of polynomials or even iteration of a single polynomial: I have considered these options for the sequence of SSFRs in [**?**].

4. This picture is in accordance with the conservation laws in ZEO and allows the creation of Universes as from nothing. CDs do not pop up from vacuum but dream-CDs transform to real ones.

It is difficult to avoid the question of whether the notion of state function reduction could be reduced to a classical choice selecting one P_k: quantum jump as choice between dreams to be realized. This option would lead to purely classical probability theory and it would be however very difficult to understand what determines the transition probabilities.

13.5.3 The notion of magnetic body

Magnetic body (MB) would carrying dark matter would serve as the boss controlling ordinary matter at flux tubes.

1. MB has as building bricks magnetic flux quanta. Typically flux tubes and flux sheets. It consists of two kinds of flux quanta. Flux can be vanishing, which corresponds to Maxwellian case. The flux can be also non-vanishing and quantized and corresponds to monopole flux. In monopole case magnetic field requires no current to create it. This option is not possible in Maxwellian world. These flux tubes play a key role in TGD Universe in all scales.

2. Also Earth's magnetic field with nominal value $B_E = .5$ Gauss would have these two parts. Monopole part corresponds to the "endogenous" magnetic field $B_{end} = .2$ Gauss explaining strange effects of ELF em radiation to the physiology and behavior of vertebrates [J6]. The presence of this part identifiable as monopole flux explains why Earth has magnetic field: this field should have decayed long time ago in Maxwellian world since it requires currents to generate it and they disappear. Magnetic fields of permanent magnets could have a monopole part consisting of flux quanta. Electromagnets would not have it.

3. MB would carry dark matter as $h_{eff} = n \times h_0$ phases and act as a "boss" controlling ordinary matter [L99]. Communication to and control of biological body (ordinary matter) would be based on dark photons, which can transform to ordinary photons and vice versa. Molecular transitions would be one form of control.

4. Dark photons with large h_{eff} serve as as communication and control tools. Josephson frequencies would be involved with the communication of sensory data to MB and cyclotron frequencies with control by MB. Dark photons are assumed to transform to bio-photons [L9, L8] with energies covering visible and UV associated with the transitions of bio-molecules. The control by MB which layers having size even larger than that of Earth means that remote mental interactions are routine in living matter. EEG would be a particular example of these communications: without MB it is difficult to understand why brain would use such large amounts of energy to send signals to outer space.

5. The experiments of Blackman and others led originally to the notion of h_{eff} hierarchy. The large effects of radiation at ELF frequencies could be understood iin terms of cyclotron transitions in $B_{end} = .2$ Gauss if the value of h in $E = hf$ is replaced with h_{eff}, which would be rather large and possibly assignable to gravitational flux tubes with $\hbar_{eff} = \hbar_{gr} = GMm/v_0$.

   MB would control BB by cyclotron radiation - possibly via genome accompanied by dark genome at flux tubes parallel to the DNA strands. Cyclotron Bose-Einstein condensates of bosonic ions, Cooper pairs of fermionic ions, and Cooper pairs of protons and electrons would appear in living matter and $h_{eff} = h_{gr}$ hypothesis predicts universal energy spectrum in the range of bio-photon energies.

   Cell membrane could act as generalized Josephson junction generating dark Jophson radiation with energies given by the sum for ordinary Josephson energy and of the difference of cyclotron energies for flux tubes at the two sides of the membrane. The variation of the membrane potential would induce variation of the Josephson frequency and code the sensory information at cell membrane to a dark photon signal sent to MB.

6. In ZEO field body and MB correspond to 4-D rather than 3-D field patterns. Quantum states are replaced by quantum counterparts of behaviors and biological functions. The basic mechanism used by MB would be generation of conscious holograms by using dark photon reference beams from MB and their reading. In ZEO also the time reversals of these processes are possible and make possible to understand memory as communications with geometric past. Sensory perception and memory recall would be time reversals of each other and correspond to sequences of SSRs. Motor action would correspond to BSRs.

13.5.4 Life is not mere chemistry

The dogma about biology as mere bio-chemistry is given up in TGD framework.

1. Bio-catalysis remains a mystery in bio-chemical approach. MB carrying dark matter could provide the needed mechanisms.

   According to TGD view about catalysis, the U-shaped flux tubes associated with the MBs of reactants reconnect to a pair of flux tubes connecting the molecules [L76]. This happens if there is cyclotron resonance for dark cyclotron radiation assignable to massless extremals (MEs) associated with U-shaped flux tubes. This requires that the flux tubes have same strength of magnetic field and therefore same thickness by flux quantization. The same value of h_{eff} guarantees resonance. The next step is the shortening of the flux tubes by a reduction of h_{eff} and liberating energy kicking the reactants over the potential wall making the process extremely slow otherwise.

2. Also valence bonds and hydrogen bonds could correspond to magnetic flux tubes characterized by $h_{eff} = h_{em} = n \times h_0$, where n is now rather small number ($h = 6h_0$). This leads to a model for valence bond energies of atom with n increasing as one moves to right along the row of the periodic table providing insights to the biological roles of various molecules in biology [L55]. For instance, the molecules involving atoms towards right end of the periodic table would be natural carriers of metabolic energy whereas at the left end of row would be naturally involved with biocontrol via cyclotron frequencies.

3. The physics of water is full of anomalies [L7]. TGD suggests an explanation [L56] in terms of flux tubes assignable to hydrogen bonds [L56, L75]. These flux tubes could correspond

also to values of $h_{eff} > h$ so that these flux tube could be long and give rise to long range quantal correlations. Water could be seen as a manyphase system. The MBs assignable to water molecule clusters could mimick the cyclotron frequency spectrum of invader molecules and make possible water memory and primitive immune system based on reconnections of U-shaped flux tubes of water cluster and invader molecule [L111]. In this framework water would represent a primitive life form.

In Pollack effect [I76] exclusion zones (EZs) are induced at the boundary between gel phase and water by energy feed such as IR radiation. The negative charge of EZs is explained as a formation of flux tubes carrying dark protons having interpretation as dark nuclei. A simple model for linear dark proton triplets predicts their states to be in 1-1 correspondence with DNA, RNA, tRNA, and amino-acids and the numbers of codons coding for given amino-acid are predicted to be same as for vertebrate genetic code [L73, L98]. The model thus predicts deep connections between nuclear physics, condensed matter physics, chemistry, and biology usually thought to be rather disjoin disciplines.

EZs are able remove impurities from interior in conflict with second law. TGD based explanation of the mystery is change of the arrow of time induced by TGD counterpart of ordinary state function reduction in ZEO) [L115]: self-organization would be dissipation with reversed arrow of time at at the magnetic body (MB) of system acting as master and forcing time reversed evolution at the level of ordinary bio-matter serving as a slave.

DNA has one negative charge per nucleotide, microtubules are negatively charged, also cell is negatively charged, ATP carries 3 units of negative charge. This together with ZEO suggests that Pollack effect plays a key role in bio-control and macroscopic SFRs play a key role in living matter.

Chapter i

Appendix

A-1 Introduction

Originally this appendix was meant to be a purely technical summary of basic facts but in its recent form it tries to briefly summarize those basic visions about TGD which I dare to regarded stabilized. I have added illustrations making it easier to build mental images about what is involved and represented briefly the key arguments. This chapter is hoped to help the reader to get fast grasp about the concepts of TGD.

The basic properties of embedding space and related spaces are discussed and the relationship of CP_2 to the standard model is summarized. The basic vision is simple: the geometry of the embedding space $H = M^4 \times CP_2$ geometrizes standard model symmetries and quantum numbers. The assumption that space-time surfaces are basic objects, brings in dynamics as dynamics of 3-D surfaces based on the induced geometry. Second quantization of free spinor fields of H induces quantization at the level of H, which means a dramatic simplification.

The notions of induction of metric and spinor connection, and of spinor structure are discussed. Many-sheeted space-time and related notions such as topological field quantization and the relationship many-sheeted space-time to that of GRT space-time are discussed as well as the recent view about induced spinor fields and the emergence of fermionic strings. Also the relationship to string models is discussed briefly.

Various topics related to p-adic numbers are summarized with a brief definition of p-adic manifold and the idea about generalization of the number concept by gluing real and p-adic number fields to a larger book like structure analogous to adele [L50, L51]. In the recent view of quantum TGD [L144], both notions reduce to physics as number theory vision, which relies on $M^8 - H$ duality [L101, L102] and is complementary to the physics as geometry vision.

Zero energy ontology (ZEO) [L92] [K93] has become a central part of quantum TGD and leads to a TGD inspired theory of consciousness as a generalization of quantum measurement theory having quantum biology as an application. Also these aspects of TGD are briefly discussed.

A-2 Embedding space $M^4 \times CP_2$

Space-times are regarded as 4-surfaces in $H = M^4 \times CP_2$ the Cartesian product of empty Minkowski space - the space-time of special relativity - and compact 4-D space CP_2 with size scale of order 10^4 Planck lengths. One can say that embedding space is obtained by replacing each point m of empty Minkowski space with 4-D tiny CP_2. The space-time of general relativity is replaced by a 4-D surface in H which has very complex topology. The notion of many-sheeted space-time gives an idea about what is involved.

Fig. 1. Embedding space $H = M^4 \times CP_2$ as Cartesian product of Minkowski space M^4 and complex projective space CP_2. `http://tgdtheory.fi/appfigures/Hoo.jpg`

Denote by M^4_+ and M^4_- the future and past directed lightcones of M^4. Denote their intersection, which is not unique, by CD. In zero energy ontology (ZEO) [L92, L126] [K93] causal diamond

(CD) is defined as cartesian product $CD \times CP_2$. Often I use CD to refer just to $CD \times CP_2$ since CP_2 factor is relevant from the point of view of ZEO.

Fig. 2. Future and past light-cones M^4_+ and M^4_-. Causal diamonds (CD) are defined as their intersections. `http://tgdtheory.fi/appfigures/futurepast.jpg`

Fig. 3. Causal diamond (CD) is highly analogous to Penrose diagram but simpler. `http://tgdtheory.fi/appfigures/penrose.jpg`

A rather recent discovery was that CP_2 is the only compact 4-manifold with Euclidian signature of metric allowing twistor space with Kähler structure. M^4 is in turn is the only 4-D space with Minkowskian signature of metric allowing twistor space with Kähler structure [A33] so that $H = M^4 \times CP_2$ is twistorially unique.

One can loosely say that quantum states in a given sector of "world of classical worlds" (WCW) are superpositions of space-time surfaces inside CDs and that positive and negative energy parts of zero energy states are localized and past and future boundaries of CDs. CDs form a hierarchy. One can have CDs within CDs and CDs can also overlap. The size of CD is characterized by the proper time distance between its two tips. One can perform both translations and also Lorentz boosts of CD leaving either boundary invariant. Therefore one can assign to CDs a moduli space and speak about wave function in this moduli space.

In number theoretic approach it is natural to restrict the allowed Lorentz boosts to some discrete subgroup of Lorentz group and also the distances between the tips of CDs to multiples of CP_2 radius defined by the length of its geodesic. Therefore the moduli space of CDs discretizes. The quantization of cosmic recession velocities for which there are indications, could relate to this quantization.

A-2.1 Basic facts about CP_2

CP_2 as a four-manifold is very special. The following arguments demonstrate that it codes for the symmetries of standard models via its isometries and holonomies.

CP_2 as a manifold

CP_2, the complex projective space of two complex dimensions, is obtained by identifying the points of complex 3-space C^3 under the projective equivalence

$$(z^1, z^2, z^3) \equiv \lambda(z^1, z^2, z^3) \ . \tag{A-2.1}$$

Here λ is any non-zero complex number. Note that CP_2 can be also regarded as the coset space $SU(3)/U(2)$. The pair z^i/z^j for fixed j and $z^i \neq 0$ defines a complex coordinate chart for CP_2. As j runs from 1 to 3 one obtains an atlas of three coordinate charts covering CP_2, the charts being holomorphically related to each other (e.g. CP_2 is a complex manifold). The points $z^3 \neq 0$ form a subset of CP_2 homoeomorphic to R^4 and the points with $z^3 = 0$ a set homeomorphic to S^2. Therefore CP_2 is obtained by "adding the 2-sphere at infinity to R^4".

Besides the standard complex coordinates $\xi^i = z^i/z^3$, $i = 1, 2$ the coordinates of Eguchi and Freund [A28] will be used and their relation to the complex coordinates is given by

$$\begin{aligned} \xi^1 &= z + it \ , \\ \xi^2 &= x + iy \ . \end{aligned} \tag{A-2.2}$$

These are related to the "spherical coordinates" via the equations

$$\begin{aligned} \xi^1 &= rexp(i\frac{(\Psi+\Phi)}{2})cos(\frac{\Theta}{2}) \ , \\ \xi^2 &= rexp(i\frac{(\Psi-\Phi)}{2})sin(\frac{\Theta}{2}) \ . \end{aligned} \tag{A-2.3}$$

The ranges of the variables r, Θ, Φ, Ψ are $[0, \infty], [0, \pi], [0, 4\pi], [0, 2\pi]$ respectively.

Considered as a real four-manifold CP_2 is compact and simply connected, with Euler number Euler number 3, Pontryagin number 3 and second $b = 1$.

Fig. 4. CP_2 as manifold. `http://tgdtheory.fi/appfigures/cp2.jpg`

Metric and Kähler structure of CP_2

In order to obtain a natural metric for CP_2, observe that CP_2 can be thought of as a set of the orbits of the isometries $z^i \to exp(i\alpha)z^i$ on the sphere S^5: $\sum z^i \bar{z}^i = R^2$. The metric of CP_2 is obtained by projecting the metric of S^5 orthogonally to the orbits of the isometries. Therefore the distance between the points of CP_2 is that between the representative orbits on S^5.

The line element has the following form in the complex coordinates

$$ds^2 = g_{a\bar{b}} d\xi^a d\bar{\xi}^b \ , \tag{A-2.4}$$

where the Hermitian, in fact Kähler metric $g_{a\bar{b}}$ is defined by

$$g_{a\bar{b}} = R^2 \partial_a \partial_{\bar{b}} K \ , \tag{A-2.5}$$

where the function K, Kähler function, is defined as

$$\begin{aligned} K &= log(F) \ , \\ F &= 1 + r^2 \ . \end{aligned} \tag{A-2.6}$$

The Kähler function for S^2 has the same form. It gives the S^2 metric $dzd\bar{z}/(1+r^2)^2$ related to its standard form in spherical coordinates by the coordinate transformation $(r, \phi) = (tan(\theta/2), \phi)$.

The representation of the CP_2 metric is deducible from S^5 metric is obtained by putting the angle coordinate of a geodesic sphere constant in it and is given

$$\frac{ds^2}{R^2} = \frac{(dr^2 + r^2\sigma_3^2)}{F^2} + \frac{r^2(\sigma_1^2 + \sigma_2^2)}{F} \ , \tag{A-2.7}$$

where the quantities σ_i are defined as

$$\begin{aligned} r^2\sigma_1 &= Im(\xi^1 d\xi^2 - \xi^2 d\xi^1) \ , \\ r^2\sigma_2 &= -Re(\xi^1 d\xi^2 - \xi^2 d\xi^1) \ , \\ r^2\sigma_3 &= -Im(\xi^1 d\bar{\xi}^1 + \xi^2 d\bar{\xi}^2) \ . \end{aligned} \tag{A-2.8}$$

R denotes the radius of the geodesic circle of CP_2. The vierbein forms, which satisfy the defining relation

$$s_{kl} = R^2 \sum_A e_k^A e_l^A \ , \tag{A-2.9}$$

are given by

$$\begin{aligned} e^0 &= \tfrac{dr}{F} \ , \quad e^1 = \tfrac{r\sigma_1}{\sqrt{F}} \ , \\ e^2 &= \tfrac{r\sigma_2}{\sqrt{F}} \ , \quad e^3 = \tfrac{r\sigma_3}{F} \ . \end{aligned} \tag{A-2.10}$$

The explicit representations of vierbein vectors are given by

$$\begin{aligned} e^0 &= \frac{dr}{F} \ , & e^1 &= \frac{r(sin\Theta cos\Psi d\Phi + sin\Psi d\Theta)}{2\sqrt{F}} \ , \\ e^2 &= \frac{r(sin\Theta sin\Psi d\Phi - cos\Psi d\Theta)}{2\sqrt{F}} \ , & e^3 &= \frac{r(d\Psi + cos\Theta d\Phi)}{2F} \ . \end{aligned} \tag{A-2.11}$$

The explicit representation of the line element is given by the expression

$$ds^2/R^2 = \frac{dr^2}{F^2} + \frac{r^2}{4F^2}(d\Psi + cos\Theta d\Phi)^2 + \frac{r^2}{4F}(d\Theta^2 + sin^2\Theta d\Phi^2) \ . \tag{A-2.12}$$

From this expression one finds that at coordinate infinity $r = \infty$ line element reduces to $\frac{r^2}{4F}(d\Theta^2 + sin^2\Theta d\Phi^2)$ of S^2 meaning that 3-sphere degenerates metrically to 2-sphere and one can say that CP_2 is obtained by adding to R^4 a 2-sphere at infinity.

The vierbein connection satisfying the defining relation

$$de^A = -V^A_B \wedge e^B \ , \tag{A-2.13}$$

is given by

$$\begin{aligned} V_{01} &= -\frac{e^1}{r} \ , & V_{23} &= \frac{e^1}{r} \ , \\ V_{02} &= -\frac{e^2}{r} \ , & V_{31} &= \frac{e^2}{r} \ , \\ V_{03} &= (r - \frac{1}{r})e^3 \ , & V_{12} &= (2r + \frac{1}{r})e^3 \ . \end{aligned} \tag{A-2.14}$$

The representation of the covariantly constant curvature tensor is given by

$$\begin{aligned} R_{01} &= e^0 \wedge e^1 - e^2 \wedge e^3 \ , & R_{23} &= e^0 \wedge e^1 - e^2 \wedge e^3 \ , \\ R_{02} &= e^0 \wedge e^2 - e^3 \wedge e^1 \ , & R_{31} &= -e^0 \wedge e^2 + e^3 \wedge e^1 \ , \\ R_{03} &= 4e^0 \wedge e^3 + 2e^1 \wedge e^2 \ , & R_{12} &= 2e^0 \wedge e^3 + 4e^1 \wedge e^2 \ . \end{aligned} \tag{A-2.15}$$

Metric defines a real, covariantly constant, and therefore closed 2-form J

$$J = -is_{a\bar{b}} d\xi^a d\bar{\xi}^b \ , \tag{A-2.16}$$

the so called Kähler form. Kähler form J defines in CP_2 a symplectic structure because it satisfies the condition

$$J^k_{\ r} J^{rl} = -s^{kl} \ . \tag{A-2.17}$$

The condition states that J and g give representations of real unit and imaginary units related by the formula $i^2 = -1$.

Kähler form is expressible locally in terms of Kähler gauge potential

$$J = dB \ , \tag{A-2.18}$$

where B is the so called Kähler potential, which is not defined globally since J describes homological magnetic monopole.

$dJ = ddB = 0$ gives the topological half of Maxwell equations (vanishing of magnetic charges and Faraday's induction law) and self-duality $*J = J$ reduces the remaining equations to $dJ = 0$. Hence the Kähler form can be regarded as a curvature form of a $U(1)$ gauge potential B carrying a magnetic charge of unit $1/2g$ (g denotes the gauge coupling).

The magnetic flux of J through a 2-surface in CP_2 is proportional to its homology equivalence class, which is integer valued. The explicit representations of J and B are given by

$$\begin{aligned} B &= 2re^3 \ , \\ J &= 2(e^0 \wedge e^3 + e^1 \wedge e^2) = \frac{r}{F^2} dr \wedge (d\Psi + cos\Theta d\Phi) + \frac{r^2}{2F} sin\Theta d\Theta \wedge d\Phi \ . \end{aligned} \tag{A-2.19}$$

The vierbein curvature form and Kähler form are covariantly constant and have in the complex coordinates only components of type (1, 1).

Useful coordinates for CP_2 are the so called canonical (or symplectic or Darboux) coordinates in which the Kähler potential and Kähler form have very simple expressions

$$\begin{aligned} B &= \sum_{k=1,2} P_k dQ_k \ , \\ J &= \sum_{k=1,2} dP_k \wedge dQ_k \ . \end{aligned} \tag{A-2.20}$$

The relationship of the canonical coordinates to the "spherical" coordinates is given by the equations

$$\begin{aligned} P_1 &= -\frac{1}{1+r^2} \ , \\ P_2 &= -\frac{r^2 cos\Theta}{2(1+r^2)} \ , \\ Q_1 &= \Psi \ , \\ Q_2 &= \Phi \ . \end{aligned} \tag{A-2.21}$$

Spinors In CP_2

CP_2 doesn't allow spinor structure in the conventional sense [A24]. However, the coupling of the spinors to a half odd multiple of the Kähler potential leads to a respectable spinor structure. Because the delicacies associated with the spinor structure of CP_2 play a fundamental role in TGD, the arguments of Hawking are repeated here.

To see how the space can fail to have an ordinary spinor structure consider the parallel transport of the vierbein in a simply connected space M. The parallel propagation around a closed curve with a base point x leads to a rotated vierbein at x: $e^A = R^A_B e^B$ and one can associate to each closed path an element of $SO(4)$.

Consider now a one-parameter family of closed curves $\gamma(v) : v \in (0, 1)$ with the same base point x and $\gamma(0)$ and $\gamma(1)$ trivial paths. Clearly these paths define a sphere S^2 in M and the element $R^A_B(v)$ defines a closed path in $SO(4)$. When the sphere S^2 is contractible to a point e.g., homologically trivial, the path in $SO(4)$ is also contractible to a point and therefore represents a trivial element of the homotopy group $\Pi_1(SO(4)) = Z_2$.

For a homologically nontrivial 2-surface S^2 the associated path in $SO(4)$ can be homotopically nontrivial and therefore corresponds to a nonclosed path in the covering group Spin(4) (leading from the matrix 1 to -1 in the matrix representation). Assume this is the case.

Assume now that the space allows spinor structure. Then one can parallel propagate also spinors and by the above construction associate a closed path of Spin(4) to the surface S^2. Now, however this path corresponds to a lift of the corresponding $SO(4)$ path and cannot be closed. Thus one ends up with a contradiction.

From the preceding argument it is clear that one could compensate the non-allowed -1-factor associated with the parallel transport of the spinor around the sphere S^2 by coupling it to a gauge potential in such a way that in the parallel transport the gauge potential introduces a compensating -1-factor. For a $U(1)$ gauge potential this factor is given by the exponential

$exp(i2\Phi)$, where Φ is the magnetic flux through the surface. This factor has the value -1 provided the $U(1)$ potential carries half odd multiple of Dirac charge $1/2g$. In case of CP_2 the required gauge potential is half odd multiple of the Kähler potential B defined previously. In the case of $M^4 \times CP_2$ one can in addition couple the spinor components with different chiralities independently to an odd multiple of $B/2$.

Geodesic sub-manifolds of CP_2

Geodesic sub-manifolds are defined as sub-manifolds having common geodesic lines with the embedding space. As a consequence the second fundamental form of the geodesic manifold vanishes, which means that the tangent vectors h^k_α (understood as vectors of H) are covariantly constant quantities with respect to the covariant derivative taking into account that the tangent vectors are vectors both with respect to H and X^4.

In [A45] a general characterization of the geodesic sub-manifolds for an arbitrary symmetric space G/H is given. Geodesic sub-manifolds are in 1-1-correspondence with the so called Lie triple systems of the Lie-algebra g of the group G. The Lie triple system t is defined as a subspace of g characterized by the closedness property with respect to double commutation

$$[X,[Y,Z]] \in t \ \text{ for } \ X,Y,Z \in t \ . \tag{A-2.22}$$

$SU(3)$ allows, besides geodesic lines, two nonequivalent (not isometry related) geodesic spheres. This is understood by observing that $SU(3)$ allows two nonequivalent $SU(2)$ algebras corresponding to subgroups $SO(3)$ (orthogonal 3×3 matrices) and the usual isospin group $SU(2)$. By taking any subset of two generators from these algebras, one obtains a Lie triple system and by exponentiating this system, one obtains a 2-dimensional geodesic sub-manifold of CP_2.

Standard representatives for the geodesic spheres of CP_2 are given by the equations

$$S^2_I \ : \ \xi^1 = \bar{\xi}^2 \ \text{ or equivalently } \ (\Theta = \pi/2, \Psi = 0) \ ,$$

$$S^2_{II} \ : \ \xi^1 = \xi^2 \ \text{ or equivalently } \ (\Theta = \pi/2, \Phi = 0) \ .$$

The non-equivalence of these sub-manifolds is clear from the fact that isometries act as holomorphic transformations in CP_2. The vanishing of the second fundamental form is also easy to verify. The first geodesic manifold is homologically trivial: in fact, the induced Kähler form vanishes identically for S^2_I. S^2_{II} is homologically nontrivial and the flux of the Kähler form gives its homology equivalence class.

A-2.2 CP_2 geometry and Standard Model symmetries

Identification of the electro-weak couplings

The delicacies of the spinor structure of CP_2 make it a unique candidate for space S. First, the coupling of the spinors to the $U(1)$ gauge potential defined by the Kähler structure provides the missing $U(1)$ factor in the gauge group. Secondly, it is possible to couple different H-chiralities independently to a half odd multiple of the Kähler potential. Thus the hopes of obtaining a correct spectrum for the electromagnetic charge are considerable. In the following it will be demonstrated that the couplings of the induced spinor connection are indeed those of the GWS model [B15] and in particular that the right handed neutrinos decouple completely from the electro-weak interactions.

To begin with, recall that the space H allows to define three different chiralities for spinors. Spinors with fixed H-chirality $e = \pm 1$, CP_2-chirality l, r and M^4-chirality L, R are defined by the condition

$$\begin{aligned} \Gamma\Psi &= e\Psi \ , \\ e &= \pm 1 \ , \end{aligned} \tag{A-2.23}$$

where Γ denotes the matrix $\Gamma_9 = \gamma_5 \otimes \gamma_5$, $1 \otimes \gamma_5$ and $\gamma_5 \otimes 1$ respectively. Clearly, for a fixed H-chirality CP_2- and M^4-chiralities are correlated.

The spinors with H-chirality $e = \pm 1$ can be identified as quark and lepton like spinors respectively. The separate conservation of baryon and lepton numbers can be understood as a consequence of generalized chiral invariance if this identification is accepted. For the spinors with a definite H-chirality one can identify the vielbein group of CP_2 as the electro-weak group: $SO(4)$ having as its covering group $SU(2)_L \times SU(2)_R$.

The covariant derivatives are defined by the spinorial connection

$$A = V + \frac{B}{2}(n_+ 1_+ + n_- 1_-) \ . \tag{A-2.24}$$

Here V and B denote the projections of the vielbein and Kähler gauge potentials respectively and $1_{+(-)}$ projects to the spinor H-chirality $+(-)$. The integers $n_\pm$ are odd from the requirement of a respectable spinor structure.

The explicit representation of the vielbein connection V and of B are given by the equations

$$\begin{array}{lllllll} V_{01} & = & -\frac{e^1}{r} \ , & & V_{23} & = & \frac{e^1}{r} \ , \\ V_{02} & = & -\frac{e^2}{r} \ , & & V_{31} & = & \frac{e^2}{r} \ , \\ V_{03} & = & (r - \frac{1}{r})e^3 \ , & & V_{12} & = & (2r + \frac{1}{r})e^3 \ , \end{array} \tag{A-2.25}$$

and

$$B = 2re^3 \ , \tag{A-2.26}$$

respectively. The explicit representation of the vielbein is not needed here.

Let us first show that the charged part of the spinor connection couples purely left handedly. Identifying Σ_3^0 and Σ_2^1 as the diagonal (neutral) Lie-algebra generators of $SO(4)$, one finds that the charged part of the spinor connection is given by

$$A_{ch} = 2V_{23}I_L^1 + 2V_{13}I_L^2 \ , \tag{A-2.27}$$

where one have defined

$$\begin{array}{lll} I_L^1 & = & \frac{(\Sigma_{01} - \Sigma_{23})}{2} \ , \\ I_L^2 & = & \frac{(\Sigma_{02} - \Sigma_{13})}{2} \ . \end{array} \tag{A-2.28}$$

A_{ch} is clearly left handed so that one can perform the identification of the gauge potential as

$$W^\pm = \frac{2(e^1 \pm ie^2)}{r} \ , \tag{A-2.29}$$

where $W^\pm$ denotes the charged intermediate vector boson.

The covariantly constant curvature tensor is given by

$$\begin{array}{l} R_{01} = -R_{23} = e^0 \wedge e^1 - e^2 \wedge e^3 \ , \\ R_{02} = -R_{31} = e^0 \wedge e^2 - e^3 \wedge e^1 \ , \\ R_{03} = 4e^0 \wedge e^3 + 2e^1 \wedge e^2 \ , \\ R_{12} = 2e^0 \wedge e^3 + 4e^1 \wedge e^2 \ . \end{array} \tag{A-2.30}$$

The charged part of the curvature tensor is left handed.

This is to be compared with the Weyl tensor, which defines a representation of quaternionic imaginary units.

$$\begin{aligned} W_{03} = W_{12} \equiv 2I_3 = 2(e^0 \wedge e^3 + e^1 \wedge e^2) \ , \\ W_{01} = W_{23} \equiv I_1 = -e^0 \wedge e^1 - e^2 \wedge e^3 \ , \\ W_{02} = W_{31} \equiv I_2 = -e^0 \wedge e^2 - e^3 \wedge e^1 \ . \end{aligned} \tag{A-2.31}$$

The charged part of the Weyl tensor is right-handed and that the relative sign of the two terms in the curvature tensor and Weyl tensor are opposite.

Consider next the identification of the neutral gauge bosons γ and Z^0 as appropriate linear combinations of the two functionally independent quantities

$$\begin{aligned} X &= re^3 \ , \\ Y &= \frac{e^3}{r} \ , \end{aligned} \tag{A-2.32}$$

appearing in the neutral part of the spinor connection. We show first that the mere requirement that photon couples vectorially implies the basic coupling structure of the GWS model leaving only the value of Weinberg angle undetermined.

To begin with let us define

$$\begin{aligned} \bar{\gamma} &= aX + bY \ , \\ \bar{Z}^0 &= cX + dY \ , \end{aligned} \tag{A-2.33}$$

where the normalization condition

$$ad - bc = 1 \ ,$$

is satisfied. The physical fields γ and Z^0 are related to $\bar{\gamma}$ and $\bar{Z}^0$ by simple normalization factors.

Expressing the neutral part of the spinor connection in term of these fields one obtains

$$\begin{aligned} A_{nc} &= [(c+d)2\Sigma_{03} + (2d-c)2\Sigma_{12} + d(n_+1_+ + n_-1_-)]\bar{\gamma} \\ &+ [(a-b)2\Sigma_{03} + (a-2b)2\Sigma_{12} - b(n_+1_+ + n_-1_-)]\bar{Z}^0 \ . \end{aligned} \tag{A-2.34}$$

Identifying Σ_{12} and $\Sigma_{03} = 1 \times \gamma_5\Sigma_{12}$ as vectorial and axial Lie-algebra generators, respectively, the requirement that γ couples vectorially leads to the condition

$$c = -d \ . \tag{A-2.35}$$

Using this result plus previous equations, one obtains for the neutral part of the connection the expression

$$A_{nc} = \gamma Q_{em} + Z^0(I_L^3 - sin^2\theta_W Q_{em}) \ . \tag{A-2.36}$$

Here the electromagnetic charge Q_{em} and the weak isospin are defined by

$$\begin{aligned} Q_{em} &= \Sigma^{12} + \frac{(n_+1_+ + n_-1_-)}{6} \ , \\ I_L^3 &= \frac{(\Sigma^{12} - \Sigma^{03})}{2} \ . \end{aligned} \tag{A-2.37}$$

The fields γ and Z^0 are defined via the relations

$$\begin{aligned} \gamma &= 6d\bar{\gamma} = \frac{6}{(a+b)}(aX + bY) \ , \\ Z^0 &= 4(a+b)\bar{Z}^0 = 4(X - Y) \ . \end{aligned} \tag{A-2.38}$$

The value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{3b}{2(a+b)} \ , \tag{A-2.39}$$

and is not fixed completely. Observe that right handed neutrinos decouple completely from the electro-weak interactions.

The determination of the value of the Weinberg angle is a dynamical problem. The original approach was based on the assumption that it makes sense to talk about electroweak action defined at fundamental level and introduce a symmetry breaking by adding an additional term proportional to Kähler action. The recent view is that Kähler action plus volume term defines the fundamental action.

The Weinberg angle is completely fixed if one requires that the electroweak action contains no cross term of type γZ^0. This leads to a definite value for the Weinberg angle.

One can however add a symmetry breaking term proportional to Kähler action and this changes the value of the Weinberg angle. As a matter fact, color gauge action identifying color gauge field as proportional to $H^A J_{\alpha\beta}$ is proportional to Kähler action. A possible interpretation would be as a sum of electroweak and color gauge interactions.

To evaluate the value of the Weinberg angle one can express the neutral part F_{nc} of the induced gauge field as

$$F_{nc} = 2R_{03}\Sigma^{03} + 2R_{12}\Sigma^{12} + J(n_+ 1_+ + n_- 1_-) \ , \tag{A-2.40}$$

where one has

$$\begin{aligned} R_{03} &= 2(2e^0 \wedge e^3 + e^1 \wedge e^2) \ , \\ R_{12} &= 2(e^0 \wedge e^3 + 2e^1 \wedge e^2) \ , \\ J &= 2(e^0 \wedge e^3 + e^1 \wedge e^2) \ , \end{aligned} \tag{A-2.41}$$

in terms of the fields γ and Z^0 (photon and Z- boson)

$$F_{nc} = \gamma Q_{em} + Z^0(I_L^3 - sin^2\theta_W Q_{em}) \ . \tag{A-2.42}$$

Evaluating the expressions above, one obtains for γ and Z^0 the expressions

$$\begin{aligned} \gamma &= 3J - sin^2\theta_W R_{12} \ , \\ Z^0 &= 2R_{03} \ . \end{aligned} \tag{A-2.43}$$

For the Kähler field one obtains

$$J = \frac{1}{3}(\gamma + sin^2\theta_W Z^0) \ . \tag{A-2.44}$$

Expressing the neutral part of the symmetry broken YM action

$$\begin{aligned} L_{ew} &= L_{sym} + f J^{\alpha\beta} J_{\alpha\beta} \ , \\ L_{sym} &= \frac{1}{4g^2} Tr(F^{\alpha\beta} F_{\alpha\beta}) \ , \end{aligned} \tag{A-2.45}$$

where the trace is taken in spinor representation, in terms of γ and Z^0 one obtains for the coefficient X of the γZ^0 cross term (this coefficient must vanish) the expression

$$\begin{aligned} X &= -\frac{K}{2g^2} + \frac{fp}{18} \ , \\ K &= Tr\left[Q_{em}(I_L^3 - sin^2\theta_W Q_{em})\right] \ , \end{aligned} \tag{A-2.46}$$

This parameter can be calculated by substituting the values of quark and lepton charges and weak isospins.

In the general case the value of the coefficient K is given by

$$K = \sum_i \left[-\frac{(18 + 2n_i^2)sin^2\theta_W}{9} \right] \ , \tag{A-2.47}$$

where the sum is over the spinor chiralities, which appear as elementary fermions and n_i is the integer describing the coupling of the spinor field to the Kähler potential. The cross term vanishes provided the value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{9\sum_i 1}{(fg^2 + 2\sum_i(18 + n_i^2))} \ . \tag{A-2.48}$$

In the scenario where both leptons and quarks are elementary fermions the value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{9}{(\frac{fg^2}{2} + 28)} \ . \tag{A-2.49}$$

The bare value of the Weinberg angle is 9/28 in this scenario, which is not far from the typical value 9/24 of GUTs at high energies [B3]. The experimental value at the scale length scale of the electron can be deduced from the ratio of W and Z boson masses as $sin^2\theta_W = 1 - (m_W/m_Z)^2 \simeq .22290$. This ratio and also the weak boson masses depend on the length scale.

If one interprets the additional term proportional to J as color action, one could perhaps interpret the value of Weinberg angle as expressing a connection between strong and weak coupling constant evolution. The limit $f \to 0$ should correspond to an infinite value of color coupling strength and at this limit one would have $sin^2\theta_W = \frac{9}{28}$ for $f/g^2 \to 0$. This does not make sense since the Weinberg angle is in the standard model much smaller in QCD scale Λ corresponding roughly to pion mass scale. The Weinberg angle is in principle predicted by the p-adic coupling constant evolution fixed by the number theoretical vision of TGD.

One could however have a sum of electroweak action, correction terms changing the value of Weinberg angle, and color action and coupling constant evolution could be understood in terms of the coupling parameters involved.

Electroweak symmetry breaking

One of the hardest challenges in the development of the TGD based view of weak symmetry breaking was the fact that classical field equations allow space-time surfaces with finite but arbitrarily large size. For a fixed space-time surface, the induced gauge fields, including classical weak fields, are long ranged. On the other hand, the large mass for weak bosons would require a short correlation length. How can one understand this together with the fact that a photon has a long correlation length?

In zero energy ontology quantum states are superpositions of space-time surfaces as analogs of almost unique Bohr orbits of particles identified as 3-D surfaces. For some reason the superposition should be such that the quantum averages of weak gauge boson fields vanish below the weak scale whereas the quantum average of electromagnetic fields is non-vanishing.

This is indeed the case.

1. The supersymplectic symmetries form isometries of the world of classical worlds (WCW) and they act in CP_2 degrees of freedom as symplectic transformations leaving the CP_2 symplectic form J invariant and therefore also its contribution to the electromagnetic field since this part is the same for all space-time surfaces in the superposition of space-time surfaces as a representation of supersymplectic isometry group (as a special case a representation of color group).

2. In TGD, color and electroweak symmetries acting as holonomies are not independent and for the $SU(2)_L$ part of induced spinor connection the symplectic transformations induces $SU(2)_L \times U(1)_R$ gauge transformation. This suggests that the quantum expectations of the induced weak fields over the space-time surfaces vanish above the quantum coherence scale. The averages of W and of the left handed part of Z^0 should therefore vanish.

3. $\langle Z^0 \rangle$ should vanish. For $U(1)_R$ part of Z^0, the action of gauge transformation is trivial in gauge theory. Now however the space-time surface changes under symplectic transformations and this could make the average of the right-handed part of Z^0 vanishing. The vanishing of the average of the axial part of the Z^0 is suggested by the partially conserved axial current hypothesis.

One can formulate this picture quantitatively.

1. The electromagnetic field [L152] contains, besides the induced Kähler form, also the induced curvature form R_{12}, which couples vectorially. Conserved vector current hypothesis suggests that the average of R_{12} is non-vanishing. One can express the neutral part of the induced gauge field in terms of induced spinor curvature and Kähler form J as

$$\begin{aligned} R_{03} &= 2(2e^0 \wedge e^3 + e^1 \wedge e^2) = J + 2e^0 \wedge e^3 \ , \\ J &= 2(e^0 \wedge e^3 + e^1 \wedge e^2) \ , \\ R_{12} &= 2(e^0 \wedge e^3 + 2e^1 \wedge e^2) = 3J - 2e^0 \wedge e^3 \quad , \end{aligned} \tag{A-2.50}$$

2. The induced fields γ and Z^0 (photon and Z- boson) can be expressed as

$$\begin{aligned} \gamma &= 3J - sin^2\theta_W R_{12} \ , \\ Z^0 &= 2R_{03} = 2(J + 2e^0 \wedge e^3) \end{aligned} \tag{A-2.51}$$

$$per. \tag{A-2.52}$$

The condition $\langle Z^0 \rangle = 0$ gives $2\langle e^0 \wedge e^3 \rangle = -2J$ and this in turn gives $\langle R_{12} \rangle = 4J$. The average over γ would be

$$\langle \gamma \rangle = (3 - 4sin^2\theta_W)J \ .$$

For $sin^2\theta_W = 3/4$ $langle\gamma\rangle$ would vanish.

The quantum averages of classical weak fields quite generally vanish. What about correlation functions?

1. One expects that the correlators of classical weak fields as color invariants, and perhaps even symplectic invariants, are non-vanishing below the Compton length since in this kind of situation the points in the correlation function belong to the same 3-surface representing particle, such as hadron.

2. The intuitive picture is that in longer length scales one has disjoint 3-surfaces with a size scale of Compton length. If the states associated with two disjoint 3-surfaces are separately color invariant there are no correlations in color degrees of freedom and correlators reduce to the products of expectations of classical weak fields and vanish. This could also hold when the 3-surfaces are connected by flux tube bonds.

   Below the Compton length weak bosons would thus behave as correlated massless fields. The Compton lengths of weak bosons are proportional to the value of effective Planck constant h_{eff} and in living systems the Compton lengths are proposed to be even of the order of cell size. This would explain the mysterious chiral selection in living systems requiring large parity violation.

3. What about the averages and correlators of color gauge fields? Classical color gauge fields are proportional to the products of Hamiltonians of color isometries induced Kähler form and the expectations of color Hamiltonians give vanishing average above Compton length and therefore vanishing average. Correlators are non-vanishing below the hadron scale. Gluons do not propagate in long scales for the same reason as weak bosons. This is implied by color confinement, which has also classical description in the sense that 3-surfaces have necessarily a finite size.

   A large value of h_{eff} allows colored states even in biological scales below the Compton length since in this kind of situation the points in the correlation function belong to the same 3-surface representing particle, such as dark hadron.

Discrete symmetries

The treatment of discrete symmetries C, P, and T is based on the following requirements:

1. Symmetries must be realized as purely geometric transformations.

2. Transformation properties of the field variables should be essentially the same as in the conventional quantum field theories [B4] .

   The action of the reflection P on spinors of is given by

$$\Psi \rightarrow P\Psi = \gamma^0 \otimes \gamma^0 \Psi \ . \tag{A-2.53}$$

in the representation of the gamma matrices for which γ^0 is diagonal. It should be noticed that W and Z^0 bosons break parity symmetry as they should since their charge matrices do not commute with the matrix of P.

The guess that a complex conjugation in CP_2 is associated with T transformation of the physicist turns out to be correct. One can verify by a direct calculation that pure Dirac action is invariant under T realized according to

$$\begin{aligned} m^k &\rightarrow T(M^k) \ , \\ \xi^k &\rightarrow \bar{\xi}^k \ , \\ \Psi &\rightarrow \gamma^1\gamma^3 \otimes 1\Psi \ . \end{aligned} \tag{A-2.54}$$

The operation bearing closest resemblance to the ordinary charge conjugation corresponds geometrically to complex conjugation in CP_2:

$$\begin{aligned} \xi^k &\rightarrow \bar{\xi}^k \ , \\ \Psi &\rightarrow \Psi^\dagger \gamma^2\gamma^0 \otimes 1 \ . \end{aligned} \tag{A-2.55}$$

As one might have expected symmetries CP and T are exact symmetries of the pure Dirac action.

A-3 Induction procedure and many-sheeted space-time

Since the classical gauge fields are closely related in TGD framework, it is not possible to have space-time sheets carrying only single kind of gauge field. For instance, em fields are accompanied by Z^0 fields for extremals of Kähler action.

Classical em fields are always accompanied by Z^0 field and some components of color gauge field. For extremals having homologically non-trivial sphere as a CP_2 projection em and Z^0 fields are the only non-vanishing electroweak gauge fields. For homologically trivial sphere only W fields are non-vanishing. Color rotations does not affect the situation.

For vacuum extremals all electro-weak gauge fields are in general non-vanishing although the net gauge field has U(1) holonomy by 2-dimensionality of the CP_2 projection. Color gauge field has $U(1)$ holonomy for all space-time surfaces and quantum classical correspondence suggest a weak form of color confinement meaning that physical states correspond to color neutral members of color multiplets.

A-3.1 Induction procedure for gauge fields and spinor connection

Induction procedure for gauge potentials and spinor structure is a standard procedure of bundle theory. If one has embedding of some manifold to the base space of a bundle, the bundle structure can be induced so that it has as a base space the imbedded manifold, whose points have as fiber the fiber if embedding space at their image points. In the recent case the embedding of space-time surface to embedding space defines the induction procedure. The induced gauge potentials and gauge fields are projections of the spinor connection of the embedding space to the space-time surface (see `http://tgdtheory.fi/appfigures/induct.jpg`).

Induction procedure makes sense also for the spinor fields of embedding space and one obtains geometrization of both electroweak gauge potentials and of spinors. The new element is induction of gamma matrices which gives their projections at space-time surface.

As a matter fact, the induced gamma matrices cannot appear in the counterpart of massless Dirac equation. To achieve super-symmetry, Dirac action must be replaced with Kähler-Dirac action for which gamma matrices are contractions of the canonical momentum currents of Kähler action with embedding space gamma matrices. Induced gamma matrices in Dirac action would correspond to 4-volume as action.

Fig. 9. Induction of spinor connection and metric as projection to the space-time surface. `http://tgdtheory.fi/appfigures/induct.jpg`.

A-3.2 Induced gauge fields for space-times for which CP_2 projection is a geodesic sphere

If one requires that space-time surface is an extremal of Kähler action and has a 2-dimensional CP_2 projection, only vacuum extremals and space-time surfaces for which CP_2 projection is a geodesic sphere, are allowed. Homologically non-trivial geodesic sphere correspond to vanishing W fields and homologically non-trivial sphere to non-vanishing W fields but vanishing γ and Z^0. This can be verified by explicit examples.

$r = \infty$ surface gives rise to a homologically non-trivial geodesic sphere for which e_0 and e_3 vanish imply the vanishing of W field. For space-time sheets for which CP_2 projection is $r = \infty$ homologically non-trivial geodesic sphere of CP_2 one has

$$\gamma = (\frac{3}{4} - \frac{sin^2(\theta_W)}{2})Z^0 \simeq \frac{5Z^0}{8} \quad .$$

The induced W fields vanish in this case and they vanish also for all geodesic sphere obtained by $SU(3)$ rotation.

$Im(\xi^1) = Im(\xi^2) = 0$ corresponds to homologically trivial geodesic sphere. A more general representative is obtained by using for the phase angles of standard complex CP_2 coordinates constant values. In this case e^1 and e^3 vanish so that the induced em, Z^0, and Kähler fields vanish but induced W fields are non-vanishing. This holds also for surfaces obtained by color rotation. Hence one can say that for non-vacuum extremals with 2-D CP_2 projection color rotations and weak symmetries commute.

A-3.3 Many-sheeted space-time

TGD space-time is many-sheeted: in other words, there are in general several space-sheets which have projection to the same M^4 region. Second manner to say this is that CP_2 coordinates are many-valued functions of M^4 coordinates. The original physical interpretation of many-sheeted space-time time was not correct: it was assumed that single sheet corresponds to GRT space-time and this obviously leads to difficulties since the induced gauge fields are expressible in terms of only four embedding space coordinates.

Fig. 10. Illustration of many-sheeted space-time of TGD. `http://tgdtheory.fi/appfigures/manysheeted.jpg`

Superposition of effects instead of superposition of fields

The first objection against TGD is that superposition is not possible for induced gauge fields and induced metric. The resolution of the problem is that it is effects which need to superpose, not the fields.

Test particle topologically condenses simultaneously to all space-time sheets having a projection to same region of M^4 (that is touches them). The superposition of effects of fields at various space-time sheets replaces the superposition of fields.This is crucial for the understanding also how GRT space-time relates to TGD space-time, which is also in the appendix of this book).

Wormhole contacts

Wormhole contacts are key element of many-sheeted space-time. One does not expect them to be stable unless there is non-trivial Kähler magnetic flux flowing through then so that the throats look like Kähler magnetic monopoles.

Fig. 11. Wormhole contact. `http://tgdtheory.fi/appfigures/wormholecontact.jpg`

Since the flow lines of Kähler magnetic field must be closed this requires the presence of another wormhole contact so that one obtains closed monopole flux tube decomposing to two Minkowskian pieces at the two space-time sheets involved and two wormhole contacts with Euclidian signature of the induced metric. These objects are identified as space-time correlates of elementary particles and are clearly analogous to string like objects.

The relationship between the many-sheeted space-time of TGD and of GRT space-time

The space-time of general relativity is single-sheeted and there is no need to regard it as surface in H although the assumption about representability as vacuum extremal gives very powerful constraints in cosmology and astrophysics and might make sense in simple situations.

The space-time of GRT can be regarded as a long length scale approximation obtained by lumping together the sheets of the many-sheeted space-time to a region of M^4 and providing it with an effective metric obtained as sum of M^4 metric and deviations of the induced metrics of various space-time sheets from M^4 metric. Also induced gauge potentials sum up in the similar manner so that also the gauge fields of gauge theories would not be fundamental fields.

Fig. 12. The superposition of fields is replaced with the superposition of their effects in many-sheeted space-time. `http://tgdtheory.fi/appfigures/fieldsuperpose.jpg`

Space-time surfaces of TGD are considerably simpler objects that the space-times of general relativity and relate to GRT space-time like elementary particles to systems of condensed matter physics. Same can be said about fields since all fields are expressible in terms of embedding space coordinates and their gradients, and general coordinate invariance means that the number of bosonic field degrees is reduced locally to 4. TGD space-time can be said to be a microscopic description whereas GRT space-time a macroscopic description. In TGD complexity of space-time topology replaces the complexity due to large number of fields in quantum field theory.

Topological field quantization and the notion of magnetic body

Topological field quantization also TGD from Maxwell's theory. TGD predicts topological light rays ("massless extremals (MEs)") as space-time sheets carrying waves or arbitrary shape propagating

with maximal signal velocity in single direction only and analogous to laser beams and carrying light-like gauge currents in the generi case. There are also magnetic flux quanta and electric flux quanta. The deformations of cosmic strings with 2-D string orbit as M^4 projection gives rise to magnetic flux tubes carrying monopole flux made possible by CP_2 topology allowing homological Kähler magnetic monopoles.

Fig. 13. Topological quantization for magnetic fields replaces magnetic fields with bundles of them defining flux tubes as topological field quanta. `http://tgdtheory.fi/appfigures/field.jpg`

The imbeddability condition for say magnetic field means that the region containing constant magnetic field splits into flux quanta, say tubes and sheets carrying constant magnetic field. Unless one assumes a separate boundary term in Kähler action, boundaries in the usual sense are forbidden except as ends of space-time surfaces at the boundaries of causal diamonds. One obtains typically pairs of sheets glued together along their boundaries giving rise to flux tubes with closed cross section possibly carrying monopole flux.

These kind of flux tubes might make possible magnetic fields in cosmic scales already during primordial period of cosmology since no currents are needed to generate these magnetic fields: cosmic string would be indeed this kind of objects and would dominated during the primordial period. Even superconductors and maybe even ferromagnets could involve this kind of monopole flux tubes.

A-3.4 Embedding space spinors and induced spinors

One can geometrize also fermionic degrees of freedom by inducing the spinor structure of $M^4 \times CP_2$.

CP_2 does not allow spinor structure in the ordinary sense but one can couple the opposite H-chiralities of H-spinors to an $n = 1$ ($n = 3$) integer multiple of Kähler gauge potential to obtain a respectable modified spinor structure. The em charges of resulting spinors are fractional (integer valued) and the interpretation as quarks (leptons) makes sense since the couplings to the induced spinor connection having interpretation in terms electro-weak gauge potential are identical to those assumed in standard model.

The notion of quark color differs from that of standard model.

1. Spinors do not couple to color gauge potential although the identification of color gauge potential as projection of $SU(3)$ Killing vector fields is possible. This coupling must emerge only at the effective gauge theory limit of TGD.

2. Spinor harmonics of embedding space correspond to triality $t = 1$ ($t = 0$) partial waves. The detailed correspondence between color and electroweak quantum numbers is however not correct as such and the interpretation of spinor harmonics of embedding space is as representations for ground states of super-conformal representations. The wormhole pairs associated with physical quarks and leptons must carry also neutrino pair to neutralize weak quantum numbers above the length scale of flux tube (weak scale or Compton length). The total color quantum numbers or these states must be those of standard model. For instance, the color quantum numbers of fundamental left-hand neutrino and lepton can compensate each other for the physical lepton. For fundamental quark-lepton pair they could sum up to those of physical quark.

The well-definedness of em charge is crucial condition.

1. Although the embedding space spinor connection carries W gauge potentials one can say that the embedding space spinor modes have well-defined em charge. One expects that this is true for induced spinor fields inside wormhole contacts with 4-D CP_2 projection and Euclidian signature of the induced metric.

2. The situation is not the same for the modes of induced spinor fields inside Minkowskian region and one must require that the CP_2 projection of the regions carrying induced spinor field is such that the induced W fields and above weak scale also the induced Z^0 fields vanish in order to avoid large parity breaking effects. This condition forces the CP_2 projection to be 2-dimensional. For a generic Minkowskian space-time region this is achieved only if the

spinor modes are localized at 2-D surfaces of space-time surface - string world sheets and possibly also partonic 2-surfaces.

3. Also the Kähler-Dirac gamma matrices appearing in the modified Dirac equation must vanish in the directions normal to the 2-D surface in order that Kähler-Dirac equation can be satisfied. This does not seem plausible for space-time regions with 4-D CP_2 projection.

4. One can thus say that strings emerge from TGD in Minkowskian space-time regions. In particular, elementary particles are accompanied by a pair of fermionic strings at the opposite space-time sheets and connecting wormhole contacts. Quite generally, fundamental fermions would propagate at the boundaries of string world sheets as massless particles and wormhole contacts would define the stringy vertices of generalized Feynman diagrams. One obtains geometrized diagrammatics, which brings looks like a combination of stringy and Feynman diagrammatics.

5. This is what happens in the the generic situation. Cosmic strings could serve as examples about surfaces with 2-D CP_2 projection and carrying only em fields and allowing delocalization of spinor modes to the entire space-time surfaces.

A-3.5 About induced gauge fields

In the following the induced gauge fields are studied for general space-time surface without assuming the preferred extremal property (Bohr orbit property). Therefore the following arguments are somewhat obsolete in their generality.

Space-times with vanishing em, Z^0, or Kähler fields

The following considerations apply to a more general situation in which the homologically trivial geodesic sphere and extremal property are not assumed. It must be emphasized that this case is possible in TGD framework only for a vanishing Kähler field.

Using spherical coordinates (r, Θ, Ψ, Φ) for CP_2, the expression of Kähler form reads as

$$\begin{aligned} J &= \frac{r}{F^2} dr \wedge (d\Psi + cos(\Theta) d\Phi) + \frac{r^2}{2F} sin(\Theta) d\Theta \wedge d\Phi \ , \\ F &= 1 + r^2 \ . \end{aligned} \tag{A-3.1}$$

The general expression of electromagnetic field reads as

$$\begin{aligned} F_{em} &= (3+2p)\frac{r}{F^2} dr \wedge (d\Psi + cos(\Theta) d\Phi) + (3+p)\frac{r^2}{2F} sin(\Theta) d\Theta \wedge d\Phi \ , \\ p &= sin^2(\Theta_W) \ , \end{aligned} \tag{A-3.2}$$

where Θ_W denotes Weinberg angle.

1. The vanishing of the electromagnetic fields is guaranteed, when the conditions

$$\begin{aligned} \Psi &= k\Phi \ , \\ (3+2p)\frac{1}{r^2 F}(d(r^2)/d\Theta)(k + cos(\Theta)) &+ (3+p) sin(\Theta) = 0 \ , \end{aligned} \tag{A-3.3}$$

hold true. The conditions imply that CP_2 projection of the electromagnetically neutral space-time is 2-dimensional. Solving the differential equation one obtains

$$\begin{aligned} r &= \sqrt{\frac{X}{1-X}} \ , \\ X &= D\left[|\frac{k+u}{C}|\right]^{\epsilon} \ , \\ u &\equiv cos(\Theta) \ , \ C = k + cos(\Theta_0) \ , \ D = \frac{r_0^2}{1+r_0^2} \ , \ \epsilon = \frac{3+p}{3+2p} \ , \end{aligned} \tag{A-3.4}$$

where C and D are integration constants. $0 \leq X \leq 1$ is required by the reality of r. $r = 0$ would correspond to $X = 0$ giving $u = -k$ achieved only for $|k| \leq 1$ and $r = \infty$ to $X = 1$ giving $|u + k| = [(1 + r_0^2)/r_0^2)]^{(3+2p)/(3+p)}$ achieved only for

$$sign(u+k) \times [\frac{1+r_0^2}{r_0^2}]^{\frac{3+2p}{3+p}} \leq k+1 \ ,$$

where $sign(x)$ denotes the sign of x.

The expressions for Kähler form and Z^0 field are given by

$$\begin{aligned} J &= -\frac{p}{3+2p} X du \wedge d\Phi \ , \\ Z^0 &= -\frac{6}{p} J \ . \end{aligned} \tag{A-3.5}$$

The components of the electromagnetic field generated by varying vacuum parameters are proportional to the components of the Kähler field: in particular, the magnetic field is parallel to the Kähler magnetic field. The generation of a long range Z^0 vacuum field is a purely TGD based feature not encountered in the standard gauge theories.

2. The vanishing of Z^0 fields is achieved by the replacement of the parameter ϵ with $\epsilon = 1/2$ as becomes clear by considering the condition stating that Z^0 field vanishes identically. Also the relationship $F_{em} = 3J = -\frac{3}{4}\frac{r^2}{F} du \wedge d\Phi$ is useful.

3. The vanishing Kähler field corresponds to $\epsilon = 1, p = 0$ in the formula for em neutral space-times. In this case classical em and Z^0 fields are proportional to each other:

$$\begin{aligned} Z^0 &= 2e^0 \wedge e^3 = \frac{r}{F^2}(k+u)\frac{\partial r}{\partial u} du \wedge d\Phi = (k+u) du \wedge d\Phi \ , \\ r &= \sqrt{\frac{X}{1-X}} \ , \ X = D|k+u| \ , \\ \gamma &= -\frac{p}{2} Z^0 \ . \end{aligned} \tag{A-3.6}$$

For a vanishing value of Weinberg angle ($p = 0$) em field vanishes and only Z^0 field remains as a long range gauge field. Vacuum extremals for which long range Z^0 field vanishes but em field is non-vanishing are not possible.

The effective form of CP_2 metric for surfaces with 2-dimensional CP_2 projection

The effective form of the CP_2 metric for a space-time having vanishing em,Z^0, or Kähler field is of practical value in the case of vacuum extremals and is given by

$$\begin{aligned} ds^2_{eff} &= (s_{rr}(\frac{dr}{d\Theta})^2 + s_{\Theta\Theta})d\Theta^2 + (s_{\Phi\Phi} + 2ks_{\Phi\Psi})d\Phi^2 = \frac{R^2}{4}[s^{eff}_{\Theta\Theta}d\Theta^2 + s^{eff}_{\Phi\Phi}d\Phi^2] \ , \\ s^{eff}_{\Theta\Theta} &= X \times \left[\frac{\epsilon^2(1-u^2)}{(k+u)^2} \times \frac{1}{1-X} + 1 - X\right] \ , \\ s^{eff}_{\Phi\Phi} &= X \times \left[(1-X)(k+u)^2 + 1 - u^2\right] \ , \end{aligned} \tag{A-3.7}$$

and is useful in the construction of vacuum embedding of, say Schwartchild metric.

Topological quantum numbers

Space-times for which either em, Z^0, or Kähler field vanishes decompose into regions characterized by six vacuum parameters: two of these quantum numbers (ω_1 and ω_2) are frequency type parameters, two (k_1 and k_2) are wave vector like quantum numbers, two of the quantum numbers (n_1 and n_2) are integers. The parameters ω_i and n_i will be referred as electric and magnetic quantum numbers. The existence of these quantum numbers is not a feature of these solutions alone but represents a much more general phenomenon differentiating in a clear cut manner between TGD and Maxwell's electrodynamics.

The simplest manner to avoid surface Kähler charges and discontinuities or infinities in the derivatives of CP_2 coordinates on the common boundary of two neighboring regions with different vacuum quantum numbers is topological field quantization, 3-space decomposes into disjoint topological field quanta, 3-surfaces having outer boundaries with possibly macroscopic size.

Under rather general conditions the coordinates Ψ and Φ can be written in the form

$$\begin{aligned} \Psi &= \omega_2 m^0 + k_2 m^3 + n_2\phi + \text{Fourier expansion} \ , \\ \Phi &= \omega_1 m^0 + k_1 m^3 + n_1\phi + \text{Fourier expansion} \ . \end{aligned} \tag{A-3.8}$$

m^0,m^3 and ϕ denote the coordinate variables of the cylindrical M^4 coordinates) so that one has $k = \omega_2/\omega_1 = n_2/n_1 = k_2/k_1$. The regions of the space-time surface with given values of the vacuum parameters ω_i,k_i and n_i and m and C are bounded by the surfaces at which space-time surface becomes ill-defined, say by $r > 0$ or $r < \infty$ surfaces.

The space-time surface decomposes into regions characterized by different values of the vacuum parameters r_0 and Θ_0. At $r = \infty$ surfaces n_2,ω_2 and m can change since all values of Ψ correspond to the same point of CP_2: at $r = 0$ surfaces also n_1 and ω_1 can change since all values of Φ correspond to same point of CP_2, too. If $r = 0$ or $r = \infty$ is not in the allowed range space-time surface develops a boundary.

This implies what might be called topological quantization since in general it is not possible to find a smooth global embedding for, say a constant magnetic field. Although global embedding exists it decomposes into regions with different values of the vacuum parameters and the coordinate u in general possesses discontinuous derivative at $r = 0$ and $r = \infty$ surfaces. A possible manner to avoid edges of space-time is to allow field quantization so that 3-space (and field) decomposes into disjoint quanta, which can be regarded as structurally stable units a 3-space (and of the gauge field). This doesn't exclude partial join along boundaries for neighboring field quanta provided some additional conditions guaranteeing the absence of edges are satisfied.

For instance, the vanishing of the electromagnetic fields implies that the condition

$$\Omega \equiv \frac{\omega_2}{n_2} - \frac{\omega_1}{n_1} = 0 \ , \tag{A-3.9}$$

is satisfied. In particular, the ratio ω_2/ω_1 is rational number for the electromagnetically neutral regions of space-time surface. The change of the parameter n_1 and n_2 (ω_1 and ω_2) in general generates magnetic field and therefore these integers will be referred to as magnetic (electric) quantum numbers.

A-4 The relationship of TGD to QFT and string models

The recent view of the relationship of TGD to QFT and string models has developed slowly during years and it seems that in a certain sense TGD means a return to roots: instead of QFT like description involving path integral one would have wave mechanics for 3-surfaces.

A-4.1 TGD as a generalization of wave mechanism obtained by replacing point-like particles with 3-surfaces

The first vision of TGD was as a generalization of quantum field theory (string models) obtained by replacing pointlike particles (strings) as fundamental objects with 3-surfaces.

The later work has revealed that TGD could be seen as a generalization of the wave mechanism based on the replacement of a point-like particle with 3-D surface. This is due to holography implied by general coordinate invariance. The definition of the metric of the "world of classical worlds" (WCW) must assign a unique or at least almost unique space-time surface to a given 3-surface. This 4-surface is analogous to Bohr orbit so that also Bohr orbitology becomes an exact part of quantum physics. The failure of strict determinism forces to replace 3-surfaces with 4-surfaces and this leads to zero energy ontology (ZEO) in which quantum states are superpositions of space-time surfaces [K43, K20, K72] [L128, L144].

Fig. 5. TGD replaces point-like particles with 3-surfaces. `http://tgdtheory.fi/appfigures/particletgd.jpg`

A-4.2 Extension of superconformal invariance

The fact that light-like 3-surfaces are effectively metrically 2-dimensional and thus possess generalization of 2-dimensional conformal symmetries with light-like radial coordinate defining the analog of second complex coordinate suggests that this generalization could work and extend the super-conformal symmetries to their 4-D analogs.

The boundary $\delta M^4_+ = S^2 \times R_+$- of 4-D light-cone M^4_+ is also metrically 2-dimensional and allows extended conformal invariance. Also the group of isometries of light-cone boundary and of light-like 3-surfaces is infinite-dimensional since the conformal scalings of S^2 can be compensated by S^2-local scaling of the light-like radial coordinate of R_+. These simple facts mean that 4-dimensional Minkowski space and 4-dimensional space-time surfaces are in a completely unique position as far as symmetries are considered.

In fact, this leads to a generalization of the Kac-Moody type symmetries of string models. $\delta M^4_+ \times CP_2$ allows huge supersymplectic symmetries for which the radial light-like coordinate of δM^4_+ plays the role of complex string coordinate in string models. These symmetries are assumed to act as isometries of WCW.

A-4.3 String-like objects and strings

String like objects obtained as deformations of cosmic strings $X^2 \times Y^2$, where X^2 is minimal surface in M^4 and Y^2 a holomorphic surface of CP_2 are fundamental extremals of Kähler action having string world sheet as M^4 projections. Cosmic strings dominate the primordial cosmology of the TGD Universe and the inflationary period corresponds to the transition to radiation dominated cosmology for which space-time sheets with 4-D M^4 projection dominate.

Also genuine string-like objects emerge from TGD. The conditions that the em charge of modes of induces spinor fields is well-defined requires in the generic case the localization of the modes at 2-D surfaces -string world sheets and possibly also partonic 2-surfaces. This in Minkowskian space-time regions.

Fig. 6. Well-definedness of em charge forces the localization of induced spinor modes to 2-D surfaces in generic situations in Minkowskian regions of space-time surface. `http://tgdtheory.fi/appfigures/fermistring.jpg`

A-4.4 TGD view of elementary particles

The TGD based view about elementary particles has two key aspects.

1. The space-time correlates of elementary particles are identified as pairs of wormhole contacts with Euclidean signature of metric and having 4-D CP_2 projection. Their throats behave effectively as Kähler magnetic monopoles so that wormhole throats must be connected by Kähler magnetic flux tubes with monopole flux so that closed flux tubes are obtained.

2. At the level of H Fermion number is carried by the modes of the induced spinor field. In space-time regions with Minkowski signature the modes are localized at string world sheets connecting the wormhole contacts.

Fig. 7. TGD view about elementary particles. a) Particle orbit corresponds to a 4-D generalization of a world line or b) with its light-like 3-D boundary (holography). c) Particle world lines have Euclidean signature of the induced metric. d) They can be identified as wormhole contacts. e) The throats of wormhole contacts carry effective Kähler magnetic charges so that wormhole contacts must appear as pairs in order to obtain closed flux tubes. f) Wormhole contacts are accompanied by fermionic strings connecting the throats at the same sheet: the strings do not extend inside the wormhole contacts. `http://tgdtheory.fi/appfigures/elparticletgd.jpg`

Particle interactions involve both stringy and QFT aspects.

1. The boundaries of string world sheets correspond to fundamental fermions. This gives rise to massless propagator lines in generalized Feynman diagrammatics. One can speak of "long" string connecting wormhole contacts and having a hadronic string as a physical counterpart. Long strings should be distinguished from wormhole contacts which due to their superconformal invariance behave like "short" strings with length scale given by CP_2 size, which is 10^4 times longer than Planck scale characterizing strings in string models.

2. Wormhole contact defines basic stringy interaction vertex for fermion-fermion scattering. The propagator is essentially the inverse of the superconformal scaling generator L_0. Wormhole contacts containing fermion and antifermion at its opposite throats behave like virtual bosons so that one has BFF type vertices typically.

3. In topological sense one has 3-vertices serving as generalizations of 3-vertices of Feynman diagrams. In these vertices 4-D "lines" of generalized Feynman diagrams meet along their 3-D ends. One obtains also the analogs of stringy diagrams but stringy vertices do not have the usual interpretation in terms of particle decays but in terms of propagation of particles along two different routes.

Fig. 8. a) TGD analogs of Feynman and string diagrammatics at the level of space-time topology. b) The 4-D analogs of both string diagrams and QFT diagrams appear but the interpretation of the analogs stringy diagrams is different. `http://tgdtheory.fi/appfigures/tgdgraphs.jpg`

A-5 About the selection of the action defining the Kähler function of the "world of classical worlds" (WCW)

The proposal is that space-time surfaces correspond to preferred extremals of some action principle, being analogous to Bohr orbits, so that they are almost deterministic. The action for the preferred extremal would define the Kähler function of WCW [K43, K72].

How unique is the choice of the action defining WCW Kähler metric? The problem is that twistor lift strongly suggests the identification of the preferred extremals as 4-D surfaces having 4-D generalization of complex structure and that a large number of general coordinate invariant actions constructible in terms of the induced geometry have the same preferred extremals.

A-5.1 Could twistor lift fix the choice of the action uniquely?

The twistor lift of TGD [L52] [L128, L133, L134] generalizes the notion of induction to the level of twistor fields and leads to a proposal that the action is obtained by dimensional reduction of the action having as its preferred extremals the counterpart of twistor space of the space-time surface identified as 6-D surface in the product $T(M^4) \times T(CP_2)$ twistor spaces of $T(M^4)$ and

$T(CP_2)$ of M^4 and CP_2. Only M^4 and CP_2 allow a twistor space with Kähler structure [A33] so that TGD would be unique. Dimensional reduction is forced by the condition that the 6-surface has S^2-bundle structure characterizing twistor spaces and the base space would be the space-time surface.

1. Dimensional reduction of 6-D Kähler action implies that at the space-time level the fundamental action can be identified as the sum of Kähler action and volume term (cosmological constant). Other choices of the action do not look natural in this picture although they would have the same preferred extremals.

2. Preferred extremals are proposed to correspond to minimal surfaces with singularities such that they are also extremals of 4-D Kähler action outside the singularities. The physical analogue are soap films spanned by frames and one can localize the violation of the strict determinism and of strict holography to the frames.

3. The preferred extremal property is realized as the holomorphicity characterizing string world sheets, which generalizes to the 4-D situation. This in turn implies that the preferred extremals are the same for any general coordinate invariant action defined on the induced gauge fields and induced metric apart from possible extremals with vanishing CP_2 Kähler action.

   For instance, 4-D Kähler action and Weyl action as the sum of the tensor squares of the components of the Weyl tensor of CP_2 representing quaternionic imaginary units constructed from the Weyl tensor of CP_2 as an analog of gauge field would have the same preferred extremals and only the definition of Kähler function and therefore Kähler metric of WCW would change. One can even consider the possibility that the volume term in the 4-D action could be assigned to the tensor square of the induced metric representing a quaternionic or octonionic real unit.

Action principle does not seem to be unique. On the other hand, the WCW Kähler form and metric should be unique since its existence requires maximal isometries.

Unique action is not the only way to achieve this. One cannot exclude the possibility that the Kähler gauge potential of WCW in the complex coordinates of WCW differs only by a complex gradient of a holomorphic function for different actions so that they would give the same Kähler form for WCW. This gradient is induced by a symplectic transformation of WCW inducing a U(1) gauge transformation. The Kähler metric is the same if the symplectic transformation is an isometry.

Symplectic transformations of WCW could give rise to inequivalent representations of the theory in terms of action at space-time level. Maybe the length scale dependent coupling parameters of an effective action could be interpreted in terms of a choice of WCW Kähler function, which maximally simplifies the computations at a given scale.

1. The 6-D analogues of electroweak action and color action reducing to Kähler action in 4-D case exist. The 6-D analog of Weyl action based on the tensor representation of quaternionic imaginary units does not however exist. One could however consider the possibility that only the base space of twistor space $T(M^4)$ and $T(CP_2)$ have quaternionic structure.

2. Kähler action has a huge vacuum degeneracy, which clearly distinguishes it from other actions. The presence of the volume term removes this degeneracy. However, for minimal surfaces having CP_2 projections, which are Lagrangian manifolds and therefore have a vanishing induced Kähler form, would be preferred extremals according to the proposed definition. For these 4-surfaces, the existence of the generalized complex structure is dubious.

   For the electroweak action, the terms corresponding to charged weak bosons eliminate these extremals and one could argue that electroweak action or its sum with the analogue of color action, also proportional Kähler action, defines the more plausible choice. Interestingly, also the neutral part of electroweak action is proportional to Kähler action.

Twistor lift strongly suggests that also M^4 has the analog of Kähler structure. M^8 must be complexified by adding a commuting imaginary unit i. In the E^8 subspace, the Kähler structure of E^4 is defined in the standard sense and it is proposed that this generalizes to M^4 allowing also

generalization of the quaternionic structure. M^4 Kähler structure violates Lorentz invariance but could be realized at the level of moduli space of these structures.

The minimal possibility is that the M^4 Kähler form vanishes: one can have a different representation of the Kähler gauge potential for it obtained as generalization of symplectic transformations acting non-trivially in M^4. The recent picture about the second quantization of spinors of $M^4 \times CP_2$ assumes however non-trivial Kähler structure in M^4.

A-5.2 Two paradoxes

TGD view leads to two apparent paradoxes.

1. If the preferred extremals satisfy 4-D generalization of holomorphicity, a very large set of actions gives rise to the same preferred extremals unless there are some additional conditions restricting the number of preferred extremals for a given action.

2. WCW metric has an infinite number of zero modes, which appear as parameters of the metric but do not contribute to the line element. The induced Kähler form depends on these degrees of freedom. The existence of the Kähler metric requires maximal isometries, which suggests that the Kähler metric is uniquely fixed apart from a conformal scaling factor Ω depending on zero modes. This cannot be true: galaxy and elementary particle cannot correspond to the same Kähler metric.

Number theoretical vision and the hierarchy of inclusions of HFFs associated with supersymplectic algebra actings as isometries of WcW provide equivalent realizations of the measurement resolution. This solves these paradoxes and predicts that WCW decomposes into sectors for which Kähler metrics of WCW differ in a natural way.

The hierarchy subalgebras of supersymplectic algebra implies the decomposition of WCW into sectors with different actions

Supersymplectic algebra of $\delta M^4_+ \times CP_2$ is assumed to act as isometries of WCW [L144]. There are also other important algebras but these will not be discussed now.

1. The symplectic algebra A of $\delta M^4_+ \times CP_2$ has the structure of a conformal algebra in the sense that the radial conformal weights with non-negative real part, which is half integer, label the elements of the algebra have an interpretation as conformal weights.

   The super symplectic algebra A has an infinite hierarchy of sub-algebras [L144] such that the conformal weights of sub-algebras $A_{n(SS)}$ are integer multiples of the conformal weights of the entire algebra. The superconformal gauge conditions are weakened. Only the subalgebra $A_{n(SS)}$ and the commutator $[A_{n(SS)}, A]$ annihilate the physical states. Also the corresponding classical Noether charges vanish for allowed space-time surfaces.

   This weakening makes sense also for ordinary superconformal algebras and associated Kac-Moody algebras. This hierarchy can be interpreted as a hierarchy symmetry breakings, meaning that sub-algebra $A_{n(SS)}$ acts as genuine dynamical symmetries rather than mere gauge symmetries. It is natural to assume that the super-symplectic algebra A does not affect the coupling parameters of the action.

2. The generators of A correspond to the dynamical quantum degrees of freedom and leave the induced Kähler form invariant. They affect the induced space-time metric but this effect is gravitational and very small for Einsteinian space-time surfaces with 4-D M^4 projection.

   The number of dynamical degrees of freedom increases with $n(SS)$. Therefore WCW decomposes into sectors labelled by $n(SS)$ with different numbers of dynamical degrees of freedom so that their Kähler metrics cannot be equivalent and cannot be related by a symplectic isometry. They can correspond to different actions.

Number theoretic vision implies the decomposition of WCW into sectors with different actions

The number theoretical vision leads to the same conclusion as the hierarchy of HFFs. The number theoretic vision of TGD based on $M^8 - H$ duality [L144] predicts a hierarchy with levels labelled by the degrees $n(P)$ of rational polynomials P and corresponding extensions of rationals characterized by Galois groups and by ramified primes defining p-adic length scales.

These sequences allow us to imagine several discrete coupling constant evolutions realized at the level H in terms of action whose coupling parameters depend on the number theoretic parameters.

1. Coupling constant evolution with respect to $n(P)$

The first coupling constant evolution would be with respect to $n(P)$.

1. The coupling constants characterizing action could depend on the degree $n(P)$ of the polynomial defining the space-time region by $M^8 - H$ duality. The complexity of the space-time surface would increase with $n(P)$ and new degrees of freedom would emerge as the number of the rational coefficients of P.

2. This coupling constant evolution could naturally correspond to that assignable to the inclusion hierarchy of hyperfinite factors of type II_1 (HFFs). I have indeed proposed [L144] that the degree $n(P)$ equals to the number $n(braid)$ of braids assignable to HFF for which super symplectic algebra subalgebra $A_{n(SS)}$ with radial conformal weights coming as $n(SS)$-multiples of those of entire algebra A. One would have $n(P) = n(braid) = n(SS)$. The number of dynamical degrees of freedom increases with n which just as it increases with $n(P)$ and $n(SS)$.

3. The actions related to different values of $n(P) = n(braid) = n(SS)$ cannot define the same Kähler metric since the number of allowed space-time surfaces depends on $n(SS)$.

   WCW could decompose to sub-WCWs corresponding to different actions, a kind of theory space. These theories would not be equivalent. A possible interpretation would be as a hierarchy of effective field theories.

4. Hierarchies of composite polynomials define sequences of polynomials with increasing values of $n(P)$ such that the order of a polynomial at a given level is divided by those at the lower levels. The proposal is that the inclusion sequences of extensions are realized at quantum level as inclusion hierarchies of hyperfinite factors of type II_1.

   A given inclusion hierarchy corresponds to a sequence $n(SS)_i$ such that $n(SS)_i$ divides $n(SS)_{i+1}$. Therefore the degree of the composite polynomials increases very rapidly. The values of $n(SS)_i$ can be chosen to be primes and these primes correspond to the degrees of so called prime polynomials [L136] so that the decompositions correspond to prime factorizations of integers. The "densest" sequence of this kind would come in powers of 2 as $n(SS)_i = 2^i$. The corresponding p-adic length scales (assignable to maximal ramified primes for given $n(SS)_i$) are expected to increase roughly exponentially, say as 2^{r2^i}. $r = 1/2$ would give a subset of scales $2^{r/2}$ allowed by the p-adic length scale hypothesis. These transitions would be very rare.

   A theory corresponding to a given composite polynomial would contain as sub-theories the theories corresponding to lower polynomial composites. The evolution with respect to $n(SS)$ would correspond to a sequence of phase transitions in which the action genuinely changes. For instance, color confinement could be seen as an example of this phase transition.

5. A subset of p-adic primes allowed by the p-adic length scale hypothesis $p \simeq 2^k$ defining the proposed p-adic length scale hierarchy could relate to n_S changing phase transition. TGD suggests a hierarchy of hadron physics corresponding to a scale hierarchy defined by Mersenne primes and their Gaussian counterparts [K51, K52]). Each of them would be characterized by a confinement phase transition in which n_S and therefore also the action changes.

2. Coupling constant evolutions with respect to ramified primes for a given value of $n(P)$

For a given value of $n(P)$, one could have coupling constant sub-evolutions with respect to the set of ramified primes of P and dimensions $n = h_{eff}/h_0$ of algebraic extensions. The action would only change by U(1) gauge transformation induced by a symplectic isometry of WCW. Coupling parameters could change but the actions would be equivalent.

The choice of the action in an optimal manner in a given scale could be seen as a choice of the most appropriate effective field theory in which radiative corrections would be taken into account. One can interpret the possibility to use a single choice of coupling parameters in terms of quantum criticality.

The range of the p-adic length scales labelled by ramified primes and effective Planck constants h_{eff}/h_0 is finite for a given value of $n(SS)$.

The first coupling constant evolution of this kind corresponds to ramified primes defining p-adic length scales for given $n(SS)$.

1. Ramified primes are factors of the discriminant $D(P)$ of P, which is expressible as a product of non-vanishing root differents and reduces to a polynomial of the n coefficients of P. Ramified primes define p-adic length scales assignable to the particles in the amplitudes scattering amplitudes defined by zero energy states.

   P would represent the space-time surface defining an interaction region in $N-$-particle scattering. The N ramified primes dividing $D(P)$ would characterize the p-adic length scales assignable to these particles. If $D(P)$ reduces to a single ramified prime, one has elementary particle [L136], and the forward scattering amplitude corresponds to the propagator.

   This would give rise to a multi-scale p-adic length scale evolution of the amplitudes analogous to the ordinary continuous coupling constant evolution of n-point scattering amplitudes with respect to momentum scales of the particles. This kind of evolutions extend also to evolutions with respect to $n(SS)$.

2. According to [L136], physical constraints require that $n(P)$ and the maximum size of the ramified prime of P correlate.

   A given rational polynomial of degree $n(P)$ can be always transformed to a polynomial with integer coefficients. If the integer coefficients are smaller than $n(P)$, there is an upper bound for the ramified primes. This assumption also implies that finite fields become fundamental number fields in number theoretical vision [L136].

3. p-Adic length scale hypothesis [L145] in its basic form states that there exist preferred primes $p \simeq 2^k$ near some powers of 2. A more general hypothesis states that also primes near some powers of 3 possibly also other small primes are preferred physically. The challenge is to understand the origin of these preferred scales.

   For polynomials P with a given degree $n(P)$ for which discriminant $D(P)$ is prime, there exists a maximal ramified prime. Numerical calculations suggest that the upper bound depends exponentially on $n(P)$.

   Could these maximal ramified primes satisfy the p-adic length scale hypothesis or its generalization? The maximal prime defines a fixed point of coupling constant evolution in accordance with the earlier proposal. For instance, could one think that one has $p \simeq 2^k$, $k = n(SS)$? Each p-adic prime would correspond to a p-adic coupling constant sub-evolution representable in terms of symplectic isometries.

Also the dimension n of the algebraic extension associated with P, which is identified in terms of effective Planck constant $h_{eff}/h_0 = n$ labelling different phases of the ordinary matter behaving like dark matter, could give rise to coupling constant evolution for given $n(SS)$. The range of allowed values of n is finite. Note however that several polynomials of a given degree can correspond to the same dimension of extension.

Number theoretic discretization of WCW and maxima of WCW Kähler function

Number theoretic approach involves a unique discretization of space-time surface and also of WCW. The question is how the points of the discretized WCW correspond to the preferred extremals.

1. The exponents of Kähler function for the maxima of Kähler function, which correspond to the universal preferred extremals, appear in the scattering amplitudes. The number theoretical approach involves a unique discretization of space-time surfaces defining the WCW coordinates of the space-time surface regarded as a point of WCW.

   In [L144] it is assumed that these WCW points appearing in the number theoretical discretization correspond to the maxima of the Kähler function. The maxima would depend on the action and would differ for ghd maxima associated with different actions unless they are not related by symplectic WCW isometry.

2. The symplectic transformations of WCW acting as isometries are assumed to be induced by the symplectic transformations of $\delta M^4_+ \times CP_2$ [K43, K20]. As isometries they would naturally permute the maxima with each other.

A-6 Number theoretic vision of TGD

Physics as number theory vision is complementary to the physics as geometry vision and has developed gradually since 1993. Langlands program is the counterpart of this vision in mathematics [L141].

The notion of p-adic number fields emerged with the motivation coming from the observation that elementary particle mass scales and mass ratios could be understood in terms of the so-called p-adic length scale hypothesis [K55, K46, K19]. The fusion of the various p-adic physics leads to what I call adelic physics [L50, L51]. Later the hypothesis about hierarchy of Planck constants labelling phases of ordinary matter behaving like dark matter emerged [K22, K23, K24, K25].

Eventually this led to that the values of effective Planck constant could be identified as the dimension of an algebraic extension of rationals assignable to polynomials with rational coefficients. This led to the number theoretic vision in which so-called $M^8 - H$ duality [L101, L102] plays a key role. M^8 (actually a complexification of real M^8) is analogous to momentum space so that the duality generalizes momentum position duality for point-like particles. M^8 has an interpretation as complexified octonions.

The dynamics of 4-surfaces in M^8 is coded by polynomials with rational coefficients, whose roots define mass shells H^3 of $M^4 \subset M^8$. It has turned out that the polynomials satisfy stringent additional conditions and one can speak of number theoretic holography [L136, L141]. Also the ordinary $3 \rightarrow 4$ holography is needed to assign 4-surfaces with these 3-D mass shells. The number theoretic dynamics is based on the condition that the normal space of the 4-surface in M^8 is associative (quaternionic) and contains a commutative complex sub-space. This makes it possible to assign to this surface space-time surface in $H = M^4 \times CP_2$.

At the level of H the space-time surfaces are by holography preferred extremals and are assumed to be determined by the twistor lift of TGD [L52] giving rise to an action which is sum of the Kähler action and volume term. The preferred extremals would be minimal surfaces analogous to soap films spanned by frames. Outside frames they would be simultaneous extremals of the Kähler action, which requires a generalization of the holomorphy characterizing string world sheets.

In the following only p-adic numbers and hierarchy of Planck constants will be discussed.

A-6.1 p-Adic numbers and TGD

p-Adic number fields

p-Adic numbers (p is prime: 2, 3, 5, ...) can be regarded as a completion of the rational numbers using a norm, which is different from the ordinary norm of real numbers [A21]. p-Adic numbers are representable as power expansion of the prime number p of form

$$x = \sum_{k \geq k_0} x(k) p^k, \; x(k) = 0, ..., p-1 \; . \tag{A-6.1}$$

The norm of a p-adic number is given by

$$|x| \quad = \quad p^{-k_0(x)} \quad . \tag{A-6.2}$$

Here $k_0(x)$ is the lowest power in the expansion of the p-adic number. The norm differs drastically from the norm of the ordinary real numbers since it depends on the lowest pinary digit of the p-adic number only. Arbitrarily high powers in the expansion are possible since the norm of the p-adic number is finite also for numbers, which are infinite with respect to the ordinary norm. A convenient representation for p-adic numbers is in the form

$$x \quad = \quad p^{k_0}\varepsilon(x) \quad , \tag{A-6.3}$$

where $\varepsilon(x) = k + ...$ with $0 < k < p$, is p-adic number with unit norm and analogous to the phase factor $exp(i\phi)$ of a complex number.

The distance function $d(x,y) = |x-y|_p$ defined by the p-adic norm possesses a very general property called ultra-metricity:

$$d(x,z) \quad \leq \quad max\{d(x,y), d(y,z)\} \quad . \tag{A-6.4}$$

The properties of the distance function make it possible to decompose R_p into a union of disjoint sets using the criterion that x and y belong to same class if the distance between x and y satisfies the condition

$$d(x,y) \quad \leq \quad D \quad . \tag{A-6.5}$$

This division of the metric space into classes has following properties:

1. Distances between the members of two different classes X and Y do not depend on the choice of points x and y inside classes. One can therefore speak about distance function between classes.

2. Distances of points x and y inside single class are smaller than distances between different classes.

3. Classes form a hierarchical tree.

Notice that the concept of the ultra-metricity emerged in physics from the models for spin glasses and is believed to have also applications in biology [B14]. The emergence of p-adic topology as the topology of the effective space-time would make ultra-metricity property basic feature of physics.

Canonical correspondence between p-adic and real numbers

The basic challenge encountered by p-adic physicist is how to map the predictions of the p-adic physics to real numbers. p-Adic probabilities provide a basic example in this respect. Identification via common rationals and canonical identification and its variants have turned out to play a key role in this respect.

1. Basic form of the canonical identification

There exists a natural continuous map $I : R_p \to R_+$ from p-adic numbers to non-negative real numbers given by the "pinary" expansion of the real number for $x \in R$ and $y \in R_p$ this correspondence reads

$$\begin{aligned} y \quad &= \quad \sum_{k>N} y_k p^k \to x = \sum_{k<N} y_k p^{-k} \quad , \\ y_k \quad &\in \quad \{0,1,..,p-1\} \quad . \end{aligned} \tag{A-6.6}$$

This map is continuous as one easily finds out. There is however a little difficulty associated with the definition of the inverse map since the pinary expansion like also decimal expansion is not unique ($1 = 0.999...$) for the real numbers x, which allow pinary expansion with finite number of pinary digits

$$\begin{aligned} x &= \sum_{k=N_0}^{N} x_k p^{-k} \ , \\ x &= \sum_{k=N_0}^{N-1} x_k p^{-k} + (x_N - 1)p^{-N} + (p-1)p^{-N-1} \sum_{k=0,..} p^{-k} \ . \end{aligned} \tag{A-6.7}$$

The p-adic images associated with these expansions are different

$$\begin{aligned} y_1 &= \sum_{k=N_0}^{N} x_k p^{k} \ , \\ y_2 &= \sum_{k=N_0}^{N-1} x_k p^{k} + (x_N - 1)p^{N} + (p-1)p^{N+1} \sum_{k=0,..} p^{k} \\ &= y_1 + (x_N - 1)p^N - p^{N+1} \ , \end{aligned} \tag{A-6.8}$$

so that the inverse map is either two-valued for p-adic numbers having expansion with finite pinary digits or single valued and discontinuous and non-surjective if one makes pinary expansion unique by choosing the one with finite pinary digits. The finite pinary digit expansion is a natural choice since in the numerical work one always must use a pinary cutoff on the real axis.

2. The topology induced by canonical identification

The topology induced by the canonical identification in the set of positive real numbers differs from the ordinary topology. The difference is easily understood by interpreting the p-adic norm as a norm in the set of the real numbers. The norm is constant in each interval $[p^k, p^{k+1})$ (see **Fig. A-6.1**) and is equal to the usual real norm at the points $x = p^k$: the usual linear norm is replaced with a piecewise constant norm. This means that p-adic topology is coarser than the usual real topology and the higher the value of p is, the coarser the resulting topology is above a given length scale. This hierarchical ordering of the p-adic topologies will be a central feature as far as the proposed applications of the p-adic numbers are considered.

Ordinary continuity implies p-adic continuity since the norm induced from the p-adic topology is rougher than the ordinary norm. p-Adic continuity implies ordinary continuity from right as is clear already from the properties of the p-adic norm (the graph of the norm is indeed continuous from right). This feature is one clear signature of the p-adic topology.

Fig. 14. The real norm induced by canonical identification from 2-adic norm. `http://tgdtheory.fi/appfigures/norm.png`

The linear structure of the p-adic numbers induces a corresponding structure in the set of the non-negative real numbers and p-adic linearity in general differs from the ordinary concept of linearity. For example, p-adic sum is equal to real sum only provided the summands have no common pinary digits. Furthermore, the condition $x +_p y < max\{x, y\}$ holds in general for the p-adic sum of the real numbers. p-Adic multiplication is equivalent with the ordinary multiplication only provided that either of the members of the product is power of p. Moreover one has $x \times_p y < x \times y$ in general. The p-Adic negative -1_p associated with p-adic unit 1 is given by $(-1)_p = \sum_k (p-1)p^k$ and defines p-adic negative for each real number x. An interesting possibility is that p-adic linearity might replace the ordinary linearity in some strongly nonlinear systems so these systems would look simple in the p-adic topology.

These results suggest that canonical identification is involved with some deeper mathematical structure. The following inequalities hold true:

$$\begin{aligned} (x+y)_R &\leq x_R + y_R \ , \\ |x|_p|y|_R \leq (xy)_R &\leq x_R y_R \ , \end{aligned} \tag{A-6.9}$$

where $|x|_p$ denotes p-adic norm. These inequalities can be generalized to the case of $(R_p)^n$ (a linear vector space over the p-adic numbers).

$$\begin{aligned} (x+y)_R &\leq x_R + y_R \ , \\ |\lambda|_p|y|_R \leq (\lambda y)_R &\leq \lambda_R y_R \ , \end{aligned} \tag{A-6.10}$$

where the norm of the vector $x \in T_p^n$ is defined in some manner. The case of Euclidian space suggests the definition

$$(x_R)^2 = (\sum_n x_n^2)_R \ . \tag{A-6.11}$$

These inequalities resemble those satisfied by the vector norm. The only difference is the failure of linearity in the sense that the norm of a scaled vector is not obtained by scaling the norm of the original vector. Ordinary situation prevails only if the scaling corresponds to a power of p.

These observations suggests that the concept of a normed space or Banach space might have a generalization and physically the generalization might apply to the description of some non-linear systems. The nonlinearity would be concentrated in the nonlinear behavior of the norm under scaling.

3. Modified form of the canonical identification

The original form of the canonical identification is continuous but does not respect symmetries even approximately. This led to a search of variants which would do better in this respect. The modification of the canonical identification applying to rationals only and given by

$$I_Q(q = p^k \times \frac{r}{s}) = p^k \times \frac{I(r)}{I(s)} \tag{A-6.12}$$

is uniquely defined for rationals, maps rationals to rationals, has also a symmetry under exchange of target and domain. This map reduces to a direct identification of rationals for $0 \leq r < p$ and $0 \leq s < p$. It has turned out that it is this map which most naturally appears in the applications. The map is obviously continuous locally since p-adically small modifications of r and s mean small modifications of the real counterparts.

Canonical identification is in a key role in the successful predictions of the elementary particle masses. The predictions for the light elementary particle masses are within extreme accuracy same for I and I_Q but I_Q is theoretically preferred since the real probabilities obtained from p-adic ones by I_Q sum up to one in p-adic thermodynamics.

4. Generalization of number concept and notion of embedding space

TGD forces an extension of number concept: roughly a fusion of reals and various p-adic number fields along common rationals is in question. This induces a similar fusion of real and p-adic embedding spaces. Since finite p-adic numbers correspond always to non-negative reals n-dimensional space R^n must be covered by 2^n copies of the p-adic variant R_p^n of R^n each of which projects to a copy of R_+^n (four quadrants in the case of plane). The common points of p-adic and real embedding spaces are rational points and most p-adic points are at real infinity.

Real numbers and various algebraic extensions of p-adic number fields are thus glued together along common rationals and also numbers in algebraic extension of rationals whose number belong to the algebraic extension of p-adic numbers. This gives rise to a book like structure with rationals and various algebraic extensions of rationals taking the role of the back of the book. Note that Neper number is exceptional in the sense that it is algebraic number in p-adic number field Q_p satisfying $e^p \ mod \ p = 1$.

Fig. 15. Various number fields combine to form a book like structure. `http://tgdtheory.fi/appfigures/book.jpg`

For a given p-adic space-time sheet most points are literally infinite as real points and the projection to the real embedding space consists of a discrete set of rational points: the interpretation in terms of the unavoidable discreteness of the physical representations of cognition is natural. Purely local p-adic physics implies real p-adic fractality and thus long range correlations for the real space-time surfaces having enough common points with this projection.

p-Adic fractality means that M^4 projections for the rational points of space-time surface X^4 are related by a direct identification whereas CP_2 coordinates of X^4 at these points are related by I, I_Q or some of its variants implying long range correlates for CP_2 coordinates. Since only a discrete set of points are related in this manner, both real and p-adic field equations can be satisfied and there are no problems with symmetries. p-Adic effective topology is expected to be a good approximation only within some length scale range which means infrared and UV cutoffs. Also multi-p-fractality is possible.

The notion of p-adic manifold

The notion of p-adic manifold is needed in order to fuse real physics and various p-adic physics to a larger structure which suggests that real and p-adic number fields should be glued together along common rationals bringing in mind adeles. The notion is problematic because p-adic topology is totally disconnected implying that p-adic balls are either disjoint or nested so that ordinary definition of manifold using p-adic chart maps fails. A cure is suggested to be based on chart maps from p-adics to reals rather than to p-adics (see the appendix of the book)

The chart maps are interpreted as cognitive maps, "thought bubbles".

Fig. 16. The basic idea between p-adic manifold. `http://tgdtheory.fi/appfigures/padmanifold.jpg`

There are some problems.

1. Canonical identification does not respect symmetries since it does not commute with second pinary cutoff so that only a discrete set of rational points is mapped to their real counterparts by chart map arithmetic operations which requires pinary cutoff below which chart map takes rationals to rationals so that commutativity with arithmetics and symmetries is achieved in finite resolution: above the cutoff canonical identification is used

2. Canonical identification is continuous but does not map smooth p-adic surfaces to smooth real surfaces requiring second pinary cutoff so that only a discrete set of rational points is mapped to their real counterparts by chart map requiring completion of the image to smooth preferred extremal of Kähler action so that chart map is not unique in accordance with finite measurement resolution

3. Canonical identification violates general coordinate invariance of chart map: (cognition-induced symmetry breaking) minimized if p-adic manifold structure is induced from that for p-adic embedding space with chart maps to real embedding space and assuming preferred coordinates made possible by isometries of embedding space: one however obtains several inequivalent p-adic manifold structures depending on the choice of coordinates: these cognitive representations are not equivalent.

A-6.2 Hierarchy of Planck constants and dark matter hierarchy

Hierarchy of Planck constants was motivated by the "impossible" quantal effects of ELF em fields on vertebrate cyclotron energies $E = hf = \hbar \times eB/m$ are above thermal energy is possible only if $\hbar$ has value much larger than its standard value. Also Nottale's finding that planetary orbits migh be understood as Bohr orbits for a gigantic gravitational Planck constant.

Hierachy of Planck constant would mean that the values of Planck constant come as integer multiples of ordinary Planck constant: $h_{eff} = n \times h$. The particles at magnetic flux tubes characterized by h_{eff} would correspond to dark matter which would be invisible in the sense that only particle with same value of h_{eff} appear in the same vertex of Feynman diagram.

Hierarchy of Planck constants would be due to the non-determism of the Kähler action predicting huge vacuum degeneracy allowing all space-time surfaces which are sub-manfolds of any $M^4 \times Y^2$, where Y^2 is Lagrangian sub-manifold of CP_2. For agiven Y^2 one obtains new manifolds Y^2 by applying symplectic transformations of CP_2.

Non-determinism would mean that the 3-surface at the ends of causal diamond (CD) can be connected by several space-time surfaces carrying same conserved Kähler charges and having same values of Kähler action. Conformal symmetries defined by Kac-Moody algebra associated with the embedding space isometries could act as gauge transformations and respect the light-likeness property of partonic orbits at which the signature of the induced metric changes from Minkowskian to Euclidian (Minkowskianb space-time region transforms to wormhole contact say). The number of conformal equivalence classes of these surfaces could be finite number n and define discrete physical degree of freedom and one would have $h_{eff} = n \times h$. This degeneracy would mean "second quantization" for the sheets of n-furcation: not only one but several sheets can be realized.

This relates also to quantum criticality postulated to be the basic characteristics of the dynamics of quantum TGD. Quantum criticalities would correspond to an infinite fractal hierarchy of broken conformal symmetries defined by sub-algebras of conformal algebra with conformal weights coming as integer multiples of n. This leads also to connections with quantum criticality and hierarchy of broken conformal symmetries, p-adicity, and negentropic entanglement which by consistency with standard quantum measurement theory would be described in terms of density matrix proportional $n \times n$ identity matrix and being due to unitary entanglement coefficients (typical for quantum computing systems).

Formally the situation could be described by regarding space-time surfaces as surfaces in singular n-fold singular coverings of embedding space. A stronger assumption would be that they are expressible as as products of n_1 -fold covering of M^4 and n_2-fold covering of CP_2 meaning analogy with multi-sheeted Riemann surfaces and that M^4 coordinates are n_1-valued functions and CP_2 coordinates n_2 -valued functions of space-time coordinates for $n = n_1 \times n_2$. These singular coverings of embedding space form a book like structure with singularities of the coverings localizable at the boundaries of causal diamonds defining the back of the book like structure.

Fig. 17. Hierarchy of Planck constants. `http://tgdtheory.fi/appfigures/planckhierarchy.jpg`

A-6.3 $M^8 - H$ duality as it is towards the end of 2021

The view of $M^8 - H$ duality (see Appendix 12.4.6) has changed considerably towards the end 2021 [L128] after the realization that this duality is the TGD counterpart of momentum position duality of wave mechanics, which is lost in QFTs. Therefore M^8 and also space-time surface is analogous to momentum space. This forced us to give up the original simple identification of the points $M^4 \subset M^4 \times E^4 = M^8$ and of $M^4 \times CP_2$ so that it respects Uncertainty Principle (UP).

The first improved guess for the duality map was the replacement with the inversion $p^k \to m^k = \hbar_{eff} p^k/p^2$ conforming in spirit with UP but turned out to be too naive.

The improved form [L128] of the $M^8 - H$ duality map takes mass shells $p^2 = m^2$ of $M^4 \subset M^8$ to cds with size $L(m) = \hbar_{eff}/m$ with a common center. The slicing by mass shells is mapped to a Russian doll like slicing by cds. Therefore would be no CDs in M^8 contrary to what I believed first.

Quantum classical correspondence (QCC) inspires the proposal that the point $p^k \in M^8$ is mapped to a geodesic line corresponding to momentum p^k starting from the common center of cds. Its intersection with the opposite boundary of cd with size $L(m)$ defines the image point. This is not yet quite enough to satisfy UP but the additional details [L128] are not needed in the sequel.

The 6-D brane-like special solutions in M^8 are of special interest in the TGD inspired theory of consciousness. They have an M^4 projection which is $E = E_n$ 3-ball. Here E_n is a root of the real polynomial P defining $X^4 \subset M^8_c$ (M^8 is complexified to M^8_c) as a "root" of its octonionic continuation [L101, L102]. E_n has an interpretation as energy, which can be complex. The original interpretation was as moment of time. For this interpretation, $M^8 - H$ duality would be a linear identification and these hyper planes would be mapped to hyperplanes in $M^4 \subset H$.

This motivated the term "very special moment in the life of self" for the image of the $E = E_n$ section of $X^4 \subset M^8$ [L84]. This notion does not make sense at the level M^8 anymore.

The modified $M^8 - H$ duality forces us to modify the original interpretation [L128]. The point $(E_n, p = 0)$ is mapped $(t_n = \hbar_{eff}/E_n, 0)$. The momenta (E_n, p) in $E = E_n$ plane are mapped to the boundary of cd and correspond to a continuous time interval at the boundary of CD: "very special moment" becomes a "very special time interval".

The quantum state however corresponds to a set of points corresponding to quark momenta, which belong to a cognitive representation and are therefore algebraic integers in the extension determined by the polynomial. These active points in E_n are mapped to a discrete set at the boundary of cd(m). A "very special moment" is replaced with a sequence of "very special moments".

So called Galois confinement [L117] forces the total momenta for bound states of quarks and antiquarks to be rational integers invariant under Galois group of extension of rationals determined by the polynomial P [L128]. These states correspond to states at boundaries of sub-CDs so that one obtains a hierarchy. Galois confinement provides a universal number theoretic mechanism for the formation of bound states.

A-7 Zero energy ontology (ZEO)

ZEO is implied by the holography forced in the TGD framework by general coordinate invariance.

A-7.1 Basic motivations and ideas of ZEO

The following gives a brief summary of ZEO [L92] [K93].

1. In ZEO quantum states are not 3-dimensional but superpositions of 4-dimensional deterministic time evolutions connecting ordinary initial 3-dimensional states. By holography they are equivalent to pairs of ordinary 3-D states identified as initial and final states of time evolution. One can say that in the TGD framework general coordinate invariance implies holography and the slight failure of its determinism in turn forces ZEO.

   Quantum jumps replace this state with a new one: a superposition of deterministic time evolutions is replaced with a new superposition. Classical determinism of individual time evolution is not violated and this solves the basic paradox of quantum measurement theory. There are two kinds of quantum jumps: ordinary ("big") state function reductions (BSFRs) changing the arrow of time and "small" state function reductions (SSFRs) (weak measurements) preserving it and giving rise to the analog of Zeno effect [L92].

2. To avoid getting totally confused it is good to emphasize some aspects of ZEO.

   (a) ZEO does not mean that physical states in the usual 3-D sense as snapshots of time evolution would have zero energy state pairs defining zero energy states as initial and final states have same conserved quantities such as energy. Conservation implies that one can adopt the conventions that the values of conserved quantities are opposite for these states so that their sum vanishes: one can think that incoming and outgoing particles come from geometric past and future is the picture used in quantum field theories.

   (b) ZEO means two times: subjective time as sequence of quantum jumps and geometric time as space-time coordinate. These times are identifiable but are strongly correlated.

3. In BSFRs the arrow of time is changed and the time evolution in the final state occurs backwards with respect to the time of the external observer. BSFRs can occur in all scales since TGD predicts a hierarchy of effective Planck constants with arbitrarily large values. There is empirical support for BSFRs.

   (a) The findings of Minev et al [L79] in atomic scale can be explained by the same mechanism [L79]. In BSFR a final zero energy state as a superposition of classical deterministic time evolutions emerges and for an observer with a standard arrow of time looks

like a superposition of deterministic smooth time evolutions leading to the final state. Interestingly, once this evolution has started, it cannot be stopped unless one changes the stimulus signal inducing the evolution in which case the process does not lead to anywhere: the interpretation would be that BSFR back to the initial state occurs!

(b) Libets' experiments about active aspects of consciousness [J3] can be understood. Subject person raises his finger and neural activity starts before the conscious decision to do so. In the physicalistic framework it is thought to lead to raising of the finger. The problem with the explanation is that the activity beginning .5 seconds earlier seems to be dissipation with a reversed arrow of time: from chaotic and disordered to ordered at around .15 seconds. ZEO explanation is that macroscopic quantum jump occurred and generated a signal proceeding backwards in time and generated neural activity and dissipated to randomness.

(c) Earthquakes involve a strange anomaly: they are preceded by ELF radiation. One would expect that they generate ELF radiation. The identification as BSFR would explain the anomaly [L81]. In biology the reversal of the arrow of time would occur routinely and be a central element of biological self-organization, in particular self-organized quantum criticality (see [L87, L162].

A-7.2 Some implications of ZEO

ZEO has profound implications for understanding self-organization and self-organized quantum criticality in terms of dissipation with non-standard arrow of time looking like generation of structures [L87, L162]. ZEO could also allow understanding of what planned actions - like realizing the experiment under consideration - could be.

1. Second law in the standard sense does not favor - perhaps even not allow - realization of planned actions. ZEO forces a generalization of thermodynamics: dissipation with a non-standard arrow of time for a subsystem would look like self-organization and planned action and its realization.

   Could most if not all planned action be like this - induced by BSFR in the geometric future and only apparently planned? There would be however the experience of planning and realizing induced by the signals from geometric future by a higher level in the hierarchy of conscious entities predicted by TGD! In long time scales we would be realizing our fates or wishes of higher level conscious entities rather than agents with completely free will.

2. The notion of magnetic body (MB) serving as a boss of ordinary matter would be central. MB carries dark matter as $h_{eff} = nh_0$ phases of ordinary matter with n serving as a measure for algebraic complexity of extension of rationals as its dimension and defining a kind of universal IQ. There is a hierarchy of these phases and MBs labelled by extension of rationals and the value of n.

   MBs would form a hierarchy of bosses - a realization for master slave hierarchy. Ordinary matter would be at the bottom and its coherent behavior would be induced from quantum coherence at higher levels. BSFR for higher level MB would give rise to what looks like planned actions and experienced as planned action at the lower levels of hierarchy. One could speak of planned actions inducing a cascade of planned actions in shorter time scales and eventually proceeding to atomic level.

A-8 Some notions relevant to TGD inspired consciousness and quantum biology

Below some notions relevant to TGD inspired theory of consciousness and quantum biology.

A-8.1 The notion of magnetic body

Topological field quantization inspires the notion of field body about which magnetic body is especially important example and plays key role in TGD inspired quantum biology and consciousness theory. This is a crucial departure fromt the Maxwellian view. Magnetic body brings in third level to the description of living system as a system interacting strongly with environment. Magnetic body would serve as an intentional agent using biological body as a motor instrument and sensory receptor. EEG would communicated the information from biological body to magnetic body and Libet's findings from time delays of consciousness support this view.

The following pictures illustrate the notion of magnetic body and its dynamics relevant for quantum biology in TGD Universe.

Fig. 18. Magnetic body associated with dipole field. `http://tgdtheory.fi/appfigures/fluxquant.jpg`

Fig. 19. Illustration of the reconnection by magnetic flux loops. `http://tgdtheory.fi/appfigures/reconnect1.jpg`

Fig. 20. Illustration of the reconnection by flux tubes connecting pairs of molecules. `http://tgdtheory.fi/appfigures/reconect2.jpg`

Fig. 21. Flux tube dynamics. a) Reconnection making possible magnetic body to "recognize" the presence of another magnetic body, b) braiding, knotting and linking of flux tubes making possible topological quantum computation, c) contraction of flux tube in phase transition reducing the value of h_{eff} allowing two molecules to find each other in dense molecular soup. `http://tgdtheory.fi/appfigures/fluxtubedynamics.jpg`

A-8.2 Number theoretic entropy and negentropic entanglement

TGD inspired theory of consciousness relies heavily p-Adic norm allows an to define the notion of Shannon entropy for rational probabilities (and even those in algebraic extension of rationals) by replacing the argument of logarithm of probability with its p-adic norm. The resulting entropy can be negative and the interpretation is that number theoretic entanglement entropy defined by this formula for the p-adic prime minimizing its value serves as a measure for conscious information. This negentropy characterizes two-particle system and has nothing to do with the formal negative negentropy assignable to thermodynamic entropy characterizing single particle. Negentropy Maximization Principle (NMP) implies that number theoretic negentropy increases during evolution by quantum jumps. The condition that NMP is consistent with the standard quantum measurement theory requires that negentropic entanglement has a density matrix proportional to unit matrix so that in 2-particle case the entanglement matrix is unitary.

Fig. 22. Schrödinger cat is neither dead or alive. For negentropic entanglement this state would be stable. `http://tgdtheory.fi/appfigures/cat.jpg`

A-8.3 Life as something residing in the intersection of reality and p-adicities

In TGD inspired theory of consciousness p-adic space-time sheets correspond to space-time correlates for thoughts and intentions. The intersections of real and p-adic preferred extremals consist of points whose coordinates are rational or belong to some extension of rational numbers in preferred embedding space coordinates. They would correspond to the intersection of reality and various p-adicities representing the "mind stuff" of Descartes. There is temptation to assign life to the intersection of realities and p-adicities. The discretization of the chart map assigning to real space-time surface its p-adic counterpart would reflect finite cognitive resolution.

At the level of "world of classical worlds" (WCW) the intersection of reality and various p-adicities would correspond to space-time surfaces (or possibly partonic 2-surfaces) representable in terms of rational functions with polynomial coefficients with are rational or belong to algebraic extension of rationals.

The quantum jump replacing real space-time sheet with p-adic one (vice versa) would correspond to a buildup of cognitive representation (realization of intentional action).

Fig. 23. The quantum jump replacing real space-time surface with corresponding p-adic manifold can be interpreted as formation of though, cognitive representation. Its reversal would correspond to a transformation of intention to action. `http://tgdtheory.fi/appfigures/padictoreal.jpg`

A-8.4 Sharing of mental images

The 3-surfaces serving as correlates for sub-selves can topologically condense to disjoint large space-time sheets representing selves. These 3-surfaces can also have flux tube connections and this makes possible entanglement of sub-selves, which unentangled in the resolution defined by the size of sub-selves. The interpretation for this negentropic entanglement would be in terms of sharing of mental images. This would mean that contents of consciousness are not completely private as assumed in neuroscience.

Fig. 24. Sharing of mental images by entanglement of subselves made possible by flux tube connections between topologically condensed space-time sheets associated with mental images. `http://tgdtheory.fi/appfigures/sharing.jpg`

A-8.5 Time mirror mechanism

Zero energy ontology (ZEO) is crucial part of both TGD and TGD inspired consciousness and leads to the understanding of the relationship between geometric time and experience time and how the arrow of psychological time emerges. One of the basic predictions is the possibiity of negative energy signals propagating backwards in geometric time and having the property that entropy basically associated with subjective time grows in reversed direction of geometric time. Negative energy signals inspire time mirror mechanism (see **Fig.** `http://tgdtheory.fi/appfigures/timemirror.jpg` or **Fig.** 24 in the appendix of this book) providing mechanisms of both memory recall, realization of intentational action initiating action already in geometric past, and remote metabolism. What happens that negative energy signal travels to past and is reflected as positive energy signal and returns to the sender. This process works also in the reverse time direction.

Fig. 25. Zero energy ontology allows time mirror mechanism as a mechanism of memory recall. Essentially "seeing" in time direction is in question. `http://tgdtheory.fi/appfigures/timemirror.jpg`

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