GENES AND MEMES: PART I

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April 29, 2024

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 $H = M^4 \times CP_2$ [L58]. 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 [L27, L35](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 [L59].

- 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 [K81, L42].

- 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 [K14, K39] [L54].

- 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 [L56]. 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 [L61].

- 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 [L25, L26] 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 [L60]. 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. 22**). 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 [L51], 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 [A6]. I have proposed [K33, K17, K80, K63, L59] 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 [K81, L42] 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 [L57]. 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 [L48, L49] 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 [L61].

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 [L55]. 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.

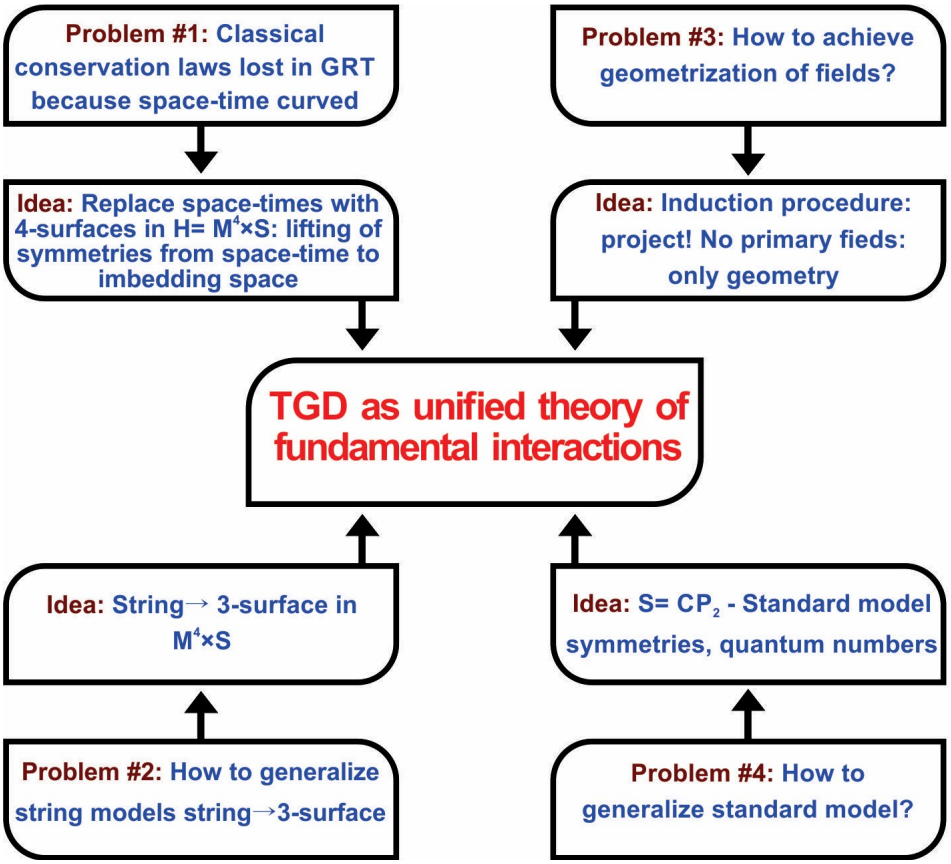


Figure 1: The problems leading to TGD as their solution.

- 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.

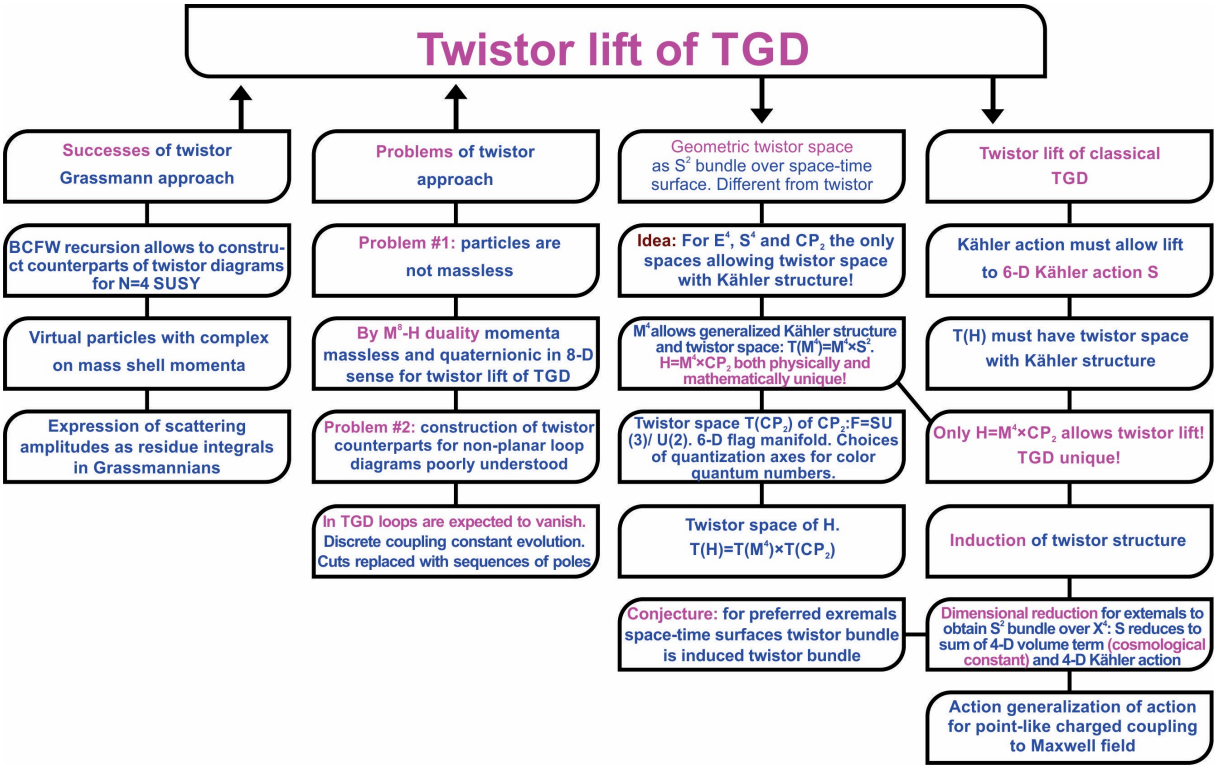


Figure 2: Twistor lift

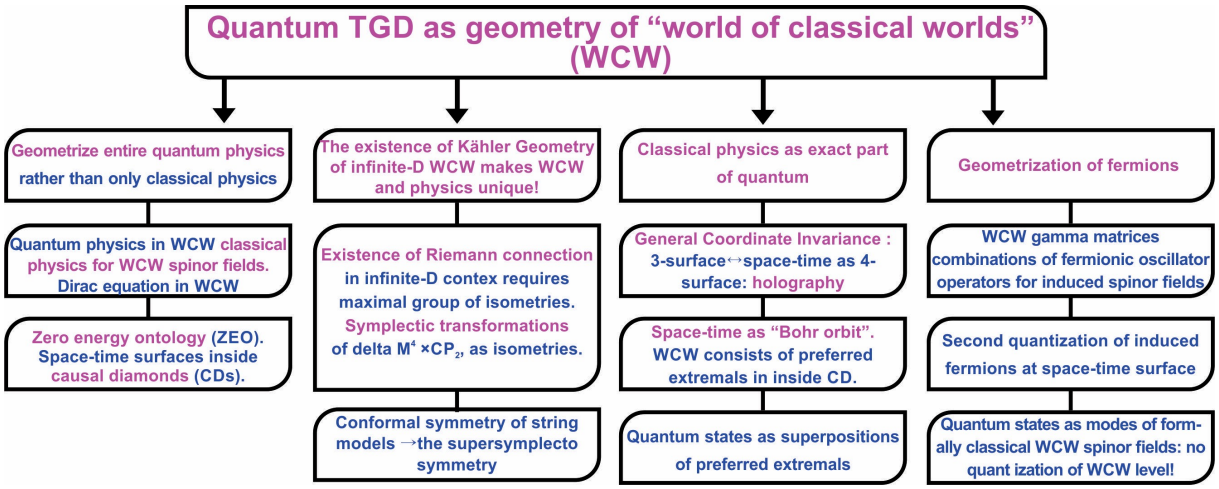


Figure 3: Geometrization of quantum physics in terms of WCW

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

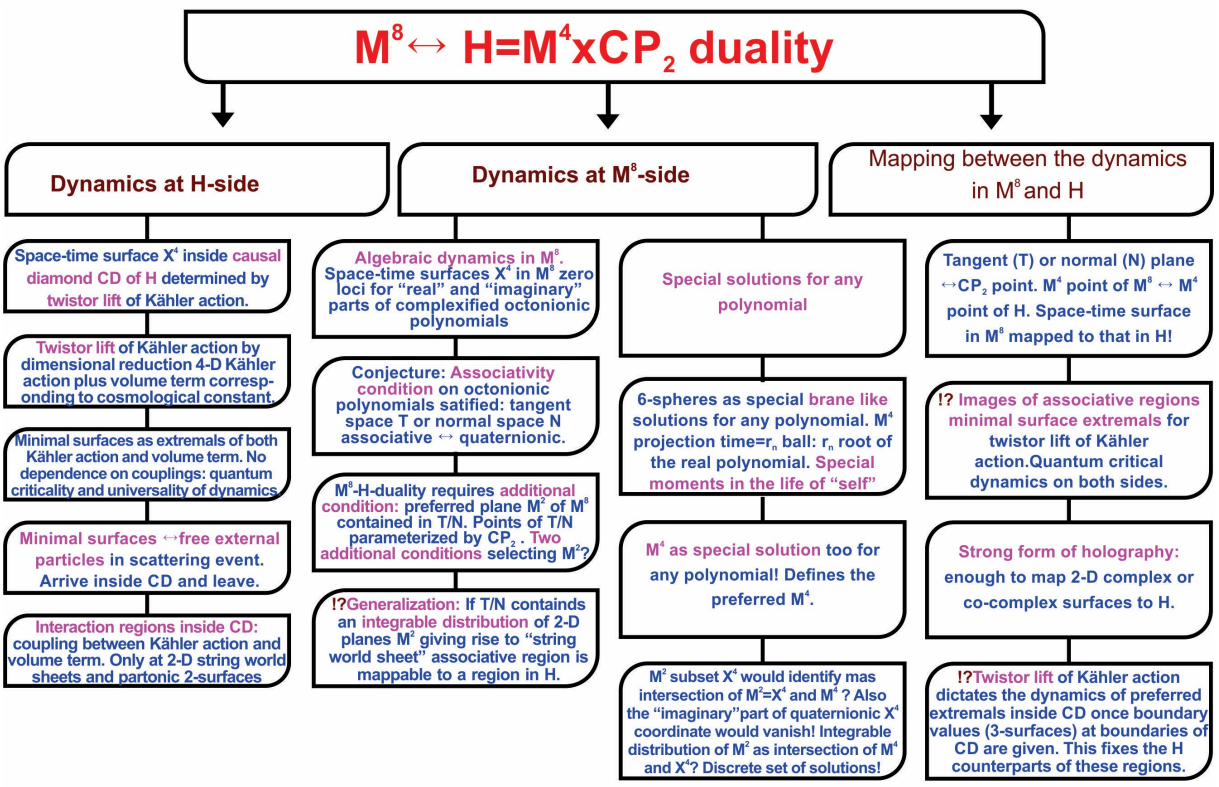


Figure 4: $M^8 - H$ duality

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

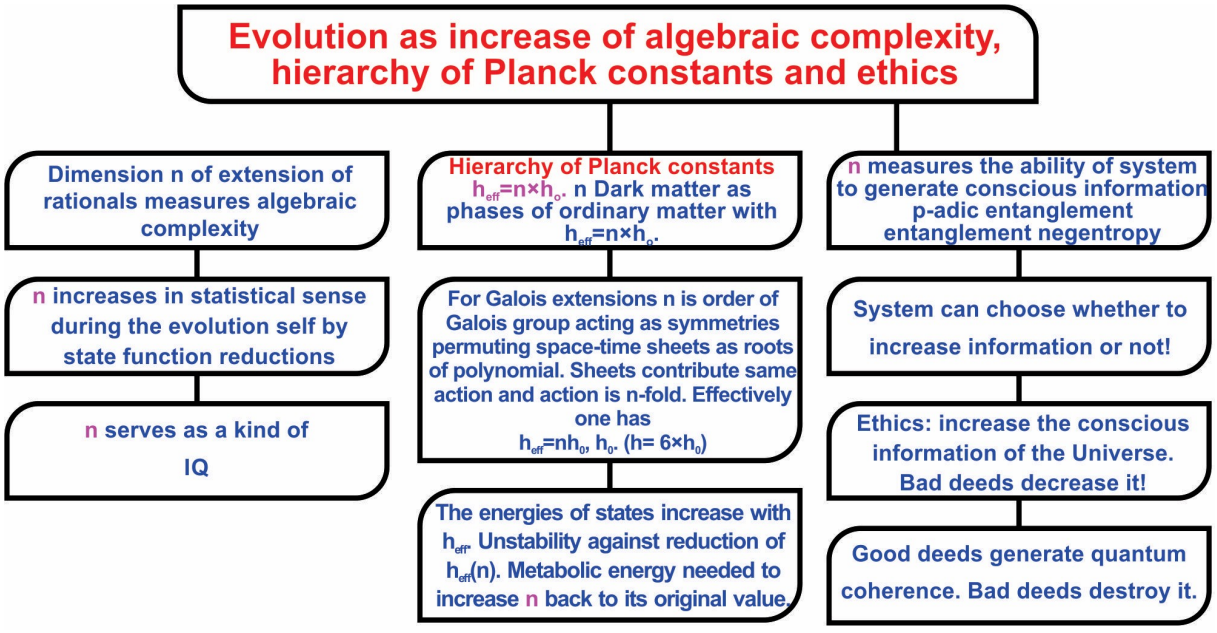


Figure 5: Number theoretic view of evolution

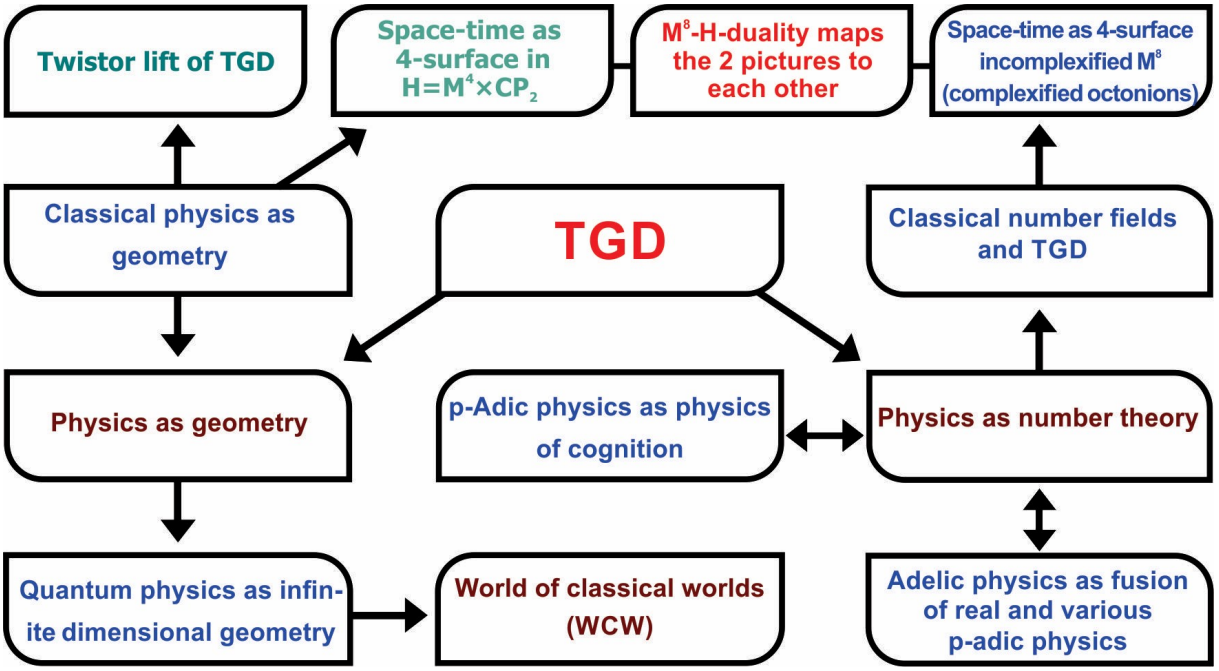


Figure 6: TGD is based on two complementary visions: physics as geometry and physics as number theory.

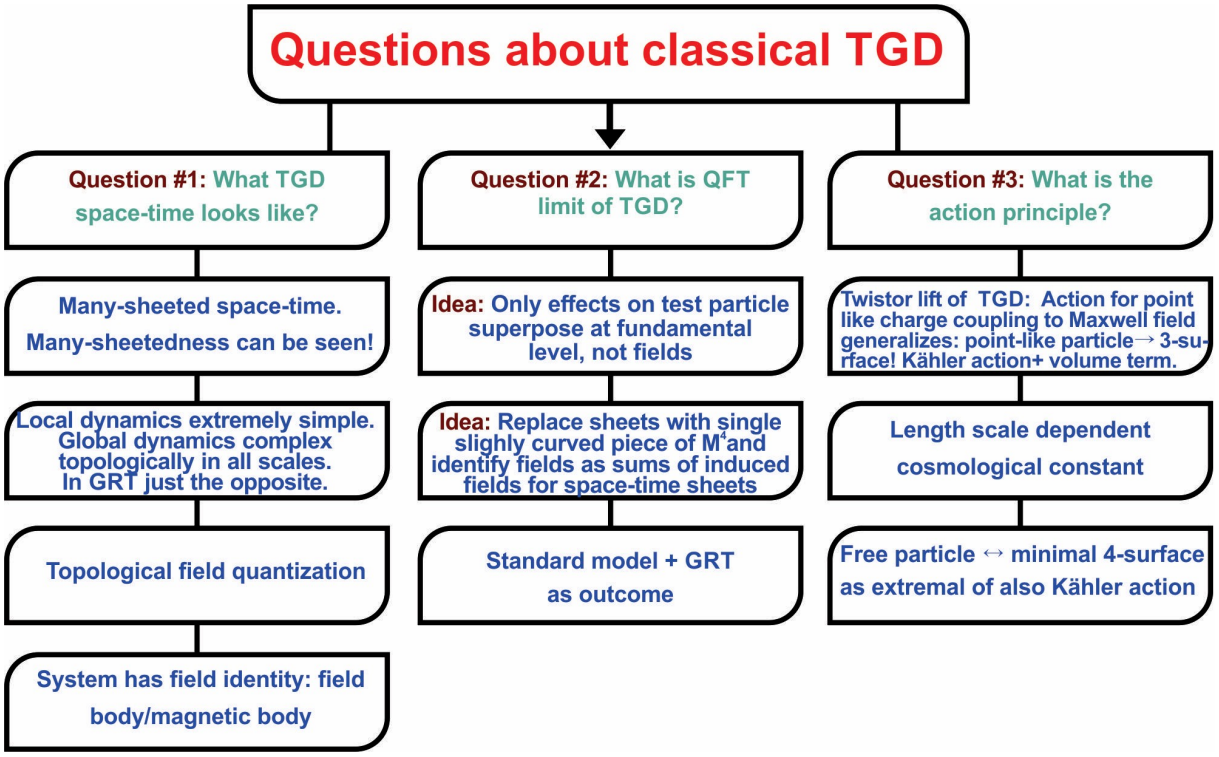


Figure 7: Questions about classical TGD.

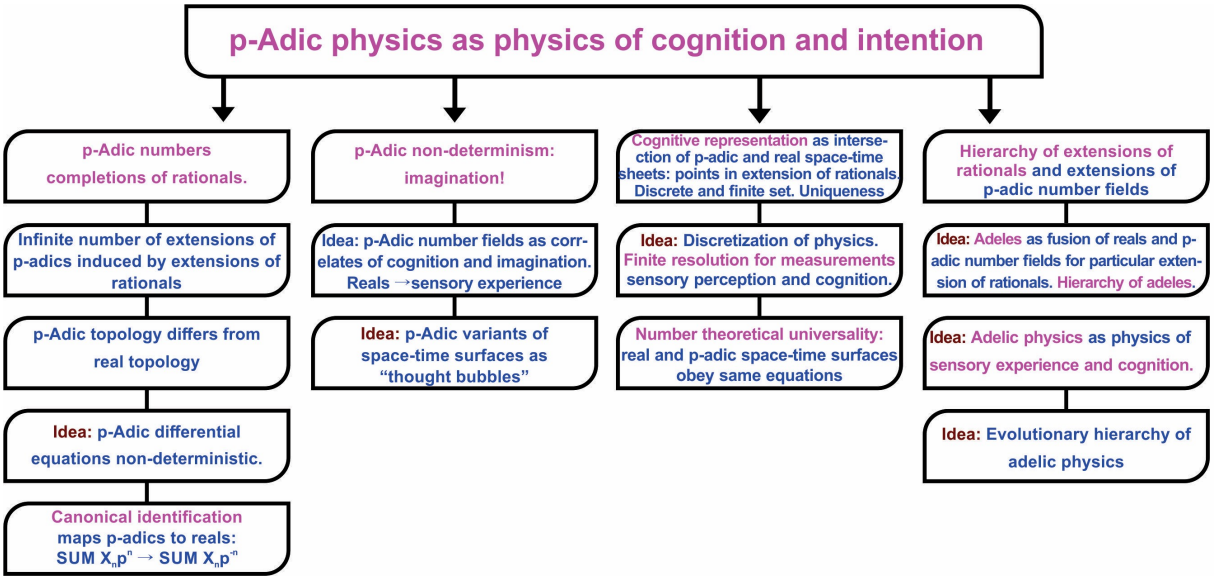


Figure 8: p-Adic physics as physics of cognition and imagination.

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.

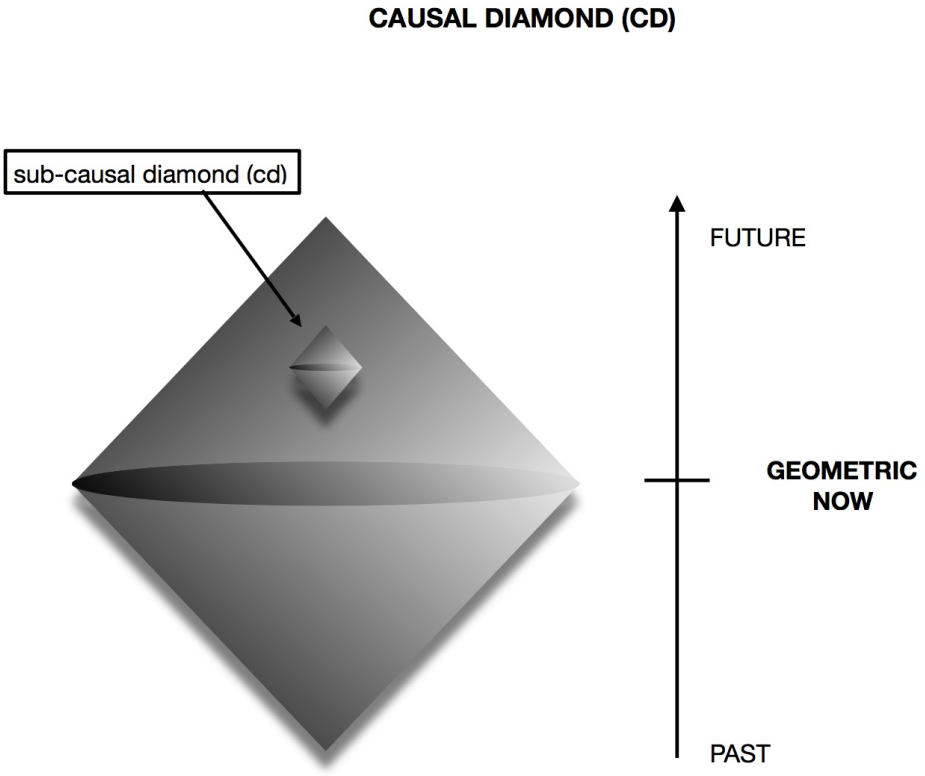


Figure 9: Causal diamond

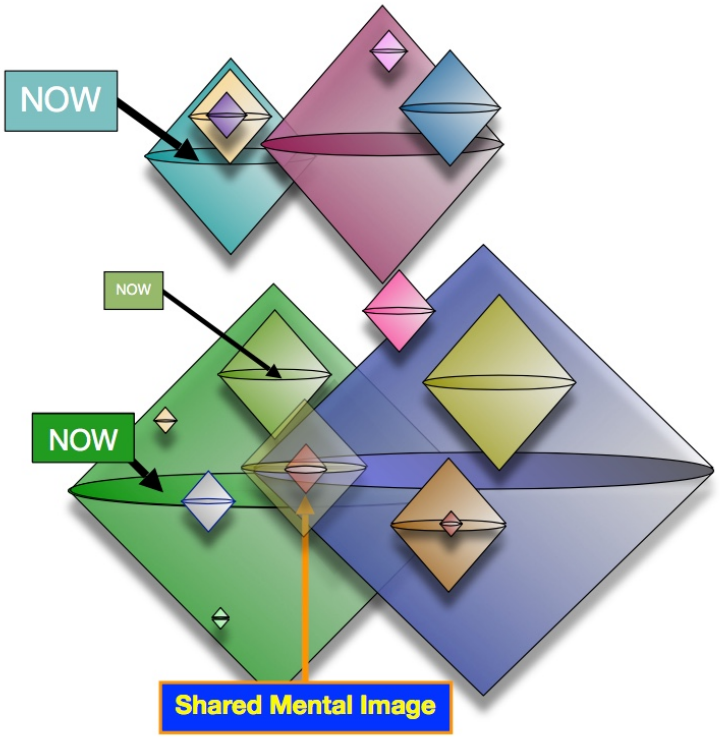


Figure 10: CDs define a fractal "conscious atlas"

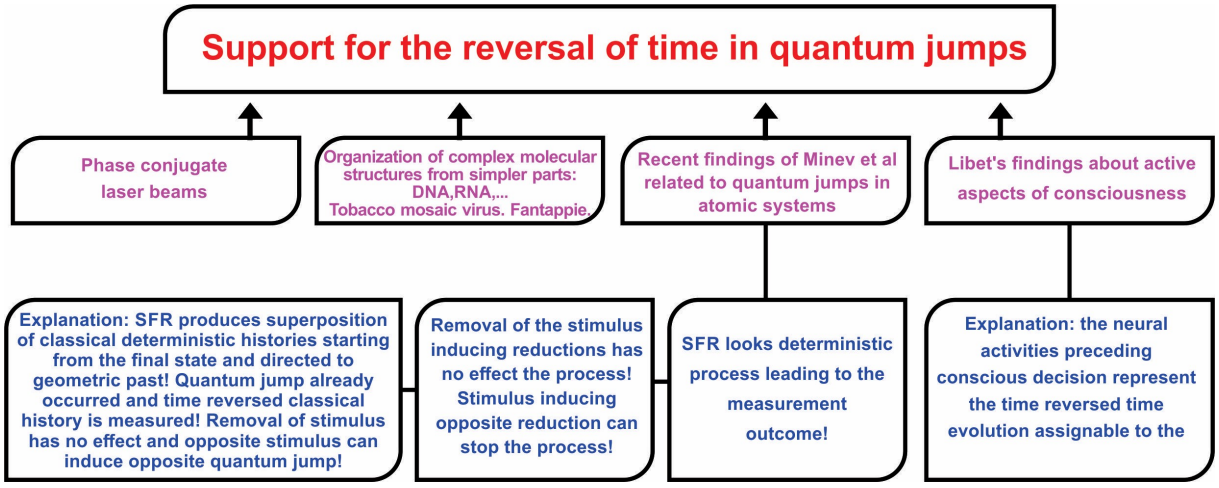


Figure 11: Time reversal occurs in BSFR

Figures

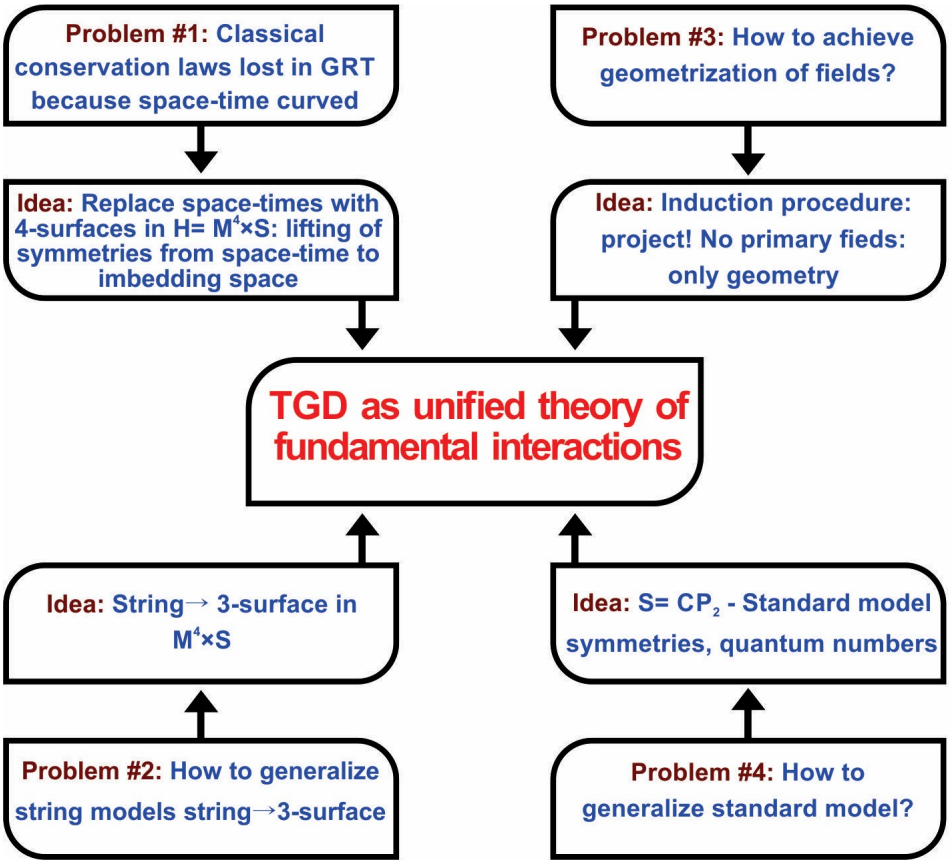
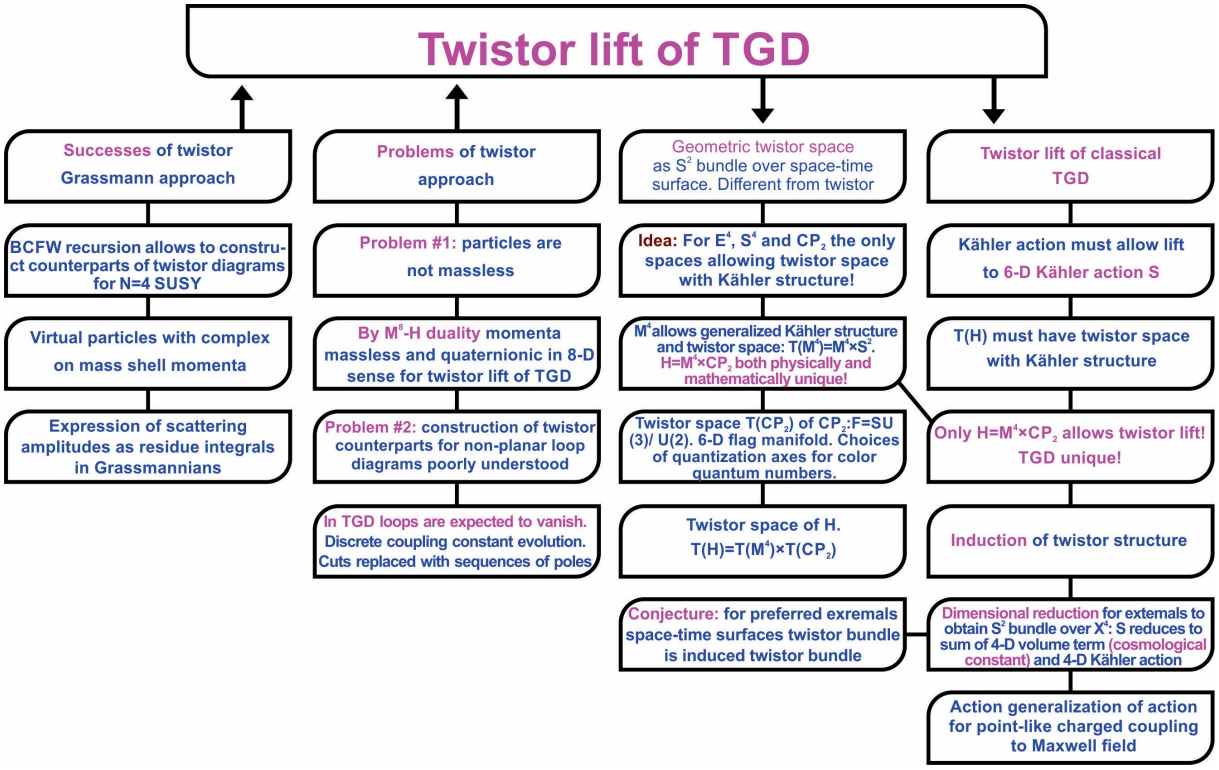


Figure 12: The problems leading to TGD as their solution.

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



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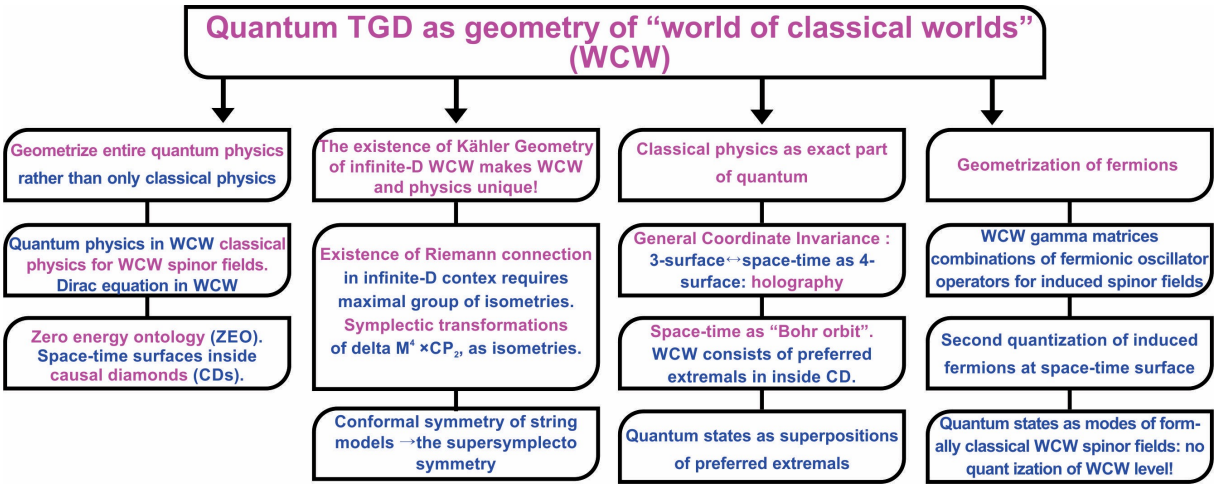


Figure 14: Geometrization of quantum physics in terms of WCW

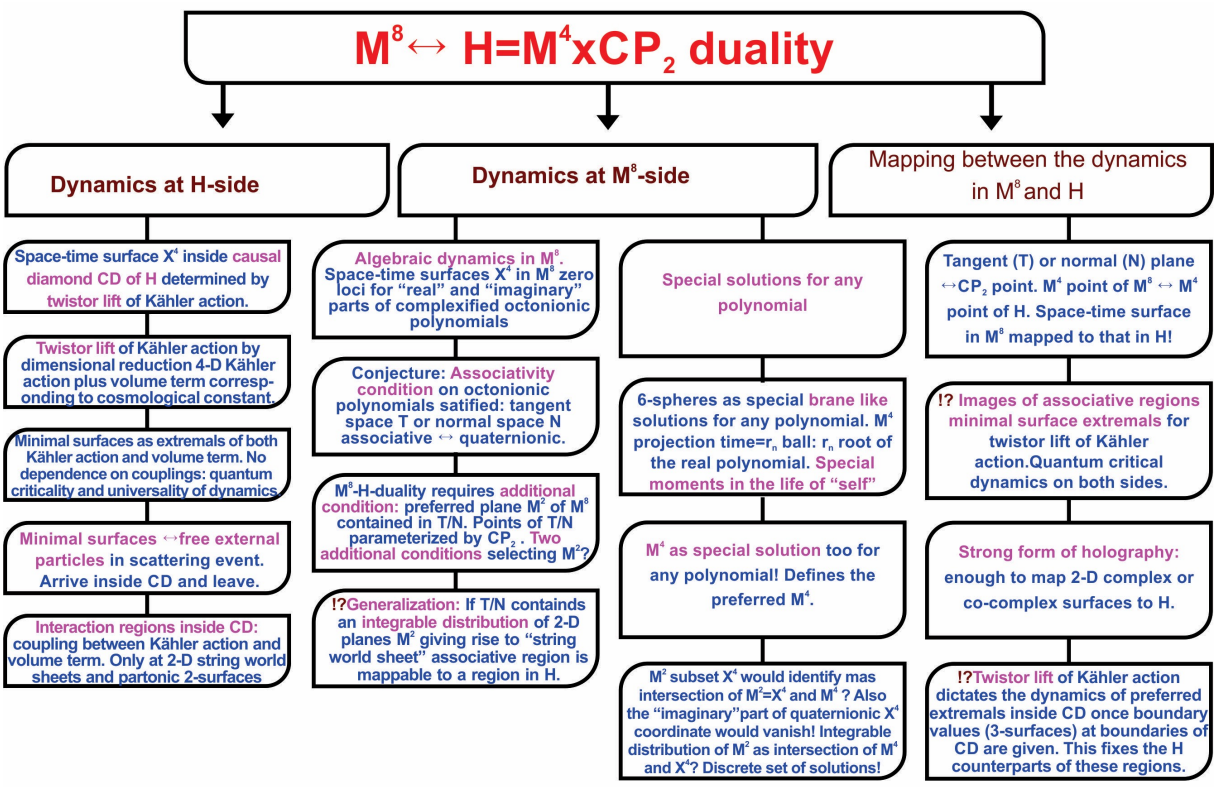


Figure 15: $M^8 - H$ duality

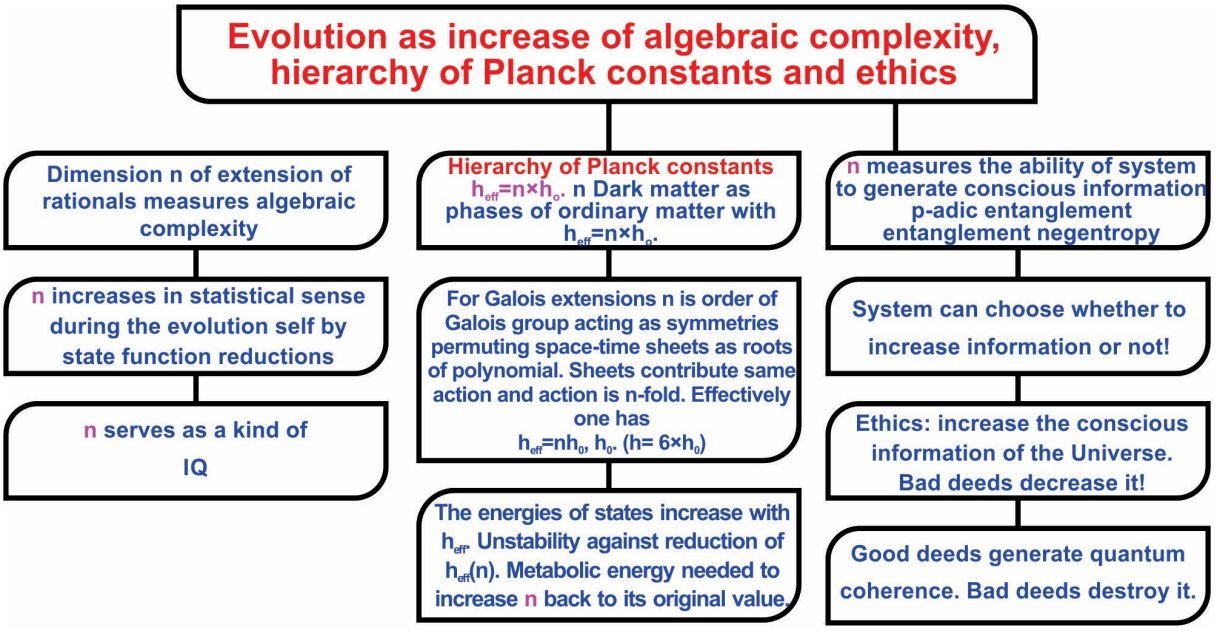


Figure 16: Number theoretic view of evolution

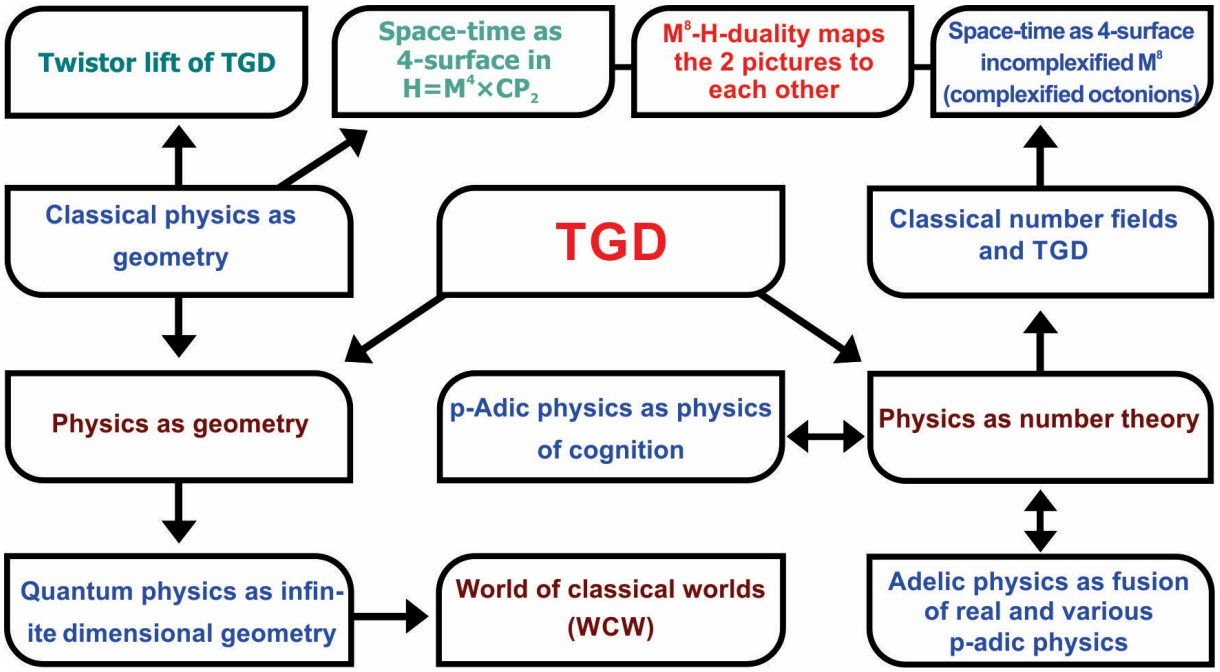


Figure 17: TGD is based on two complementary visions: physics as geometry and physics as number theory.

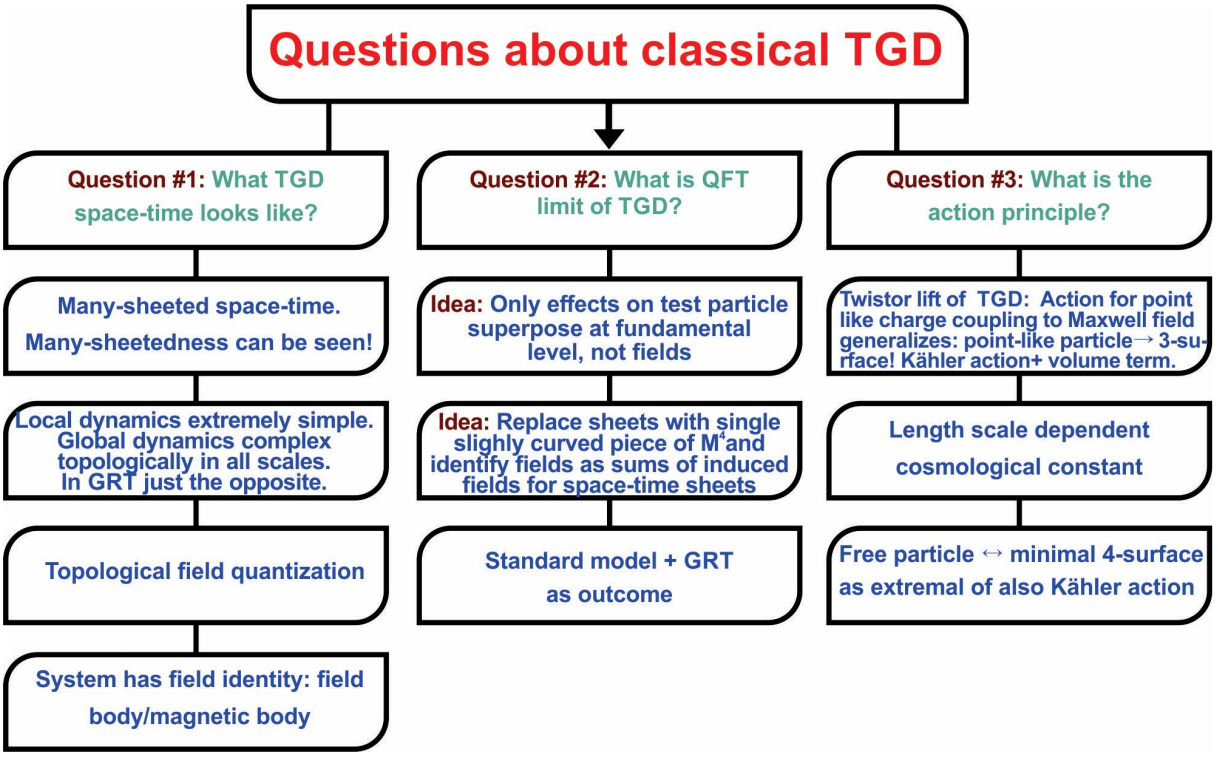


Figure 18: Questions about classical TGD.

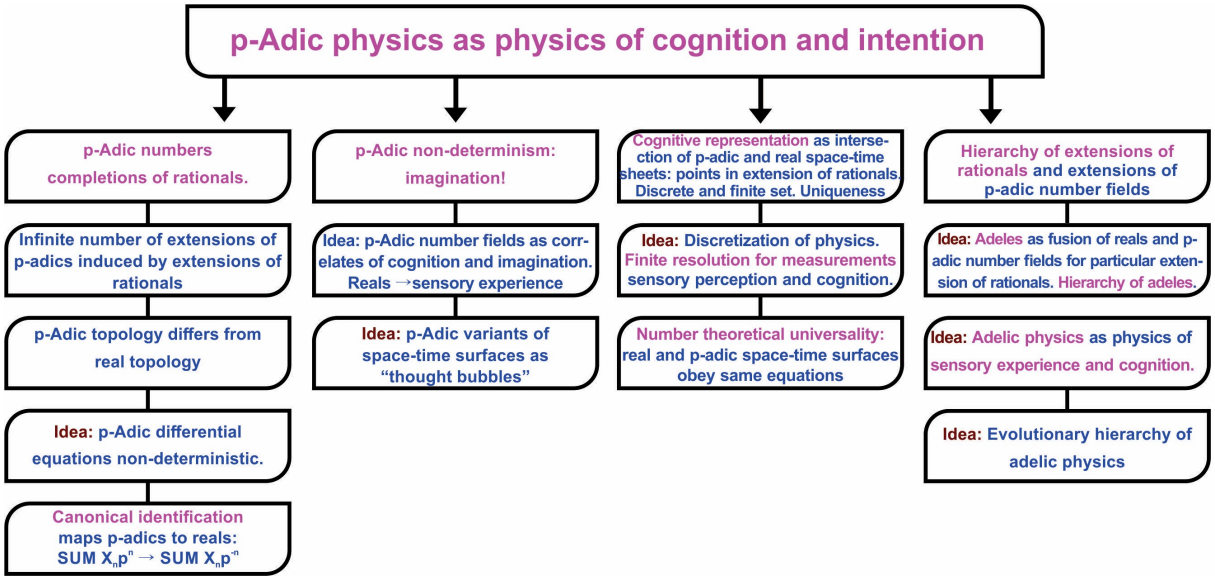


Figure 19: p-Adic physics as physics of cognition and imagination.

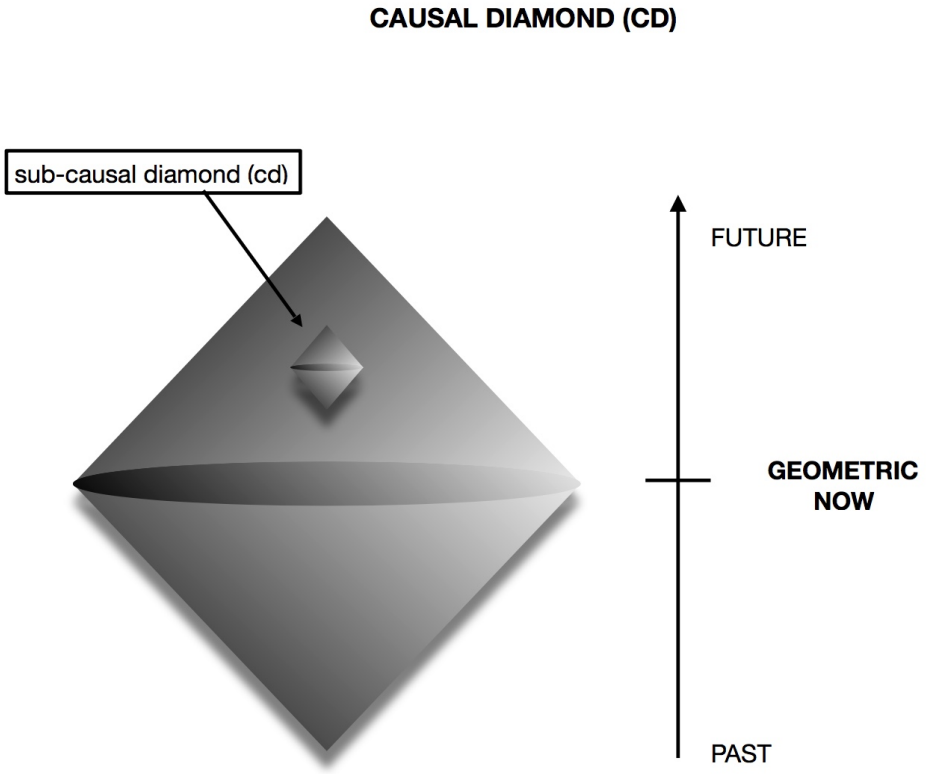
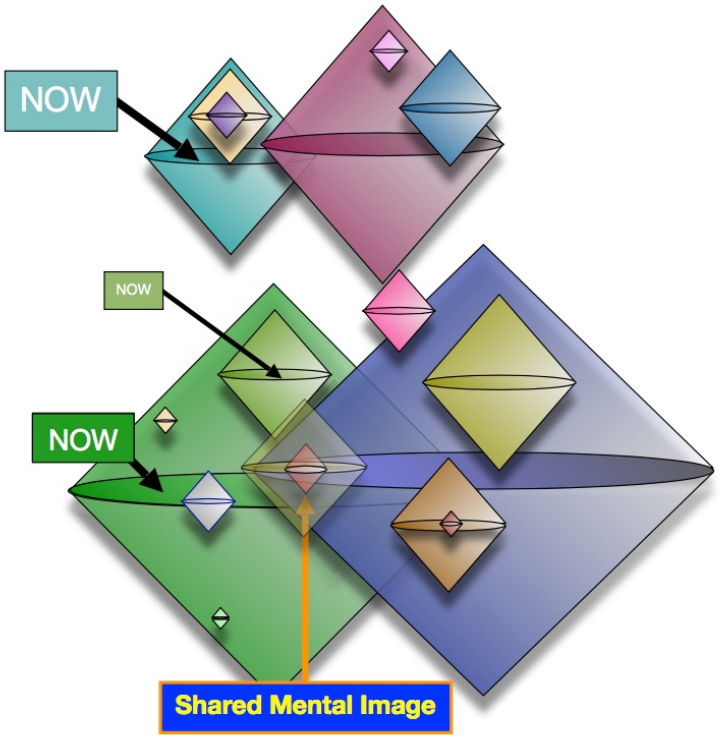


Figure 20: Causal diamond



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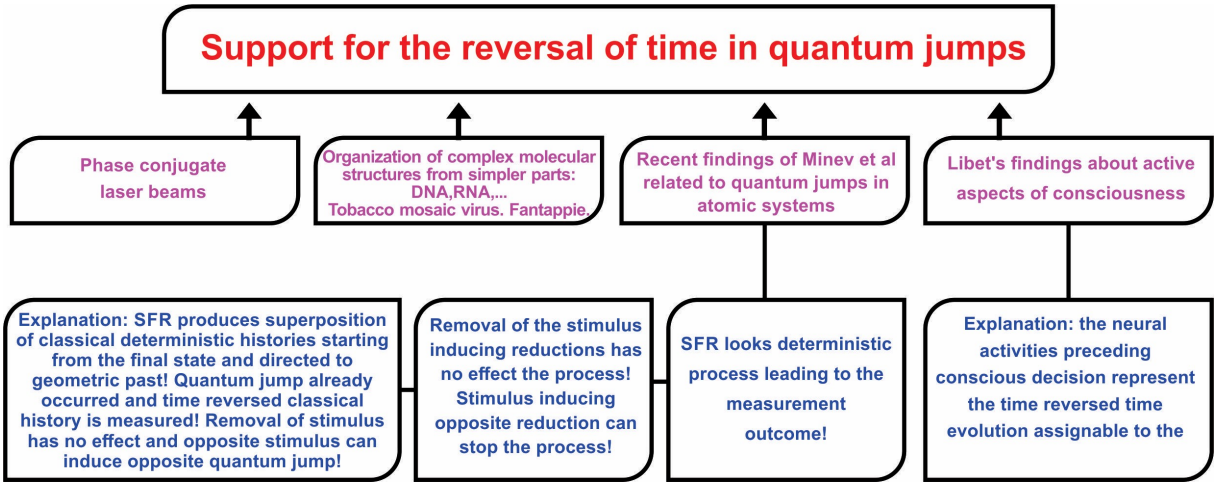

Figure 22: Time reversal occurs in BSFR

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 [A14]. 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 [A1] [B7, B5, B6]), 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 [B4]) 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 [A8, A13, A4, A12].

The identification of the space-time as a sub-manifold [A9, A16] 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 [A15, A18, A20]. 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 [K46]. 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 [K42].

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 [K66].

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 [K58, K59, K56]) 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 [K73]. 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 [A14]. 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 co-incides 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 [L34].

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 [L26]. 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 I"

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

1. The oldest layers in the stratigraphy are the vision about DNA inspired by the notion of many-sheeted space-time and the model of genetic code inspired by the notion of Combinatorial Hierarchy predicting also the existence of what I have called memetic code. The hierarchy would contain at least three levels including the predecessor of genetic code, genetic code, and what I have coined as memetic code. Surprisingly, the idea of memetic code made a comeback quite recently (2023) and might be realized at the level of DNA.

2. The chapter devoted to the notion of many-sheeted DNA represents rather old contributions and the original model is not yet realistic.

3. The discoveries of Peter Gariaev about the interaction of ordinary and laser light with genome combined with the ideas about dark matter and water memory led to a concrete model for the interaction of photons with DNA. One prediction is that it is possible to "see" dark matter by allowing ordinary matter interaction with DNA and Peter Gariaev might have already done this. In this process ordinary photons would transform to dark ones, scatter from dark matter, transform back to ordinary photons and arrive at camera. A second discovery - certainly one of the greatest surprises of my professional life - was an end product

of an attempt to understand the mechanism behind water memory for which rather strong support exists now. The idea was that dark nuclei which sizes zoomed up to atomic size scale could provide a representation of genes. The findings of the group of Luc Montagnier findings suggesting the remote replication of DNA are also discussed.

1.3 Sources

The eight online books about TGD [K77, K74, K62, K49, K11, K47, K32, K68] and nine online books about TGD inspired theory of consciousness and quantum biology [K72, K9, K55, K7, K29, K37, K40, K67, K71] 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 Genes and Memes

In this article basic TGD inspired ideas about genetic code are discussed.

1. Genetic and memetic code from the model of abstraction process

The basic numbers of genetic code are probably not accidental. This led for more than two decades ago to an attempt to construct a model for abstraction process reproducing the basic numbers of the genetic code. The simplest model for an abstraction process is based on a repeated formation of statements about statements starting from two basic statements. If one drops at each step of the construction the statement corresponding to empty set in the set theoretic realization of Boolean algebra, one obtains a hierarchy allowing to understand the basic numbers of genetic code, including the number of amino-acids. What one obtains is so called Combinatorial Hierarchy consisting of the Mersenne numbers $2, M(1) = 3, 7$,$127, 2^{127} - 1, ..$ constructed using the rule $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$. The explicitly listed ones are known to be primes. Combinatorial Hierarchy emerges from a model of abstraction process as subsequent transitions from level to meta level by forming Boolean statements about Boolean statements of level n and dropping one statement away.

The infinite hierarchy of possible genetic codes suggests the possibility of an infinite hierarchy of increasingly complex life-forms. The natural question is whether a counterpart of the genetic code could make sense for our ideas, memes. Combinatorial Hierarchy model for abstraction process predicts that memetic code should correspond to the level M_{127} of the hierarchy. This leads to a precise realization of the memetic code in terms of binary sequences. Codewords, counterparts of mRNA, correspond to 126-bit sequences. Also almost-127-bit code with $2^{127} - 1$ codons is possible.

2. Frequency and pulse representations of codes

p-Adic length scale hypothesis and identification of codes as special cases of a hierarchy of p-adic cognitive codes allows quantitative predictions. The most general assumption assigns to any prime $p \simeq 2^k$, k integer, a hierarchy of cognitive codes with codeword having a duration equal to n-ary p-adic time scale $T_p(n)$ such that the number of bits is factor k_1 of k. Codewords could be realized either as k_1 harmonics of the fundamental frequency $f_p(n) = 1/T_p(n)$ or as temporal sequences of bits of duration $\tau = T_p(n)/k_1$ represented as pulses of maximal duration τ. Pulse-frequency dichotomy corresponds to dichotomies like particle-wave, nerve pulse-EEG, and talking left brain-singing right brain.

Genetic code would correspond to $k = 2^7 - 1 = 127$ and have 6 bits (64 DNA triplets). These codewords could be realized dynamically as temporal field patterns. For genetic code primes $p \simeq 2^k$, $k = 6 \times n$ define candidates for the duration of the genetic code word if all factors of k are assumed to define a possible number of bits of the code word. The time scales come as powers of

8 so that they cover the entire range of biologically relevant time scales down to CP_2 length scale, and genetic code could appear as fractally scaled versions unlike memetic code and perhaps also outside the biological context. $k = 2 \times 126 = 2 \times 6 \times 21 = 252$ allows the representation of both 126-bit memetic codeword, 6-bit genetic codeword, and almost-7-bit genetic code word. For pulse representation genetic codon would have a duration of 50 ms whereas the bit would have duration of 8.3 ms so that the realization using nerve pulse patterns is in principle possible. Frequency representation would be realized as 6 first harmonics of the fundamental frequency $f_1 = 2^n \times 20$ Hz, where $f_1 = 20$ Hz defines the lower end of audible frequency range and also the rate for the translation of mRNA triplets to amino-acids. 126-bit memetic code allows a representation as sequence of 21 nerve pulses of duration 2.4 ms each of them accompanied by 6-bit genetic codon realized at the microtubular level (this representation of genetic code has been suggested by Koruga).

The secondary p-adic time scale associated with M_{127} is .1 seconds and defines the duration of the almost 127-bit memetic codeword. For frequency representation is realized as 127 first harmonics of $f_1 = 10$ Hz and the duration of the bit for pulse representation is .8 ms which is shorter than the duration of nerve pulse. The duration .1 seconds of code word might be identified as the minimal duration of cortical mental images, and the so called features introduced by Walter Freeman could define pulse representation of memetic code words of 127 bits. The highest frequency in the frequency representation is 1270 Hz and could define the frequency responsible for synchronous neuronal firing known to be about 1 kHz. Various numerical co-incidences suggest that language corresponds to a particular realization of memetic and genetic codes closely related to their realization at DNA level.

3. Model for the evolution of genetic code from the symmetries of the code

TGD leads to a model for the evolution of the genetic code motivated by the observation that the genetic code possesses an exact A-G and almost exact T-C permutation symmetry with respect to the third nucleotide of the DNA triplet. This leads to the hypothesis that genetic code has evolved as a fusion of doublet and singlet codes accompanied by a small breaking of the product symmetry. The hypothesis is highly predictive, and it is possible to reproduce genetic code and its variants by this mechanism in a natural manner. The mechanism has deep implications for the models of the bio-chemical evolution before genetic code: in particular a detailed model for the evolution of genetic code and pre-biotic evolution emerges.

4. Mapping memetic code to 169-bit micro-tubular code

169-bit micro-tubular code words is excellent candidate for a representation of long term memories as a temporal list of activated memes. The model for the mapping of memetic code to 169-bit microtubular code is dictated by the general ideas about realization of intentions and p-adic cognitive codes. When combined with general number theoretical arguments and physical considerations the model becomes highly unique. The prediction for the intronic representation of the memetic codon involving 9 DNA triplets as parity bits is readily testable, and also the prediction for the microtubular electric field pattern is in principle testable.

5. Genes, memes, and universal language

Also static representations of the memetic code are possible and intronic DNA could provide representation of memetic codewords as sequences of 21 DNA triplets. At DNA level memes and genes should relate like computer software and hardware. In the case of language the rules producing a given linguistic expression can be seen as the high level software, main programs, whereas words can be seen as hardware-like lower level subprograms. This leads to the idea that memetic codewords define the basic program modules producing linguistic expressions by activating genes which express themselves in terms of field patterns generating nerv pulse patterns generating words or word sequences very much analogous to proteins.

Time mirror mechanism and the structure of the computer language LISP inspire a concrete model for memes as intronic programs initiated from magnetic body and calling genes as subprograms in turn calling other genes as subprograms and generating at the lowest level field patterns generating nerve pulses patterns giving rise to the motor action producing speech. Phonemes could directly correspond to DNA triplets and define the basic building blocks of language having as such no meaning. If this view is correct, the development of spoken and written language would mean basically the emergence of a higher level of intentionality, which utilizes an already existing repertoire of memes expressed in many other manners. This would in turn suggest that animals and even plants possess some kind of languages realized at cellular level, and that even inter-species

communications using common memetic grammar and genetic vocabulary.

6. Corals and men

A strong support for the idea of interspecies communications come from the sensational finding that the genome of corals, known to be the most primitive animals having nervous system, share a large number of common genes with vertebrates whereas they share much less common genes with flies and worms. This finding challenges profoundly the existing view about the evolution of animals and adds a further mystery to the halo of mysteries surrounding Cambrian explosion.

Since corals are usually regarded as relatively simple creatures, the most obvious questions concern the function of the complex genome. The TGD inspired answer is that the common genes provide a common vocabulary making possible communications between corals and vertebrates such as fishes. The genes express themselves in terms of electromagnetic field patterns and cyclotron transitions of Ca_{++} ions giving rise to primitive EEG are crucially involved. The calcium containing skeleton possessed by both corals and vertebrates could amplify the field patterns representing genes and make possible interspecies communications.

Coral reefs can be also seen as super organisms with cells replaced by double cell layers forming the corals. This forces to consider the possibility that coral reefs are super-organisms perhaps even possessing super-neural system consisting of super-neurons defined by differentiated corals. Accordingly, in TGD Universe coral reefs could be seen as descendants of higher level intra-terrestrial life forms which boosted Cambrian explosion by horizontal transfer of genes to much simpler life forms and providing also them with a nervous system.

7. Does ontogeny recapitulate also the future phylogeny at the level of genes and memes?

Ontogeny recapitulates phylogeny means that the morphogenesis of the embryo repeats the evolutionary steps leading to the organism. One might ask whether and how this process is realized at the level of genes and memes (introns expressing themselves electromagnetically): this could provide further understanding of the mysterious "junk DNA". Combining this question with some recent puzzling findings leads to a rather radical revision of the view about evolution proceeding through random mutations.

1. The second strange finding besides coral genome reported in New Scientist (5 June, 2004) was that the removal of large portions of conserved intronic DNA from mice has no detectable effects on the basic biological functions. Conserved parts of DNA are usually thought as being an outcome of a long selection process and far from genetic trash. This could be understood if the conserved introns have been radiated from corals and the selection process has occurred already before the Cambrian explosion induced by the emergence of the corals and leading to the sudden emergence of new highly developed life forms. That mouse introns did not have any identifiable function could mean that they are still waiting for time to become ripe for their expression.

2. A third strange discovery relates to morphogenesis and is known as Ciba Geigy effect. Chemists Guido Ebner and Guido Schuerch exposed germs, seeds, and eggs to an electric field with strength in the range .5-2 kV/m. For instance, the resulting trouts appeared to resemble their ancient predecessors. The leaves of certain plants represented a series of snapshots from evolution with the oldest leaves dating back to 300 million years. This suggests that the memone and genome represent ontogeny recapitulates phylogeny principle quite concretely, and that static electric fields could provide the practical manner to activate and study the ancient morphologies. Even partial transmutation of life forms to each other might be possible (beautiful swan to ugly duckling at least!). The activation of morphologies not yet realized is probably more difficult: new memetic programs require new genetic hardware.

The resulting vision about evolution of higher organisms would be as the activation of conserved memes and genes basically inherited from corals rather than by the emergence of new genes by random mutations. Very much like learning new features of a text processing program. The explosive evolution of human civilization could correspond to a rapid shift of the activated portion of memone and genome. The fact that 95 per cent of our DNA consists of introns suggests that an enormous evolutionary potential exists also at the level of personal evolution during single life cycle. TGD view about space-time as a 4-dimensional living organism would mean that this personal evolution continues after the biological death since the 4-body of geometric past does not disappear in the biological death.

1.3.2 Many-Sheeted DNA

The problems of how genes code information about the morphology of organism and how this information is expressed, belong to the great puzzles of the developmental biology. A closely related mystery is the differentiation of cells. The notion of the genetic program is far from precise and it is not clear how close the analogy with a computer program is. There are also several problems which challenge the basic dogmas of genetics.

1. Only 1 per cent of DNA of human genome actually codes polypeptides. Eukaryote genes contain intron sequences which are transcribed into hnRNA but snipped of when hnRNA is transformed mRNA in process called slicing. The higher the evolutionary level of organism, the higher the fraction of introns is. Molecular Darwinists see introns as "junk DNA" but there is evidence that introns are far from junk. For instance, the splicing of intron contribution from hnRNA to give mRNA can give several different outcomes depending on the stage of development of the organism and introns are crucial for the effectiveness of immune system. Hence one can wonder whether intronic mRNA and protein mRNA could both form the real output of gene subprograms serving in some sense as input for other gene subprograms. This interpretation obviously conflicts with "gene-single protein" dogma in its basic form.

2. There are large amounts of highly repetitive DNA which is silent. One can wonder whether there is some fundamental mis-understanding involved. Could it be that this DNA is analogous to control DNA not transcribed to RNA and therefore not all useless. There is also active repetitive DNA.

3. There is large amount of silent DNA in control sections between genes. Could it be that this silent DNA expresses itself in some nonchemical manner? Chemical expression is very slow, translation rate being twenty aminoacids per second, and one can wonder whether life might have invented faster modes of gene expression and control of gene expression.

4. Plant genome is often by a factor of hundred longer than human genome. One could argue that the complexity of organism is measured by the length of the shortest program coding the organism. It is however not at all obvious how the genome of plants could be more redundant than human genome since repetitive sequences common to all animals are present. Introns are in fact more frequent in human genome. This suggests that some new unidentified degrees of freedom giving rise to complexity might be present and that the chemistry of DNA in the sense of standard physics is perhaps not all that is needed to understand genetic program.

5. Various self-organization processes such as self-assembly and de-assembly are very frequent in living systems. The problem how genes give rise to morphology of the organism is poorly understood. This forces to challenge the dogma of genetic determinism. One should be able to understand what is determined by genes and what is determined by self-organization and whether the genes of the standard physics are enough.

The reason why the above mentioned problems have turned out to be so untractable might be due to a wrong view about space-time. Many-sheeted space-time concept of TGD might be absolutely crucial for the expression of genetic code. Gene itself might be many-sheeted space-time structure coding faithfully the topology of the expression domain of gene. This many-sheeted structure of DNA could allow to understand the miraculous looking features of DNA replication and cell differentiation. TGD based view of evolution as p-adic evolution implied by the basic quantum theory, should be a crucial element of the picture. Together with p-adic length scale hypothesis, with Combinatorial Hierarchy model for genetic code allowing to interpret genes as Boolean statements, and general vision about quantum control and coordination based on a hierarchy of weakly coupled super conductors, the notion of many-sheeted DNA leads to precise quantitative predictions and a general model for genetic program. In particular, one can understand the mystery of introns. What interesting from the point of view of our consciousness is that it might be possible to interpret the Boolean statements represented by the exon and intron parts of genes as a physical representation for our belief system. Thus genes would code both matter– and mind like hardware of the living system.

The notion of magnetic body is central in the TGD inspired theory of living matter. Every system possesses magnetic body and there are strong reasons to believe that the magnetic body associated with human body is of order Earth size and that there could be hierarchy of these bodies with even much larger sizes. Therefore the question arises what distinguishes between the magnetic bodies of Earth and human body.

The vision about dark matter hierarchy labelled partially by a hierarchy of values of effective Planck constant coming as integer multiples of the ordinary Planck constant leads to a rather concrete view about the hierarchy of magnetic bodies and implies a natural generalization leading to the notion of super- and hyper genes. The original model assumption $\hbar_{eff} = \lambda^{k_d}\hbar_0$, $\lambda \simeq 2^{11}$, is however un-necessarily strong.

Super genes consist of genes in different cell nuclei arranged to threads along magnetic flux sheets like text lines on the page of book whereas hyper genes traverse through genomes of different organisms. Super and hyper genes provide an enormous representative capacity and together with the dark matter hierarchy allows to resolve the paradox created by the observation that human genome does not differ appreciably in size from that of wheat.

1.3.3 Model for the Findings about Hologram Generating Properties of DNA

A TGD inspired model for the strange replica structures observed when DNA sample is radiated by red, IR, and UV light using two methods by Peter Gariaev and collaborators. The first method produces what is tentatively interpreted as replica images of either DNA sample or of five red lamps used to irradiate the sample. Second method produce replica image of environment with replication in horizontal direction but only at the right hand side of the apparatus. Also a white phantom variant of the replica trajectory observed in the first experiment is observed and has in vertical direction the size scale of the apparatus.

A model is developed in order to explain the characteristic features of the replica patterns. The basic notions are magnetic body, massless extremal (topological light ray), the existence of Bose-Einstein condensates of Cooper pairs at magnetic flux tubes, and dark photons with large value of Planck constant for which macroscopic quantum coherence is possible. The hypothesis is that the first method makes part of the magnetic body of DNA sample visible whereas method II would produce replica hologram of environment using dark photons and produce also a phantom image of the magnetic tubes becoming visible by method I. Replicas would result as mirror hall effect in the sense that the dark photons would move back and forth between the part of magnetic body becoming visible by method I and serving as a mirror and the objects of environment serving also as mirrors. What is however required is that not only the outer boundaries of objects visible via ordinary reflection act as mirrors but also the parts of the outer boundary not usually visible perform mirror function so that an essentially 3-D vision providing information about the geometry of the entire object would be in question. Many-sheeted space-time allows this.

The presence of the hologram image for method II requires the self-sustainment of the reference beam only whereas the presence of phantom DNA image for method I requires the self-sustainment of both beams. Non-linear dynamics for the energy feed from DNA to the magnetic body could make possible self-sustainment for both beams simultaneously. Non-linear dynamics for beams themselves could allow for the self-sustainment of reference beam and/or reflected beam. The latter option is favored by data.

1.3.4 Quantum Model for Remote Replication

A model for remote replication of DNA is proposed. The motivating experimental discoveries are phantom DNA, the evidence for remote gene activation by scattered laser light from similar genome, and the recent findings of Montagnier's and Gariaev's groups suggesting remote DNA replication.

Phantom DNA is identified as dark nucleon sequences predicted by quantum TGD with dark nucleons defining naturally the analogs of DNA, RNA, tRNA, and amino-acids and realization of vertebrate genetic code. The notion of magnetic body defining a hierarchy of flux quanta realize as flux tubes connecting DNA nucleotides contained inside flux tubes connecting DNA codons and a condensed at flux sheets connecting DNA strands is an essential element of the model.

Dark photons with large value of Planck constant coming as integer multiple of ordinary Planck constant propagate along flux quanta connecting biomolecules: this realizes the idea about wave DNA. Biomolecules act as quantum antennas and those with common antenna frequencies interact resonantly.

Biomolecules interacting strongly - in particular DNA nucleotides- would be characterized by same frequency. An additional coding is needed to distinguish between nucleotides: in the model for DNA as topological quantum computer quarks (u,d) and their antiquarks would code for the nucleotides A,T,C, and G would take care of this. The proposed role of quarks in biophysics of course makes sense only if one accepts the new physics predicted by quantum TGD. DNA codons (nucleotide triplets) would be coded by different frequencies which correspond to different values of Planck constant for photons with same photon energy propagating along corresponding flux tubes. This allows to interpret the previously proposed TGD based realization of so called divisor code proposed by Khrennikov and Nilsson in terms of quantum antenna mechanism. Years later from this proposal a much more detailed mode emerged leading to a formula for $h_{eff} = n \times h$ making h_{eff} proportional to the mass (number) of the charged particle involved. This predicts universal energy spectrum for dark photons in the range of visible and UV photons. Dark photons can transform to ordinary ones in energy conserving manner and the outcome is identified as biophotons.

In this framework the remote replication of DNA could be understood. DNA nucleotides interact resonantly with DNA strand and attach to the ends of the flux tubes emerging from DNA strand and organized on 2-D flux sheets. In Montagnier's experiment the interaction between test tubes A and B would be mediated by dark photons between DNA and dark nucleon sequences and amplify the dark photon beam, which in turn would induce remote replication. In the experiment of Gariaev scattered laser light would help to achieve the same purpose. Dark nucleon sequences would be generated in Montagnier's experiment by the homeopathic treatment of the test tube B.

Dark nucleon sequences could characterize the magnetic body of any polar molecule in water and give it a "name" written in terms of genetic codons so that genetic code would be much more general than usually thought. The dark nucleon sequence would be most naturally assigned with the hydrogen bonds between the molecule and the surrounding ordered water being perhaps generated when this layer of ordered water melts as the molecule becomes biologically active. Water memory and the basic mechanism of homeopathy would be due to the "dropping" of the magnetic bodies of polar molecules as the water is treated homeopathically and the dark nucleon sequences could define an independent life form evolving during the sequence of repeated dilutions and mechanical agitations taking the role environmental catastrophes as driving force of evolution. The association of DNA, RNA and amino-acid sequences associated with the corresponding dark nucleon sequences would be automatic since also also they are polar molecules surrounded by ordered water layers.

The transcription of the dark nucleon sequences associated the with the polar invader molecule to ordinary DNA sequences in turn coding of proteins attaching to the invader molecules by the quantum antenna mechanism could define the basic mechanism for functioning and evolution of the immune system.

Chapter 2

Genes and Memes

2.1 Introduction

In TGD based model of consciousness genes and memes are in very similar position. The quantum self-organization process explains genetic code as an outcome of Darwinian selection basically carried out by dissipation, and also memes should be subject to similar selection. Cognitive codes would be for neuroscience what genetic code is for biology. Hence there are good motivations to guess what the precise form and realization of these codes might be if it really exists. In fact, p-adic length scale hierarchy suggests an entire fractal hierarchy of cognitive codes with quantized durations of the codeword and preferred numbers of bits per code word [**?**] . There exists however some preferred cognitive codes. A simple model for abstraction process leads to an entire hierarchy of genetic codes and one of them explains the basic numbers of the genetic code. A fascinating possibility is that the next level in the hierarchy yields memetic code and also this possibility will be studied in the sequel. Genetic and memetic codes represent particular examples associated with Mersenne primes $p = 127 = 2^7 - 1$ and $p = M_{127} = 2^{127} - 1$.

2.1.1 Combinatorial Hierarchy Of Codes

The basic numbers of genetic code are probably not accidental. This led for more than ten years ago to an attempt to construct a model for abstraction process reproducing the basic numbers of the genetic code.

Genetic code from a model for abstraction process

The simplest model for an abstraction process is based to a repeated formation of statements about statements starting from two basic statements representing the most primitive logical thoughts. If one drops at each step of construction the statement corresponding to empty set in the set theoretic realization of Boolean algebra, one obtains a hierarchy allowing to understand the basic numbers of genetic code.

The outcome is the so called Combinatorial Hierarchy [A10] consisting of the Mersenne numbers $2, M(1) = 3, 7, 127, 2^{127} - 1, ..$ constructed using the rule $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$. The explicitly listed ones are known to be primes. Combinatorial Hierarchy emerges from a model of abstraction process as sub-sequent transitions from level to meta level by forming Boolean statements about Boolean statements of level n and dropping one statement away. Combinatorial Hierarchy results also by constructing the sets of all subsets with empty set excluded starting from two element set. The set of statements at level n can be given a structure of Finite Field $G(M(n), 1)$ if $M(n)$ is prime. The multiplicative groups $Z_{M(n)-1}$ form a nested hierarchy and the coset spaces $Z_{k_n} \equiv Z_{M(n)-1}/Z_{M(n-1)-1}$ are cyclic groups ($k_n = (M(n) - 1)/(M(n - 1) - 1)$). Hilbert's conjecture states that each Mersenne number in the Combinatorial Hierarchy is prime.

Combinatorial Hierarchy based model of genetic code explains the number of DNAs and amino-acids, and the representation of words of the genetic code as triplets of 4 different lower level codewords. Genetic code corresponds to $n = 3$ level of the hierarchy with 127 statements representable as 7-bit sequences with the sequence of seven "0":s dropped away. Only the 64 6-bit

code words can be fully realized and correspond to $(M(3)+1)/2 = 64$ DNA triplets. $k_3 = 126/6 = 21$ equals to the number of amino-acids plus stopping codon. There is a natural imbedding of subgroup Z_{21} identifiable as a representation of amino-acids to the group $Z_{126=6\times 21}$.

More abstractly, at level n the counterparts of DNA triplets correspond to the set $X_{N(DNA)} \subset Z_{M(n)-1}$ of $N(DNA) = (M(n)+1)/2$ statements consistent with a fixed atomic statement (64 for $n = 3$). Atomic statement corresponds to a fixed value, assumed to be one, of a fixed bit in a bit sequence representation and a subset consisting of single element in the set theoretic representation. These statements could be regarded as statements consistent with the axiom defined by the selection of the atomic statement. The counterparts of amino-acids and stopping codon correspond to k_n theorems of a formal system defined by n^{th} level of Combinatorial Hierarchy having a unique imbedding as the group $Z_{k_n} \subset Z_{M(n)-1}$. The DNAs coding for a given "amino-acid" correspond to the special cases of the theorem.

Mapping of DNA code words to amino-acids generalizes to the mapping $x \to x^{k_{n-1}}$ in $Z_{M(n)-1}$ mapping DNA type statements to amino-acid type statements. $(M_(n)+1)/2$ DNAs can be imbedded to Z_{126} with several way. Genetic code is fixed ones this imbedding is given. For $n = 3$ one obtains ordinary genetic code defined by the map $x \to x^6$ and imbedding of the DNAs to Z_{126}. The numbers of DNA:s coding single amino-acid can be reproduced by a symmetry breaking mechanism involving the finite groups $Z_{p_{n-1}}$ and Z_{k_n} and symmetry breaking is in a well defined sense minimal. The infinite hierarchy of possible genetic codes (at least if Hilbert's conjecture holds true) suggests the possibility of an infinite hierarchy of increasingly complex life forms.

If one allows only Mersenne primes, the model for the abstraction process predicts at least one further code, which I have used to call memetic code. It corresponds to the Mersenne prime $M_{127} = 2^{127} - 1$ and has 2^{126} code words and $(2^{126} - 1)/(2^6 - 1)$ "amino-acids". The secondary p-adic time scale $T(2, M_{127})$ is .1 seconds and defines a fundamental time scale in bio-systems.

There are reasons to expect that memetic code is an especially interesting higher level cognitive code and realized in terms of field patterns. In particular intronic portion of DNA could realize memetic codewords as sequences of 21 DNA triplets and memes would define the counterparts of computer programs at DNA level whereas genes would define the counterpart of computer hardware coded into lower level programs and built only when needed. Both memes and genes could express themselves in terms of field patterns.

Memes and genes should relate like computer software and hardware. In the case of language the rules producing a given linguistic expression can be seen as the software whereas words can be seen as the hardware built from phonemes. This leads to the idea that memetic codewords define the basic program modules producing linguistic expressions by activating genes which express themselves as words or word sequences. Phonemes could directly correspond to DNA triplets and define the basic building blocks of language having as such no meaning. If this view is correct, the development of spoken and written language would mean basically the emergence of a higher level of intentionality, which utilizes an already existing repertoire of memes already expressed in many other way. This would in turn suggest that animals and even plants possess some kind of languages realized at cellular level, and that even inter-species communications using common memetic vocabulary.

Myth about Fall of Man as metaphor for codes

There are basically two genetic and memetic codes: 6-bit and almost-7-bit ($2^3 - 1$ code words represented consciously) genetic codes and 126- and almost-127 bit memetic codes. The myth about the Fall of Man provides a little bit tongue-in-cheek metaphor for the extension of 126-bit code to almost-127-bit code. God gave to Adam and Eve the moral code as a single moral law formulated as an atomic statement "Do anything but do not eat from the Tree of Good and Bad Knowledge". Adam and Eve of course did this and probably as many fractally scaled versions.

The first Fall occurred probably already at the molecular level and meant the replacement of 6-bit genetic code with almost-7-bit code: $63 = 9 \times 7$ sins beside 64 good deeds appeared (there are 9 classes of sins containing one sin for every day of the week, one of them containing the seven deadly ones!). Imagination and intentions realized as deeds emerged and Adam and Eve became moral agents. For the memetic code the replacement of 126-bit memetic code led to almost 127-bit code and the repertoire of good and bad deeds was now much more impressive: 2^{126} good deeds and $2^{126} - 1$ sins (the basic classification sins to 7 basic types makes senses still!). One can of

course wonder what was this un-doable sin with strong Gödelian flavor. A code word with only zeros cannot give rise to a conscious experience. Hence the un-doable sin could be such that the sinner cannot experience its consequences in this life, that is suicide.

Genetic code and thinking at DNA level

TGD predicts entire infinite hierarchy of selves starting from elementary particle level so that consciousness should be present also at DNA and protein level. The notion of self indeed allows to understand protein folding, which is rather mysterious phenomenon in standard physics framework.

The physical model of the genetic code constructed in [K38]. when interpreted in terms of the model for an abstraction process, suggests the interpretation of the genetic code as mapping the fundamental 64 truths to 20 basic conscious experiences, perhaps the protein level emotional experience about truth-ness: it must be emphasized that our experiences are probably not in question. Amino-acid P could correspond to the emotionally experienced truth "$G_1(P)$ or $G_2(P)$.. or $G_n(P)$ is true", where G_i code for protein P. 3 stopping sign codewords cannot be experienced emotionally as truths not non-truths (holy trinity at protein level!).

In the model for introns discussed in the chapter [K38] fermionic realization of Boolean statements plays an essential role in the genetic program of eukaryotes and suggests that Boolean mind appears already at molecular level and could correspond to the logical statements represented by genes. This Boolean mind does not correspond to our conscious logical thinking.

Does memetic code emerge at the next level of abstraction process?

The natural question is whether a counterpart of the genetic code could make sense for memes. Combinatorial Hierarchy model for abstraction process that memetic code should correspond to the level M_{127} of the hierarchy. This leads to a precise realization of the memetic code in terms of binary sequences. The secondary p-adic time scale associated with M_{127} is .1 seconds, which seems to define the duration for the immediate subjective memory. If this time scale corresponds to a sequence consisting 127 bits, the duration of single bit is 1/1270 seconds, which happens to be very near to definite p-adic time scale but is somewhat shorter than the typical duration of nerve pulse. This suggests that nerve pulse patterns as such cannot realize the full memetic code. The time scale associated with $k = 252 = 2 \times 6 \times 21$ is.05 seconds and one half of the duration of 127-bit memetic codon. $k = 252$ allows the representations of both 6- and 7-bit genetic codes and of the 126-bit memetic code.

An attractive hypothesis is that the temporal sequences for the Z^0 magnetization directions for a block cognitive antineutrinos at cell membrane space-time sheet provide a representation of the almost 127-bit memetic codeword. The conscious experience results when the Z^0 magnetization directions flip back to the direction of external Z^0 magnetic field in spin flipping cyclotron transition. $M_{127} = 2^{127} - 1$ different conscious experiences results since nothing happens if all cognitive antineutrinos are in the same direction as external Z^0 magnetic field. Z^0 magnetization direction could be altered by the Z^0 magnetic pulse associated with the Z^0 ME inducing cell membrane oscillations of nerve pulse pattern.

This raises obvious questions. Does genome have a memetic counterpart; what would be the function of the memone; what would be the memetic counterparts of the transcription and translation processes for genes? The natural guess is that memes are the basic building blocks of cognition and language. Perhaps also memes are coded by DNA, most naturally by introns, whose portion from the genome increases with the evolutionary level of organism and is 99 per cent for Homo Sapiens. The sequences of 21 DNA triplets would naturally realize 126-bit memetic codons 2^{126} memetic codons at DNA level. The prediction is that the intronic portions of the genome should consist of basic units containing 21 DNA triplets. This would also mean that the language conscious-to-us is only a tip of an iceberg. The intronic part of the DNA would be expressed in terms of MEs and involve communications between cell membrane and nucleus. The dynamics of this realization would be fast and nucleus would play the role of cellular brain.

2.1.2 The Product Model For The Evolution Of Genetic Code

It became as a surprise to me personally that the genetic code has an exact A-G permutation symmetry and an almost exact T-C permutation symmetry with respect to the third nucleotide.

Seen with the eyes of a theoretical physicist knowing the enormous importance of spontaneous symmetry breaking in physics, these simple symmetries point the way to the understanding of the basic mechanism behind the evolution of the genetic code.

This inspired a simple model for our genetic code allowing to see the genetic code as a product of much simpler doublet and singlet codes with a small symmetry breaking due to the interaction between singlets and doublets. This model, even admittedly rather formal, might have deep implications for the theories how the life at the molecular level has involved. The physical realization of this model will be also discussed briefly. A detailed discussion can be found in [**?**].

2.1.3 General Ideas About Codes And Languages

By quantum-classical correspondence space-time sheets provide a symbolic representation for the contents of consciousness. Therefore one can say that everything in principle represents and the task is to understand how these symbolic representations are generated, how codes are established, and how these symbolic representations generated the desired mental images. This obviously means a profound departure from the basic belief system of standard biology.

Computer languages form a hierarchy such that highest level languages are very flexible approaching gradually to the spoken language whereas lowest level languages are very precise and rigid. The notion of self hierarchy suggests that our spoken language is only a top of an iceberg and that below it is a hierarchy of languages ending down to the cellular level and DNA is one particular example about "computer language" realized in terms of p-adic cognitive codes, in particular genetic and memetic codes. In an attempt to understand whether and how memetic and other p-adic cognitive codes might relate to the spoken and written language one must have some general ideas codes and language.

The hierarchy of cognitive codes

p-Adic length scale hypothesis suggests an entire hierarchy of cognitive codes and languages. The primes $p \simeq 2^k$, k integer seems to be interesting physically, and prime values of k seem to be especially interesting. The codes would be characterized by the duration of the codeword given by n-ary p-adic time scale $T_p(n) = p^{(n-1)/2}T_p$, $T_p = 2^{k/2-127}T(2,127)$, $T(2,127) = .1$ seconds. The most general assumption is that number k_1 of bits of the codeword for given integer k_1 corresponds to some factor of k, the largest factor maximizing the information content. Codes could be represented either as temporal sequences of bits represented as pulses of maximal duration $T_p(n)/k_1$ or as superpositions of k_1 harmonics of $f_1 = 1/T_p(n)$, where Fourier components having intensity above/below critical value would represent bit 1/0. These representations will be referred to as pulse and frequency representations. Frequency representations would be realized in terms of topological light rays ("massless extremals", MEs) representing topologically quantized transverse radiation and pulse representations in terms of scalar wave pulses not possible in Maxwell's electrodynamics [K25]. This representational dichotomy reflects particle-wave duality and talking left brain and singing right brain dichotomy.

Memetic and genetic codes represent special examples of cognitive codes. One must distinguish between two representations: the representations involving 6 bits or almost 7 bits and 126 bits or almost 127 bits. "Almost" means that only $2^k - 1$ bit sequences rather than all 2^k bit sequences are realized as conscious bits if bits are realized as phase transitions.

Codes are always involved with classical communications involving transformation of mental images to a symbolic representation by some code. At our level of the hierarchy this symbolic representation could be speech, written language, picture, body language... This would suggest that also p-adic cognitive codes are involved with conscious communications. If these codes are realized in living systems, the bit sequences with the predicted durations and bit contents should induce biological effects serving as correlates for the conscious understanding of the message generated by the codewords at some level of the hierarchy.

TGD based view about living matter relies on the notion of field body or magnetic body associated with any system and having size much larger than the material body. Also these bodies form a fractal hierarchy. The communications from material body to field body could be based on cognitive codes. Given p-adic frequency corresponds f_p to a p-adic length scale $L_p = c/f_p$ characterizing the size of the magnetic body involved and for EEG frequencies the size scale of

Earth is natural unit. For instance, p-adic cognitive codes realized in terms of field patterns would be involved with the communication of long term declarative memories from the geometric past.

What language is?

The attempt to understand the possible role of memetic code, a rough vision about what language is, allows to eliminate several ideas which look promising at first.

1. Language involves generation of symbolic representation of a mental image by a more or less rigid code. An example of a very flexible code is code based on associations. The symbolic representation of mental image should induce in the receiver the original mental image as faithfully as possible. This requires that a lot of common context. In particular, the neurologies and biologies of the sender and receiver must resemble each other sufficiently. In the case of high level languages like ordinary language even this is not enough and only simplest verbal signals and body language are understood universally. The cognitive codes associated with say cell level communications might make possible communications between cells of even different species remaining however unconscious to us.

2. The p-adic vision about evolution of cognitive skills like spoken language is that they evolve from long time and length scales to shorter ones. First a rough sketch about the motor action is created and gradually more and more details are added. This applies also at the level of the evolution of language itself. Simple signals expressing and generating emotions evolve gradually to spoken language which evolves to written language which in turn evolves to computer languages.

3. Learning of language requires learning of the conventions assigning to a given symbol a mental image. Sharing of mental images which represent more primitive "telepathic" communication makes possible this process. The observation that even plants and cells can react to our emotions and that this reaction does not depend much on distance [J6]. suggest that the sharing of mental images is in question. This allows to consider the possibility of inter-species linguistic communications using field patterns.

4. The understanding of language requires transformation of symbolic representation to conscious experience and here the notion of conscious bit ("cbit" [K48]) realized as a phase transition or as an absence of phase transition suggests itself. Phase transition could correspond to magnetization or formation of electret state and living matter could generate these representations in various length scales.

5. In TGD Universe intentions are realized as actions by a process, which proceeds from the magnetic body downwards along the hierarchy much like a desire of a boss of some institution to the lower levels of hierarchy. At each level intention or intentions are transformed to desires communicated to the lower levels of hierarchy. Intentions have p-adic space-time sheets as space-time correlates and are transformed to real ones representing the desire.

The most plausible realization of this process is in terms of time mirror mechanism. The space-time sheets in question would correspond to negative energy topological light rays representing the propagation of signals to the geometric past and induce processes. The process would continue down to the level of neurons and even DNA level and generate the desired action as a reaction to the resulting complex of desires. The beauty of the mechanism is that the communication to the geometric past makes it instantaneous.

Spoken and written language would rely on the same process and could propagate down to the level of genome and select the memes to be expressed. The expression of these memes as field patterns would then be a process propagating upwards in the hierarchy and finally generating speech or written word. When I decide to say something say the words "time mirror", this intention is transformed to a desire communicated to the geometric past to the lower level of the self hierarchy, and that at this level this desire generates further desires communicated to the lower levels. Ultimately this process ends down to the level of cells and even cell nuclei and DNA and induces response which propagates to the higher levels as neural and other activities inducing muscular activities in speech organs and generates the words "time mirror".

The signal to the geometric past involves negative energy photons and topological light rays. The working hypothesis has been that the signal to the geometric past is only a space-time correlate for sharing of the desire to generate the action, and does not involve any code. If this is the case then only the response propagating to the geometric future would be classical signal based on some code. One must however keep mind open to the possibility that also communications to the geometric past involve code.

Conscious bits and cognitive representations

The symbols representing message must be transformed to standardized mental images. The simplest possibility is that the mental images are coded to patterns of conscious bits or cbits. The general model for sensory and other qualia suggests that conscious bits should be realized as quantum jumps sequences associated with phase transitions. In this ways same quantum number increment is occurs for many particle for single quantum jump and for sufficiently long sequence of quantum jumps. Bit 1 would correspond to the occurrence of phase transition and bit 0 to the non-occurrence of the phase transition. For a code of k bits this has important implication: the codeword containing only zeros does not generate any conscious experience so that the number of experienced code words is $2^k - 1$. This could explain why Mersenne primes seem to be define especially important p-adic time scales.

Living matter is populated by dynamical electrets so that phase transitions between ordinary and electret states at various length scales are expected to be of special importance. Also magnetization of super phases at magnetic flux tubes of say Earth's magnetic field is expected to be one mechanism producing basic qualia serving as as bits.

Computer metaphor at DNA level

Software and hardware are essential elements of the computer and at DNA level this could mean that genes code for hardware which is not stable as in case of ordinary computers. This means that computer hardware is replaced by the possibility to generate it and genes carry the information needed for this. Introns would in turn represent the software, the programs and therefore also the linguistic aspect of DNA. An interesting possibility is that introns realize memes as sequences of 21 DNA triplets. This picture allows and even suggests that even DNA level might be involved with the generation of spoken words and define the deep structure of language.

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` [L16].

2.2 Combinatorial Hierarchy And Genetic Code

It is already found that Combinatorial Hierarchy emerges as a unique hierarchy of mappings of Boolean thoughts to association sequences, which could perhaps correspond to nerve pulse patterns, or more probably, to temporal field patterns. In the following the connection of Combinatorial Hierarchy with genetic code is demonstrated.

2.2.1 Combinatorial Hierarchy As A Model For Abstraction Process

One could view the development of intelligence as a process, which takes place as sub-sequent transitions from hierarchy level to a higher hierarchy level, meta-level. First there are statements about concrete things, say numbers. Then come the statements about statements (say theorems about theorems of number theory): "If theorem A is true then theorem B is true". Then come the statements about statements about...

What is remarkable is that the so called Combinatorial Hierarchy [A10] (which emerged first in particle physics context) results from this kind of gradual abstraction process consider Z_2 valued functions. The value 1 might correspond to "true" and 0 to "not true".
i) Assume that lowest level corresponds to 2 statements.
ii) Go to the meta level and consider statements about statements (theorems about theorems in mathematics). Therefore one must consider Z_2 valued Boolean functions in Z_2 corresponding to

statements of type "P is true" and "P is not true": there are altogether 4 of them. Drop the statement represented by $(0,0)$.
iii) Again one goes to meta level and considers statements about statements about statements that is functions from 3-element set to Z_2: 7 elements altogether, when one throws away the statement represented by sequence of zero bits.
iv) Continuing this process one clearly gets Combinatorial Hierarchy.

The somewhat mysterious feature is the dropping of one statement. If the construction corresponds to the construction assigning creation of the cognitive fermion pair with the splitting of a wormhole contact connecting two space-time sheets, then the requirement that the two space-time sheets form a connected structure drops exactly one configuration (no wormhole contacts connecting the two space-time sheets) from consideration. Second interpretation would be in terms of conscious bit. If conscious bit "1" is represented as a phase transition of some kind then the sequence of "0" s is not representable as a conscious bits so that only 2^k-1 code words are representable for k bit code and the only $k-1$ bits are fully representable which suggests that only 2^{k-1} bits represent information and remaining bits could play the same role as parity bits.

There is second construction which is purely set theoretical and gives a natural explanation for the dropping of one statement. Consider subsets of the set $(0,1)$. There are 3 of them if the physically non-realizable empty set is excluded. Consider next the subsets of the 3-element set: there are $2^3-1=7$ of these sets if empty set is excluded. By continuing the process one finds that the numbers of the Combinatorial Hierarchy result. This suggests that the physical non-realizability of $(0,0,...)$ Boolean statement is basic reason for dropping it from consideration.

The numbers of the Combinatorial Hierarchy have some properties, which suggest that they are very closely related to Genetic Code.

1. The numbers $p=3=M_2,7=M_3,127=M_7,M_{127}$ are Mersenne primes. It is possible that all the Mersenne numbers $M(n+1)=M_{M(n)}$ of the sequence are primes. This implies that the statements can be given the algebraic structure of Finite Field $G(p,1)$. Therefore the set of the Boolean statements has also interpretation as a simplified model for arithmetics and the arithmetic abilities of the intelligent system grow gradually in transitions from level to meta level. As a consequence the basic conjecture

$$M(n+1) \quad = \quad M_{M(n)}=2^{M(n)}-1 \text{ prime } n=1,2,... \ , \tag{2.2.1}$$

roughly means that there is no upper bound for the arithmetic abilities of intelligent system!

2. The statements at the level p are of two types: "P is true" and "P is not true" and there are clearly $N(p)=(p+1)/2$ mutually consistent statements at level p. These numbers come as $2,4,64,2^{126},..$ for $p=3,7,127,...$ What is remarkable is that $N(7)=4$ is the number of different DNA:s and $N(127)$ is the number of different DNA sequences. This suggests that DNA: s represent physically consistent with a given atomic statement at level p.

3. The finite field $G(p,1)$ has the cyclic group Z_{p-1} as the multiplicative group of nonzero elements. The dimensions of these groups read as $1,2,6=2\cdot 3,126=6\cdot 21,...$ for Combinatorial Hierarchy. The multiplicative group of the previous level can be regarded as a subgroup of the next level multiplicative group for the lowest members of the Combinatorial Hierarchy at least: $Z_{p_n-1}\subset Z_{p_{n+1}-1}$. The reason is that $p_{n+1}-1$ is divisible by p_n-1 for the lowest Mersenne primes. In fact divisibility holds true also for $M_{127}-1$ and M_7-1. Divisibility condition gives

$$2^{126}-1 \quad = \quad 63n \ . \tag{2.2.2}$$

The condition is satisfied!: $63=3^2\cdot 7$ divides $2^{126}-1$, whose prime factorization [A11] is given by

n	1	2	3	4
$M(n)$	3	7	127	$2^{127}-1$
$N(DNA,n)=(M(n)+1)/2$	2	4	64	2^{126}
$N(amino,n)=(M(n)-1)/(M(n-1)-1)$	2	3	21	$(2^{126}-1)/63$

Table 2.1: The lowest Mersenne numbers of Combinatorial Hierarchy (known to be primes), the numbers of "DNA" k_{n-1}-plets and the numbers of "amino-acids" for these levels.

$$\begin{aligned} 2^{126}-1 &= 3^3\cdot 7^2\cdot 19\cdot 43\cdot 73\cdot 127\cdot X \ , \\ X &= 337\cdot 5419\cdot 92737\cdot 649657\cdot 77158673929 \ . \end{aligned} \tag{2.2.3}$$

Actually the divisibility follows quite generally from the following little theorem:
Theorem: $M(n)-1$ divides $M(n+1)-1$ always and $M(n)$ divides $M(n+1)-1$ if $M(n)$ is prime. The divisibility of $M(M(n))-1$ by prime $M(n)$ follows as a particular case $a=2, p=M(n)$ of Fermat's theorem stating that $a^{p-1}=1\ mod\ p$ holds true for any natural number a and any prime p. The divisibility of $M(M(n))-1$ by $M(n)-1$ is equivalent with the divisibility of $2^{M(n)-1}-1$ with $2^{M(n-1)-1}-1$. This property holds true for the lowest Mersenne numbers of the Combinatorial Hierarchy and can be proven to hold true generally by induction using the following lemma [A2]:
Lemma: The greatest common multiplier (x,y) for integers $x=2^a-1$ and $y=2^b-1$ satisfies $(2^a-1,2^b-1)=2^{(a,b)}-1$. The proof of the lemma is based on the observation that the polynomial x^n-1 ($x=2$ now) factorizes into a product of factors (x_i^n-1), where n_i is factor of n. For the polynomials x^a-1 and x^b-1 the largest common multiplier is therefore $x^{(a,b)}-1$.
For $a=M(n)-1$ and $b=M(M(n+1))-1$ lemma together with the induction assumption gives $(a,b)=2^{(M(n)-1,M(n-1)-1)}-1=2^{M(n-1)-1}-1$: the result means that $2^{M(n-1)-1}-1=M(n)-1$ divides $2^{M(n)-1}-1=M(n+1)-1$. The prime number property of Mersenne numbers is not needed in the proof.

As a consequence one has an infinite hierarchy of coset spaces $Z_{p_{n+1}-1}/Z_{p_n-1}=Z_{k_n}$, which are also cyclic groups. The first members of this hierarchy are $Z_{k_1)}=Z_2, Z_3, Z_{21}, ...$ Also the groups Z_{k_n} satisfy the condition $Z_{k_n}\subset Z_{k_{n+1}}$ for the lowest values of k with k_1 excluded and an interesting possibility is that k_n divides k_{n+1} quite generally for some number theoretic reason. What is remarkable is that $k_2=3$ is the number of DNA: s in DNA triplets and $k_3=21$ is the number of amino-acids plus stopping sign coded by DNA: s. This observation suggests that amino-acids correspond to the subset of the statements of $G(p_n,1)$ imbeddable as subgroup Z_{k_n} to Z_{p_n-1} for $p_n=127$. A little consideration shows that the map $x\to x^{k_{n-1}}$ gives a unique embedding for the amino-acid type statements to Z_{p_n-1}.

These observations suggest a general model for Genetic Code. The 64 DNA sequences give a physical representation for the statements compatible with a given atomic statement at $p=127$ level of the Combinatorial Hierarchy. The choice of these mutually compatible statements as a subset of $G(127,1)$ is by no means unique and is determined by the evolution. The 21 amino-acids (stopping sign is regarded formally as "amino-acid") at $p=127$ level correspond to the unique statements representable in the form $y=x^6$ in Z_{126} and form cyclic group Z_{21}. Genetic code can be regarded as the mapping $x\to x^6$ mapping all DNA type statements to amino acid type statements. The interpretation of the amino-acid type statements is as general axioms and DNA type statements are regarded as special cases of these axioms. Amino-acid sequences in turn are regarded as theorems derivable from axioms by constructing amino-acid sequences: the direction of the sequence is unique by the chirality of the amino-acid molecules.

The formation of theorems in formal system indeed corresponds to the formation of symbol sequences by some rules (now the rules are extremely simple, perhaps too simple!). The representability of DNA: s as triplets of 4 basic units has explanation: actually a more general the formula $N(DNA,n)=(p_n+1)/2=((p_{n-1}+1)/2)^{k_{n-1}}=N(DNA,n-1)^{N(amino,n-1)}$ holds true for all levels of the Combinatorial Hierarchy. In particular, for $p=127$ one has $64=4^3$. Actually an infinite hierarchy of Genetic Codes suggests itself: for the n: th member of the Hierarchy there

d	6	4	3	2	1
N	3	5	2	9	2

Table 2.2: The number of amino acids N associated with a given degeneracy d telling the number of DNA triplets mapped to the amino acid in genetic code. The degeneracies are always smaller than 7 as predicted by the proposed explanation of the Genetic Code.

are k_n axioms and if k_n divides k_{n+1} the axioms of level n are imbeddable as a subgroup Z_{k_n} to the group $Z_{k_{n+1}}$ of axioms at level $n+1$ and the counterpart of Gödel's Incompleteness Theorem holds true.

2.2.2 Interpretation Of Genetic Code

Finite Field Computer picture leads to the interpretation of genetic code as a map from the set of well defined truth values $X_{64} \subset G(127,1)$ (DNA: s) to the set $Z_{126}/Z_6 = Z_{21} \subset G(127,1)$ (amino-acids).

1. The interpretation of the previous observation is that amino-acids and "stopping sign" correspond to the elements x of the coset space $Y = Z_{126}/Z_6 = Z_{21}$ obtained by identifying two elements a and b of Z_{126} are identified if $a^6 = b^6$ holds true. The realization of Z_{21} as a subset of $G_{127,1}$ is obtained as the set of non-vanishing sixth powers of $G(127,1)$ elements

$$z \in Z_{21} <=> z = x^6, \quad 0 \neq x \in G(127,1) \ . \tag{2.2.4}$$

   Since a coset space is in question $d = 126/21 = 6$ elements of Z_{126} are mapped to a given element of Z_{21} in the map $x \to x^6$.

2. According to the proposed model of intelligent system DNA triplets correspond to a subset X_{64} of 64 well determined truth values of $p = 127$ logic but at this stage there is no first principle telling which subset corresponds to truth values. Let us however assume that X_{64} corresponds to subset of Z_{126} so that zero element is excluded from X_{64}.

3. With these identifications genetic code correspond to the mapping $x \to x^6$ from the set X_{64} of well defined truth values to Z_{21}

$$x \in X_{64} \quad \to \quad x^6 \in Z_{21} \ . \tag{2.2.5}$$

   The number of DNA triplets d coding same amino acid is just the number of elements of X_{64} mapped to same element of Y and this gives strong constraints for the identification of X_{64} as subset of $G(127,1)$. Clearly, genetic code is to a high degree equivalent with the identification of 64-element DNA triplets as subset of Z_{126}. The identification of X_{64} as subset of Z_{126} cannot however be determined uniquely since the group Z_6 acts as the symmetry group of the code permuting the 6 elements of Z_{21} mapped to same element of Z_{126} and leading to a code with same degeneracies d.

An important prediction is that at most six DNA triplets can correspond to same amino acid. As**Table 2.2** shows, the condition is satisfied: there are three amino acids for which DNA degeneracy d is 6. This means that it is indeed possible to realize genetic code in the proposed manner.

One can consider first simple guesses for the identification of X_{64} as a subset of $G(127,1)$. The identification as even elements $y = 2k$, $k = 0, 63$ is not possible since zero cannot belong to X_{64}: same applies to the identification as odd elements. The identification as the elements

expressible as squares $y = x^2$ is excluded for the same reason. One could include the 64^{th} DNA by identifying it as an arbitrary element of Z_{126}. All these identifications yield almost completely symmetric genetic code: $d = 3$ for all 21 amino acids except one for with one has $d = 4$ so that something more complicated is needed.

2.2.3 Genetic Code As A Result Of Geometric Symmetry Breaking

One could try to understand the pattern of degeneracies as a symmetry breaking pattern, but not in terms of group representations as is done usually but in terms of group orbits. For single DNA multiplet associated with given amino-acid the natural symmetry group is Z_6 or some of its subgroups and DNA multiplet of given amino-acid can be regarded as a union of orbits for the subgroup in question. The subgroups of $Z_{126}/Z_6 = Z_3Z_7$ in turn can transform the DNA multiplets with same degeneracy to each other and amino-acids with same degeneracy can be regarded as a union of orbits of Z_7, Z_3 or Z_1. This symmetry pattern seems to work!

1. Consider first the group Z_6 acting inside DNA multiplets associated with given amino-acid. The definition of Z_{21} implies that the DNA: as associated with $d = 6$ amino-acids must be identified as six-element orbits of Z_6 symmetry. $d = 3$, $d = 2$, $d = 1$ amino acids correspond to the breaking of Z_6 to Z_3, Z_2 and to Z_1 respectively. $d = 4$ amino-acids are however problematic since Z_6 does not have 4-element subgroup. One can interpret $d = 4$ DNA: s either as a union of two Z_2 orbits or as a union of Z_3 and Z_1 orbits: Z_1 orbit corresponds most naturally to the mirror image of one Z_3 point, when the points of Z_{126} are represented as points of unit circle. This interpretation seems to be more appropriate.

2. Consider next the group Z_{21} acting on amino-acids. The 3 $d = 6$ amino-acids could be identified as an orbit of $Z_3 \subset Z_{21}$. If one regards the 5 $d = 4$ multiplets as unions of Z_3 and Z_1 orbits one can obtain altogether $2+5$ $Z_3 \subset Z_6$ orbits, which could be regarded as Z_7 orbit. What remains is $5+2 = 7$ Z_1 orbits, which could be regarded as Z_7 orbit. Therefore it seems that amino-acids can be ordered nicely into the orbits of Z_3 and Z_7. It turns however that exact symmetry is broken and some orbits are slightly deformed or even broken to pieces.

There are good reasons for symmetry breaking.

1. Besides symmetry also redundancy of the genetic code is desirable: this means that the number of the amino-acids with small degeneracy should be as small as possible. Z_6 (or some subgroup) symmetry and redundancy are competing factors since average degeneracy is always same and symmetry tends to increase the redundancy associated with some amino acids. Therefore redundancy requirement might be one underlying reason for symmetry breaking.

2. It turns out that also the competition between symmetries Z_3 and Z_7 in Z_{27} forces either Z_7 or Z_3 symmetry breaking already before the "actual" symmetry breaking.

3. The third reason for the symmetry breaking is the constraint that the numbers of DNA triplets and amino-acids are constrained to 64 and 21 respectively. For, instance 63 DNA: s allows representation as a union 9 Z_6 orbits having $Z_3 \subset Z_{21}$ as symmetry group but for 64 DNA: s there is necessarily one Z_1 orbit present.

It would be nice if one could understand the genetic code as a small perturbation of some code with both high symmetry and high redundancy. One could even assume that the number of amino-acids before the symmetry breaking is smaller than 21 so that symmetry breaking is necessary to obtain 21 amino-acids. A geometric picture of the situation is obtained by regarding the points of Z_{126} as points $\Phi = n2\pi/126$ of a unit circle endowed with standard metric so that it becomes possible to define what "small" symmetry breaking means.

2.2.4 Symmetry Breaking Scenarios

The genetic code can be reproduced as the following symmetry breaking pattern.

1. Unbroken symmetry corresponds to the following situation. There are $6 = 3 + 3$ amino-acids with maximal degeneracy $d = 6$ and 7 amino-acids with degeneracy $d = 4$: altogether $13 < 21$ so that symmetry breaking is necessary. $d = 6$ multiplets correspond to 6 Z_6 orbits $\Phi = n2\pi/6 + k\Delta(i)$, with $\Delta(i) = k_i 2\pi/126 < 2\pi/6$. Single $d = 4$ multiplet corresponds to Z_3 orbit plus single point, which is diametrically opposite to one of the points at Z_3 orbit. More explicitly: basic $(3, 1)$ multiplet corresponds to the Z_3 orbit $\Phi_3(k) = 6\Delta + k2\pi/3$, $k = 0, 1, 2$ plus the point $\Phi_1 = 6\Delta + \pi$. By acting on this orbit with rotations $\Delta_1(i) = k_i 2\pi/126$, $i = 0, ..., 6$, $\Delta_1(i) < 2\pi/6$ one obtains 7 $d = 4$ multiplets. Obviously one must have $\Delta(i) \neq \Delta_1(j)$ for each i, j pair in order to avoid overlapping. The actual embedding of Z_6 multiplets is not relevant for the degeneracies of the genetic code and will be discussed later.

2. The first symmetry breaking is $Z_6 \to Z_2$ and occurs for 3 $d = 6$ amino-acids and leads from 3 Z_6 orbits to 9 Z_2 orbits so that 9 $d = 2$ amino-acids result. Breaking can be understood geometrically as follows. Single $d = 6$ multiplet is obtained by Z_2 action (reflection) from Z_3 orbit, say $\Phi(k) = k2\pi/3$. What happens is that two points on Z_3 orbit that for Z^3 orbit the points $\Phi(k)$ with $k = 1$ and 4 are rotated slightly with different rotation angles

$$\begin{aligned}
\Phi(1) &\to \Phi(1) + \delta_1 \ , \\
\Phi(4) \to \ & \Phi(4) + \delta_1 \ , \\
\Phi(5) &\to \Phi(5) - \delta_2 \ , \\
\Phi(6) &\to \Phi(6) - \delta_2 \ , \\
\delta_i &= \frac{k_i 2\pi}{126} \ , \\
1 < \ & k_i < 6 \ .
\end{aligned} \tag{2.2.6}$$

   Here δ_i must be chosen so that the deformed points do not coincide with already "occupied" points. Minimal symmetry breaking is obtained with $k_1 = 1 = k_2$ but would lead to overlapping. One must also have $k_1 \neq k_2$ ($k_1 = k_2$ would imply additional reflection symmetry). The symmetry breaking leads to $9 + 7 = 16$ amino acids with degeneracies $d \geq 2$.

3. The second symmetry breaking leads from 7 $d = 4$ multiplets to 5 $d = 4$ multiplets, 2 $d = 3$ multiplets and 2 $d = 1$ multiplets. What happens is that 2 basic $d = 4$ multiplets consisting of Z_3 orbit and mirror image of one of Z_3 points is deformed $d = 3$ plus $d = 1$ multiplet: this is achieved if mirror image point is slighly shifted. The deformation is obtained by performing for the basic multiplet ($\Phi_3(k) = k2\pi/3, \Phi_1 = \pi$) the deformation

$$\Phi_1 = \pi \quad \to \quad \pi \pm \delta_3 \ . \tag{2.2.7}$$

   $\delta_3 = k_3 2\pi/126$, $1 < k_3 < 6$ followed by appropriate rotation carrying broken multiplet to its own position. $k_3 = 1$ is not allowed since it would lead to overlapping and $k_3 = 2$ leads to the smallest possible symmetry breaking.

One can try to find unique embedding of X_{64} (and also try to understand the uniqueness of the genetic code) by requiring that amino-acids form orbits of Z_{21} or its subgroups. Z_3 and Z_7 are competing symmetries and not consistent with each other: the reason is that Z_3 orbits and Z_7 orbits in same basic angular range of length $2\pi/6$ necessarily overlap since between two points of Z_3 orbit there are always just 6 points so that Z_7 orbit cannot be put between two points on Z_3 orbit. Therefore one must choose between either enhanced Z_3 or Z_7 symmetry for the embedding of X_{64}.

Consider first Z_3 symmetric situation.

d	N(d)	$\Phi/\Delta = n \; mod \; 126$, $\Delta = 2\pi/126$
6	3	$n = A(i) + B(k)$, $A(i) = 21i$, $B(k) = 7k$, $i \in I$, $k \in K$
		$I = \{0, 1, .., 5\}$, $K = \{0, 1, 2\}$
2	9	$n = (A(i) + B(k) + 1 + \delta_1(i))$, $i \in I$, $k \in K$
		$\delta_1(0) = \delta_1(3) = 0$, $\delta_1(1) = \delta_1(4) = -3$, $\delta_1(2) = \delta_1(5) = 4$
4	5	$n = i + 42k$, $n = i + 63$, $i = 2, 10, 11, 17, 18$, $k \in K$
3	2	$n = i + 42k$, $i = 3, 4$, $k \in K$
1	2	$n = i + 63 + \delta_2(i)$, $i = 3, 4$, $\delta_2(3) = -1$, $\delta_2(4) = 1$

Table 2.3: Explicit form for the Z_3 symmetric embedding of X_{64} consistent with Genetic Code. The index k appearing in the formulas labels points on Z_3 orbit. The embedding is illustrated in **Fig. 2.1**.

d	N(d)	$\Phi/\Delta = n \; mod \; 126$, $\Delta = 2\pi/126$
6	3	$n = A(i) + B(k)$, $A(i) = 21i$, $B(k) = 7k + \delta_1(k)$, $i \in I$, $k \in K$
		$I = \{0, .., 5\}$, $K = \{0, 1, 2\}$, $\delta_1(1) = 5$, $\delta_1(0) = delta_1(2) = 0$
2	9	$n = A(i) + \delta_2(i) + 1 + B(k)$, $i \in I$, $k \in K$
		$\delta_2(1) = \delta_2(4) = -2$, $\delta_2(2) = \delta - 2(5) = 2$,
4	5	$n = 3 + i + 42k$, $n = i + 63$, $i = 2, ..., 6$, $k \in K$
3	2	$n = 3 + i + 42k$, $i = 1, 7$, $k \in K$
1	2	$n = i + 63 + \delta_3(i)$, $i = 1$ *or* 7, $\delta_3(1) = -1$, $\delta_3(7) = 1$

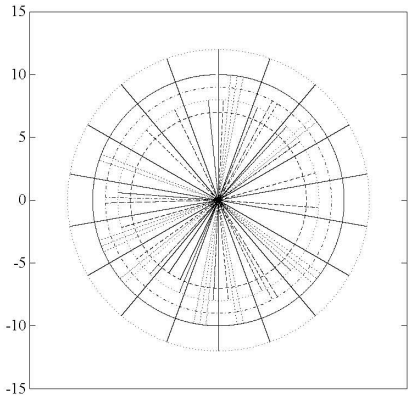
Table 2.4: Explicit form for the Z_7 type embedding of X_{64} consistent with Genetic Code. The embedding is illustrated in figure **??**.

1. $6 = 3+3$ Z_6 orbits decompose naturally into two orbits of Z_3. The first Z_3 orbit corresponds to $\Phi(k, m) = 6m \cdot 2\pi/126 + k2\pi/6$, $m = 0, 1, 2$ and second Z_3 orbit is obtained from this orbit by a rotation $\Delta\Phi = 2\pi/126$. When Z_6 orbits break down to 9 Z_2 orbits the Z_2 orbits can form 3 separate orbits of Z_3.

2. The graphical experimentation with various possibilities shows that one must split Z_7 orbit to three pieces $7 = 1 + 2 + 2 + 2$ so that the 2: s form Z_3 orbit. Therefore complete breaking of Z_7 symmetry makes possible additional Z_3 symmetry. This means that one $d = 4$ orbits arrange into 2 Z_3 orbits and one Z_1 orbit before symmetry breaking. After the symmetry breaking the 2 $d = 3$ multiplets and $d = 3$: s belonging to 5 $d = 4 : s$ form still Z_3 orbits but two $d = 1$: s are thrown out of corresponding Z_3 orbits.

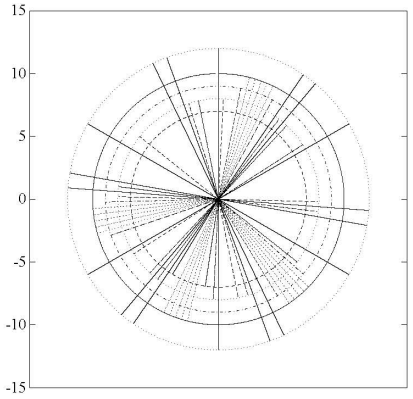
3. An example of an embedding satisfying these constraints is given by the following formulas

Consider next Z_7 type scenario. 7 $d = 4$: s can be put into single Z_7 orbit. $d = 6$ representations cannot however form neither Z_7 full orbits nor full Z_3 orbits in this case. After the symmetry breaking the 2 $d = 3$ multiplets and $d = 3$: s belonging to 5 $d = 4 : s$ form still Z_7 orbits but two $d = 1$: s are thrown out of corresponding Z_7 orbits. There exists no full Z_7 orbit consisting of amino-acids with same d after symmetry breaking so that in this sense Z_7 sceneario possesses much less symmetry than Z_3 scenario. An explicit example is given by the following formulas



1

Figure 2.1: The embedding $X_{64} \subset Z_{126}$ reproducing Genetic Code and possessing Z_3 type symmetry. The lengths of radial lines are $6 + d$, where $d = 1, 2, 3, 4, 6$ is the number of DNA: s associated with amino-acid. The angular distance between points on Z_3 (Z_7) orbits is to 20 (2.85) degrees.



1

Figure 2.2: Z_7 type embedding $X_{64} \subset Z_{126}$ reproducing Genetic Code. Symmetry breaking is much larger for this embedding although visually the embedding looks perhaps more symmetric than Z_3 type embedding.

$N(d=1)$	$N(d=2)$	$N(d=3)$	$N(d=4)$	$N(d=6)$
0	12	0	7	2
2	**9**	**2**	**5**	**3**
4	6	4	3	4
6	3	6	3	5

Table 2.5: The 4 possible genetic codes assuming unbroken initial Z_3 symmetry with numbers of amimo acids with same degeneracy.

2.2.5 In What Sense The Physical Genetic Code Is Unique?

The proposed symmetry breaking scenario is certainly not the only one. A constraint on symmetry breaking patterns comes from the requirement that all amino acids are coded. In terms of orbit multiplicities $g(k)$ (number of amino acids with same number of DNA: s) one has two conditions

$$\begin{aligned} \sum_{k=1,2,3,4,6} g(k) &= 21 \ , \\ \sum_{k=1,2,3,4,6} g(k)k = 64 \ . \end{aligned} \tag{2.2.8}$$

$k=4$ case corresponds to two Z_3 and Z_1 orbits associated with single amino acid. This gives

$$\begin{aligned} g(1) &= -22 + g(3) + 2g(4) + 4g(6) \ , \\ g(2) &= 43 - 2g(3) - 3g(4) - 5g(6) \ . \end{aligned} \tag{2.2.9}$$

This means that all possible genetic codes are labeled by the three integers $g(3), g(4)$ and $g(6)$. The conditions imply

$$\begin{aligned} g(3) + 2g(4) + 4g(6) &\geq 22 \ , \\ 2g(3) + 3g(4) + 5g(6) &\leq 43 \ . \end{aligned} \tag{2.2.10}$$

These conditions restrict the possible symmetry breaking scenarios. In particular, $g(6) \leq 8$ must hold true so that maximal symmetry corresponds to the codes with $(g(3), g(4), g(6))$ equal to $(1, 0, 8)$ or $(0, 1, 8)$.

In the proposed symmetry breaking scenario the number of DNA: s is automatically fixed to 64 and the only requirement is that deformation of X_{64} is such that the number of amino-acids is not smaller than 21. If one assumes that the only symmetry breakings are of form $6 \to 3 \cdot 2$ and $4 \to 3 + 1$ and denotes the numbers of broken $d = 6$ and $d = 4$ multiplets with k_6 and k_4 respectively the condition for 21 amino acids reads as $(6 - k_6) + 3k_6 + (7 - k_4) + 2k_4 = 21$, which gives $k_6 = 4 - k_4/2$, $k_4 = 0, 2, 4, 6$. k_4 gives the number of $d = 1$ amino-acids and $k_4/2 + 2$ gives the number of the unbroken 6 orbits: these numbers clearly measure redundancy and symmetry. The numbers of amino-acids with various degeneracies are given by

$$\begin{aligned} N(d=1) = N(3) &= k_4 \ , \\ N(2) &= 3(4 - k_4/2) \ , \\ N(4) &= 7 - k_4 \ , \\ N(6) &= 2 + k_4 \ . \end{aligned} \tag{2.2.11}$$

Table 2.5 summarizes the 4 genetic codes possible under these assumptions.

The physically realized genetic code (second row) is clearly a compromise between symmetry and redundancy. By the previous construction the physically realized code is characterized by additional symmetry: namely the group $Z_3 \subset Z_{21}$ transforming both 3 $d = 6$ amino-acids and

3 triplets of $d = 2$ amino acids to each other. For all other Z_3 type alternatives this symmetry is broken. Therefore the physical genetic code corresponds in a well defined sense to minimal symmetry breaking.

2.2.6 Hierarchy Of Genetic Codes?

Genetic Code generalizes to an entire hierarchy of genetic codes at formal level, at least.

1. The spaces $X_4 \subset X_{64} \subset X_{(M_{127}+1)/2} = X_{2^{126}} \subset ....$ an be regarded as a hierarchy of "DNA triplets".

2. The preceding results suggest that the multiplicative groups associated with the Combinatorial Hierarchy form also a hierarchy: $Z_2 \subset Z_6 \subset Z_{126} \subset Z_{M_{127}-1} \subset .....$ This is true if the dimensions divide each other: $2|6|126|M_{127}-1|.....$ 126 indeed divides $M_{127}-1 = 2(2^{126}-1)$ and the number of "amino-acids" at the third level is $(2^{126}-1)/63$! The result holds generally from Fermat's theorem ($2^{p-1} = 1 \; mod \; p$) if the Mersenne numbers of the Combinatorial Hierarchy are primes.

3. If Combinatorial Hierarchy consists of primes the coset spaces $Z_6/Z_2 = Z_3 \subset Z_{126}/Z_6 = Z_{21} \subset Z_{M_{127}-1}/Z_{126} \subset ....$ exist and form a hierarchy of "amino-acids".
   The redundancy of the genetic code could be interpreted as resulting from a hierarchy of discrete gauge symmetries: Z_{M_n-1} acts as gauge symmetry in the space $Z_{M_{M_n}-1}$.

There is still further apparent numerical co-incidence. For the first 3 levels the numbers of "amino-acids" are

$$\begin{aligned} a_0 &= 2 \; , \\ a_1 &= 3 \end{aligned} \tag{2.2.12}$$

per,

$$\begin{aligned} a_2 &= 21 \; , \\ a_3 &= ((M_{127}-1)/2)/((M_7+1)/2)) = (2^{126}-1)/63 \; . \end{aligned} \tag{2.2.13}$$

The numbers of "DNA" -n-plets (well defined truth values) are

$$\begin{aligned} d_0 &= 2 \; , \\ d_1 &= 4 = 2^2 = d_0^{a_0} \; , \\ d_2 &= 64 = 4^3 = d_1^{a_1} \; , \\ d_3 &= 2^{126} = 64^{21} = d_2^{a_2} \; . \end{aligned} \tag{2.2.14}$$

The formulas imply that one can construct the physical DNA-triplets at level 2 as $d_2 = d_1^{a_1} = 4^3$ triplets of DNA molecules. At level 3 one can construct $d_3 = d_2^{a_2} = 63^{21} = 2^{126}$ "DNA" 21-plets of 64 different DNA-triplets. More generally, DNA-plets at given level n correspond to a_{n-1}-plets of DNA formed from the DNA-plets of the previous level since the identity

$$d_n = \frac{(M_n+1)}{2} = d_{n-1}^{a_{n-1}} = 2^{a_{n-1}a_{n-2}a_{n-3}...a_0} \; . \tag{2.2.15}$$

holds true in general since the groups Z_{M_n-1} forms a hierarchy of nested subgroups.

The result means that the concrete physical representation of truth values of M_n logic as "DNA" sequences is an internal property of the Combinatorial Hierarchy. The immediate prediction is that sequences of 21 DNA-triplets should code for $a_3 = (2^{126}-1)/63$ generalized amino-acids consisting of sequences of 21 amino-acids acids: these units could be regarded as some kind of "pre-genes". The number of amino-acid sequences consisting of 21 amino-acids (of order 2^{91}

is much smaller than the number of generalized amino-acids (of order 2^{120}), which means that the ordinary amino acids cannot provide an optimal realization of DNA sequences: many generalized amino-acids have no DNA sequence as their representative. DNA sequences are known to contain passive sections, introns, which do not code DNA. An interesting question is whether these sections could represent M_{127} level sequences: if so the number of DNA triplets in these sections should be a multiple of 21.

If the lowest level of the Hierarchy is present DNA: s should be representable as doublets formed from two different $p = 3$ "pre-DNA": s and these should code for 3 different "pre-amino-acids". This kind of structure is not realized in Nature so that the $p = 7$ level of DNA: s is in this sense irreducible.

2.2.7 The Structure Of The Negation Map

The negation map mapping statement to its negation is highly non-unique unless it possesses symmetries and it is interesting to find what one can conclude about the structure of this map by symmetry arguments.

1. For each amino-acid type general statement there are six special cases of the statement. The fact that only 64 statements are actually consistent with a given atomic statement means that some special cases associated with different amino-acids correspond to statement and its negation whereas two points at given Z_6 orbit cannot correspond to a statement and its negation.

2. 62 negations of 64 DNA type statements belong to Z_{126}. One lacking negation corresponds to the zero element of $G(127, 1)$ and the second one corresponds to the excluded statement in the construction of the Combinatorial Hierarchy. One can associate to each amino-acid definite number of negations as the number of elements in the complement of DNA type statements on the Z_6 orbit defined by amino-acid (at Z_6 orbit all statements must be consistent with a fixed atomic statement). These numbers are $d_1 = 0$ for 3 $d = 6$ amino-acids, $d_1 = 2$ for 5 $d = 3 + 1$ amino-acids, $d_1 = 4$ for 9 $d = 2$ amino-acids and $d_1 = 5$ for the 2 $d = 1$ amino-acids so that negations "code" only 18 amino-acids so that duality symmetry between statements and their negations is not possible.

3. Negation must map statements at given orbit to a different orbit. It is however natural to require that points on same orbit, say A, are mapped on same orbit, say B, if possible and that the angles and ordering of points belonging to same orbit are preserved in negation map. More generally, the ordering of points on circle should be preserved.

4. For 2 $d = 3$ amino-acids, call them a and b, the Z^3 orbit a (b) is mapped to the complement of Z^3 orbit b (a). The map is unique apart from Z^3 rotation.

5. For 9 $d = 2$ amino-acids Z^2 orbits (pairs of diametrically opposite points) form 3 Z^3 orbits and Z^3 rotation plus a rotation inside Z^6 orbit gives good candidate for negation map. As a consequence 9 Z_2 orbits in the complement remains "free" and form 3 Z_3 orbits, call them G_i.

6. It is natural map $d = 6$ orbits to these free 9 Z_2 orbits in Z_3 symmetric manner, which means that the content of single Z_6 orbit i is mapped into 3 $d = 2$ orbits in G_i. Diametrically opposite point pair on Z_6 orbit is mapped to a similar point pair in G_i. The map is unique if one requires that Z_6 element on the initial orbit goes to same Z_6 element on the final orbit and this in turn makes the map of 9 Z_2 orbits unique apart from reflection.

7. The 5 $d = 3 + 1$ amino-acids form unions of diametrically opposite point pair A_i plus point pair B_i, $i = 1, ..., 5$ separated by angle of 120 degrees. Point pairs B_i can be mapped to the mirror image $\bar{B}_j$ of B_j, $j \neq i$: one can require that cyclic ordering of pairs B_i is preserved in map to remove part of the non-uniqueness. $2 + 2$ pairs A_i can be mapped to the $2 + 2$ pairs C_i in the complements of 2 $d = 1$ orbits containing 5 points each (2 diametrically opposite pairs C_i plus single point). The remaining pair, say A_{i_0}, can be mapped to zero element of $G(127, 1)$ and to the "dropped out" statement.

8. Denoting the mirror images of 2 $d = 1$ statements a and b by $\bar{a}$ and $\bar{b}$ the negation map for them reads as $(a, b) \to (\bar{b}, \bar{a})$.

2.2.8 Combinatorial Hierarchy As A Hierarchy Of Formal Systems

Usually [A5] formal system is understood as a system of symbols, axioms interpreted as allowed basic strings of symbols and rules for constructing new sequences from the symbols. In [A5] the exciting analogies between the symbol sequences of formal systems and DNA and amino acids sequences and Genetic Code were emphasized and it indeed seems that more than analogy is in question. The model for the Genetic Code suggests an interpretation of Combinatorial Hierarchy as a hierarchy of formal systems with DNA type statements identifiable as a maximal set of 64 statements consistent with an atomic statement (single bit fixed) and amino-acid type statements as basic axiom type truths. Genetic code results from the necessary but non-unique selection of these statements consistent with a fixed atomic statement and the selection of these statements could be a result of fight for survival at the level of amino-acids. The rule for forming statements in this system is simple: just form DNA sequences with building blocks consisting of a_{n-1}(number of "amino-acids" at level $n-1$) DNA-sequences of previous level. Theorems are obtained by coding these statements to amino-acid sequences.

Consider first DNA type statements.

1. It was already suggested that the elements of Finite Fields in the Combinatorial Hierarchy correspond to a hierarchy of statements about statements about.... and therefore a sequence of formal systems formed from basic formal system by successive construction of meta level statements.

2. Finite Field provides a language to construct all possible statements. As already found, the $(p+1)/2$ (p is Mersenne prime in the Combinatorial Hierarchy) statements correspond to maximal set of statements consistent with a fixed atomic statement of this formal system. This is indeed a possible interpretation. Combinatorial Hierarchy was constructed by starting from a set containing just two statements 1 and 0. In the first $p = 3$ level one forms 4 statements about these two statements and drops the one representable as $(0, 0)$. There are however 2 contradictory statements of type P and *not* P in this set so that only $2 = (p+1)/2$ statements are consistent with a given atomic statement in the real world. At the level p one has $p = M_n$ statements about lower level statements and by construction $(p-1)/2$ statements P have also their negation in the set of all possible statements so that $(p+1)/2$ consistent statements with a fixed atomic statement are possible. Thus the conclusion is that 64 DNA triplets represent the maximum number of mutually consistent statements at level $p = M_7 = 127$ of a formal system possibly having a hierarchy of meta levels.

Consider next the interpretation for the set $Z_{k_n} = Z_{p_n-1}/Z_{p_{n-1}-1}$, $k_n = (p_n-1)/(p_{n-1}+1)$ of amino-acid type statements.

1. In any formal system there are two kind of meta statements that is statements $P(Q_1, ..Q_n)$ about statements. The first class corresponds to theorems $P(Q_1, ...Q_n)$ without any reference to the particular value of statements Q_i: a simple example is general theorem stating the conditions under which an orthogonal triangle with two integer sides is Pythagorean triangle: $m^2+n^2 = l^2$ with m, n, l integers. Second class corresponds to the theorems with $(Q_1, ..., Q_n)$ possessing definite values: a simple example is previous theorem for triangle having sides $2, 1$ and 3: $2^2 + 1^2 = 3^2$. The set of "amino-acid" type statements does not depend on the choice of the choice fo the $(p+1)/2$ statements consistent with a given atomic statement and this suggests the interpretation "amino-acid" type statements as general axiom like truths without any reference to the values of the argument of the statement.

   What is special in the proposed hierarchy of formal systems that the substitution operation corresponds to the multiplication of Z_k element with the element $Z_{p_{n-1}-1}$. The introduction of mutual consistency by selecting $(p+1)/2$ special statements implies that the number of DNA: s per amino-acid corresponds to the number of special cases associated with a given "axiom" depends on the "axiom". There is still upper bound for special cases given by $p_{n-1} - 1$.

2. In a good formal system the choice of DNA type statements should be such that there is at least one statement per each truth. The most important truths (as far as survival is considered) should correspond to full $Z_{p_{n-1}-1}$ orbits.

Gödel's Incompleteness Theorem was one of the basic themes in the book of Hofstadter [A5]. Theorem states that in any sufficiently complicated formal system (, that is, practically interesting) there are truths, which are not provable. The Incompleteness Theorem seems to have its analog in bio-systems. As already observed at the level M_{127} DNA sequences consisting of 21 triplets correspond to true statements, which can be regarded as special cases of general truths, whose number is $(2^{126-1})/63 \sim 2^{120}$. Amino-acid sequences consisting of 21 amino-acids give a natural realization for a subset of these truths and the genetic code map is induced from the Genetic Code at the basic level $p = 127$. The number of the truths given by these sequences is of order $20^{21} \sim 2^{91}$ (taking into account the reduction caused by the stopping sign) and much smaller than all possible truths. The interpretation is that the number of possible theorems obtained by forming amino-acid sequences is much smaller than the number of truths. One could always add "axioms" by realizing the remaining truths in some new manner but since the number of levels in the Combinatorial Hierarchy is infinite (assuming that the Mersenne numbers in question are primes) there are always unprovable truths in the system. One can obviously classify the formal systems according to which level is the basic irreducible level inducing genetic code at higher levels.

$p = 7$ ($n = 2$) and $p = 3$ ($n = 1$) level as the defining, irreducible level are also in principle possible.

1. At level $p = 7$ 4 doublets of level $p = 3$ "DNA" code 2 "pre-amino-acids" plus stopping sign and at the next level this coding induces $2^3 = 8 < 21$ different "amino-acids" since stopping sign does not appear in theorems. If stopping sign would correspond to actual amino-acid there would be $3^3 = 27 > 21$ theorems so that the number of theorems would be larger than the number of truths!

2. At level $p = 3$ 2 "DNA": s of code one amino-acid plus stopping sign so that genetic code is one-to-one.
   An interesting possibility is that $p = 3$ and $p = 7$ levels might have been defining, irreducible levels for bio-systems at some early stage of evolution. These formal systems can be regarded as a subsystem of the full DNA-amino-acid system. RNA-triplets of form UXY, $X, Y \in \{A, C\}$ give indeed realization for $p = 7$ system: UAA codes stopping sign, UAC codes cys and UCA and UCC code ser (using the standard short hand notation for RNA: s and amino-acids [A5]). The sequences formed from these DNA: s and corresponding amino-acids indeed realize $p = 7$ formal system as subsystem of $p = 127$ system. $p = 3$ formal system can be realized as UAA coding stopping sign and UAC coding cys. An interesting possibility is that this DNA-amino-acid subsystem has formed first in the biochemical evolution. For both $p = 3$ and $p = 7$ degenerate genetic codes one has $G + C/A + U = 1/2$. $G + C/A + U$ content varies in the range $(.7, 1.5)$ for insects and in the range $(1.17, 1.56)$ in the case of fish and for younger evolutionary forms A+U content is known to increase [I42].

3. The transition to "$p = M_{127}$ life" would require the addition of a rather large number of new "amino-acids" to the set of all possible amino-acid sequences consisting of 21 amino-acids whereas DNA triplets could be simply replaced with sequences of 21 DNA triplets. In the transition to $p = 127$ life tRNA triplets binding single amino-acid would be replaced by sequences of 21 tRNA triplets binding besides amino-acid sequences suitably modified amino-acid sequences in order to achieve maximal number of "amino-acids" at level $p = 127$. Also the modification of the translation system (in ribosomes) is required so that the "reading head" recognizes a sequence of 21 mRNA-triplets instead of single mRNA triplet. An interesting question is whether biochemistry might allow this kind of extension.

2.2.9 Summary

The simple model of abstraction has rather interesting connections with genetic code.

1. Combinatorial Hierarchy results as hierarchy of abstraction levels for statements or thoughts. Lowest level A_2 corresponds to the two possible values of Boolean variable and thoughts of

the level A_{n+1} correspond to statements about statements of level n that is Boolean maps $A_n \to A_2$. If the statement corresponding to sequence of zero bits is excluded the dimensions form a series of Mersenne numbers $3, 7, 127, M_{127}, ...$ Combinatorial Hierarchy is obtained also by considering the set of subsets with empty set excluded. The hypothesis that there is no upper bound for intelligence is equivalent with the hypothesis that these numbers are primes and that the numbers $p_n - 1$ in the sequence have the property that $p_n - 1$ divides $p_{n+1} - 1$. This implies that one obtains a hierarchy of Finite Fields $G(p_n, 1)$ and their multiplicative groups Z_{p_n-1} as well as coset groups $Z_{p_n-1}/Z_{p_{n-1}-1} = Z_{k_n}$, $k_n = (p_n - 1)/(p_{n-1} - 1)$.

2. There are $(p_n + 1)/2$ statements consistent with a given atomic statement at level n and the numbers come as $2, 4, 64, ...$ These statements are referred to as "DNA" type statements for obvious reasons. The dimensions k_n comes as $2, 3, 21, ...$ The hypothesis is that amino-acid type statements correspond to the statements of $Z_{k_n} \subset Z_{p_n-1}$ and can be regarded as general theorems whereas DNA type statements correspond to special cases of these theorems and are mapped to general theorems the mapping $x \to x^{p_{n-1}-1}$ at level n. At level n the genetic code corresponds to the non-unique choice of the $(p_n + 1)/2$ DNA type statements consistent with a given atomic statement in Z_{p_n-1}.

3. Biologically Genetic Code is determined by the competition between amino-acids: each amino-acid tries to maximize the number of DNA: s coding it (amino-acids are like politicians who are representatives of one truth and DNA: s are in the role of voters). The tendency favors $Z_{p_{n-1}-1}$ (Z_6) symmetry. The physically realized code can be understood as resulting from the symmetry breaking caused by the competition between the groups $Z_{p_{n-1}-1}$ (Z_6) acting on DNA: s associated with single amino-acid and factor groups of Z_{k_n} $(Z_{21} = Z_3 Z_7)$ transforming amino-acids to each other. Instead of finite dimensional representations of Lie groups the orbits of the cyclic groups Z_n are basic objects in the symmetry breaking mechanism.

4. At level n basic objects are k_{n-1}-plets of DNA: s of level $n - 1$ and sequences of same DNA units can in principle appear at all levels of the hierarchy. At the next $k = M_{127}$ level "DNA": s could therefore be regarded as sequences of 21 DNA triplets.

5. A hierarchy of increasingly complicated formal systems is predicted if one accepts the hypothesis. For the formal system of order n n: th level of the Combinatorial Hierarchy is the defining level in the sense that the number of "amino-acids" is maximal and equal k_n. Formal systems of order $n_1 < n$ are imbeddable into the formal system of order n. The formation of amino-acid sequences corresponds to the formation of theorems. For a formal system of order n amino-acid sequences realize only a small subset of all possible k_{n_1} truths at higher levels $n_1 > n$ of the Combinatorial Hierarchy in accordance with Gödel's theorem. One can also classify all possible bio-systems according to the value of n for the corresponding formal system. The Earthly life corresponds to $n = 3$ formal system and "life of order 4" would require the addition of rather large number of new "amino-acids" to the set of all possible amino-acid sequences consisting of 21 amino-acids whereas DNA triplets could be simply replaced with sequences of 21 DNA triplets. The realization of "$n = 4$ life" requires that tRNA triplets binding single amino-acid are replaced by sequences of 21 tRNA triplets binding besides amino-acid sequences suitably modified amino-acid sequences in order to achieve maximal number of "amino-acids" at level $n = 4$. Also the modification of the reading system (in ribosomes) is required so that the "reading head" recognizes a sequence of 21 mRNA triplets instead of single mRNA triplet.

6. An open problem relates to the precise role of DNA and proteins. The model of Boolean thoughts represented in terms of the cognitive fermion pairs leads to the correspondence between fermions and mind like space-time sheets and gives Combinatorial Hierarchy a special status. What comes in mind is that DNA provides a hardware representations of thoughts analogous to a computer memory. DNA molecules would be conscious selves representing 3 basic symbols in the mind of higher level self formed by DNA triplet. DNA sequences would be selves, experiencing DNA triplets as their sub-selves. Individual DNA molecules would represent sub-sub-selves so that DNA sequence would experience only the average of the experiences of individual DNA molecules.

7. It deserves to be noticed that I Ching claims that there are 64 fundamental mental states: could it be that these mental states correspond to all possible DNA triplet selves? It this interpretation is correct then Buddhist meditators would have achieved bio-feedback at DNA level! Genetic Code itself could be interpreted as a mapping of DNA selves to protein selves: this could be perhaps regarded as kind of mimicry or conscious abstraction process. Protein selves would represent theorem like abstractions of conscious thoughts represented by DNA selves.

8. It is known that cell numbers of different cell types in nervous, muscular, adipose, gonadic and homopoietic organs concentrate themselves around powers of two – 2^n, where n in the range $20-40$ [I49]: this can be understood if they result in n regularly occurring cell divisions. It might however be that the explanation of the regularity involves something much deeper. For instance, the cell types represent various n-bit sequences.

2.3 Combinatorial Hierarchy: two decades later

Combinatorial Hierarchy (CH) [A10, A17] is a hierarchy consisting of Mersenne integers $M(n) = M_{M(n-1)} = 2^{M(n-1)} - 1$ and starting from $M_1 = 2$. The first members of the hierarchy are given by $2, 3, 7, 127, M_{127} = 2^{127} - 1$ and are primes. The conjecture of Catalan is that the hierarchy continues to some finite prime. It was proposed by Peter Noyes and Ted Bastin that the first levels of hierarchy up to M_{127} are important physically and correspond to various interactions (see `http://tinyurl.com/hszo9wb`). I have proposed the levels of CH define a hierarchy of codes containing genetic code corresponding to M_7 and also memetic code assignable to M_{127} [K30].

Pierre Noyes and Ted Bastin proposed also an argument why CH contains only the levels mentioned above. This has not been part of TGD view about CH: instead of this argument I have considered the possibility that CH does not extend beyond M_{127}. With the inspiration coming from email discussion I tried to understand the argument stating that CH contains M_{127} as the highest level and ended up with a possible interpretation of the condition. Zero energy ontology (ZEO) and the representation of quantum Boolean statements $A \to B$ as fermionic parts of positive and negative energy parts of zero energy states is essential. This led to several interesting new results.

1. To my best understanding the original argument of Noyes does not allow M_{127} level whereas prime property allows. States at M_{127} level cannot be mapped to zero energy states at M_7 level. Allowing a wild association with Gödel's theorem, one could say that that there is hube number of truths at M_{127} level not realizable as theorems at M_7 level.

   A possible interpretation is that M_{127} level corresponds to next level in the abstraction hierarchy defined by CH and to the transition from embedding space level to the level of "world of classical worlds" (WCW) in TGD. The possible non-existence of higher levels (perhaps implied if $M_{M_{127}}$ is not prime) could be perhaps interpreted by saying that there is no "world of WCWs"!

2. Rather remarkably, for M_7, which corresponds to genetic code [K30], the inequality serving as consistency condition is saturated. One can say that any set of 64 statements consistent with a given atomic statement (1 bit fixed) at M_7 level can be represented in terms of 64 Boolean maps at M_3 level representable in terms of zero energy states. One obtains an explicit identification for the Boolean algebras involved in terms of spin and isospin states of fermions in TGD framework at level M_7 so that genetic code seems to be realized at the fundamental elementary particle level thanks to the dimension $D = 8$ of embedding space. Even more, the level M_{127} corresponding to memetic code emerges in the second quantization of fermions at M_7 level. Here color triplet property of quarks and color singletness of leptons and the identification of elementary particles as pairs of wormhole contacts are in essential role.

The conclusion would be that in TGD Universe genetic code and its memetic counterpart are realized at the level of fundamental particles. Already earlier I have ended up with alternative realizations at the level of dark nucleons and sequences of 3 dark nucleons [L22].

2.3.1 Summary of Combinatorial Hierarchy

I summarize first the basics of CH.

1. One considers the space algebra of Boolean statements of n bits which can be also extended to complex linear space -quantum Boolean algebra. One can give it linear structure as Z_2 algebra for binary coefficients with Z_2 sum having set theoretic interpretation. This linear space has some basis. That the coefficient field for linear structure is Z_2 does not seem to be absolutely essential. In TGD framework one considers the linear space defined by quantum Boolean algebra with qubit interpretation generated by fermionic oscillator operators: one operator for every bit.

2. One assigns to the linear n-D space the n^2-D space of linear maps of it to itself. One can also consider the space of maps of quantum Boolean algebra to itself and also require that this defines a Boolean homomorphism. Dimensions would be the same: only coefficient field would be different.

3. To CH level, which corresponds to Mersenne prime $M(n) = M_{M(n-1)}$ ($n = 2, 3, 7, 127, 2^{127} - 1, ...$) one assigns vector space with dimension

$$D(n-1) = [(M(n-1)+1)]^2 \ ,$$

and requires that the space formed by

$$D_1(n) = \frac{(M(n)+1))}{2}$$

bit sequences, which represent a subset of mutually consistent Boolean statements as subset of $M(n)+1$ bit sequences are representable as a subset of bit sequences with $D(n-1)$ bits. This demands

$$D_1(n) \leq D(n-1)$$

giving

$$\frac{M(n)+1)}{2} \leq [M(n-1)+1]^2 \ .$$

4. This criterion is satisfied for the primes of CH up to M_7 but not for M_{127}: $2^{127} - 1 > 128^2$ so that M_{127} should not included if I have understood the criterion correctly.

   For $M_7 = 2^7 - 1 = 127$ one obtains the condition $2^6 = 64 \leq 8 \times 8 = 64$ so that condition is saturated. Remarkably, 64 is the number of DNA codons!

5. The numbers of CH are also known as Catalan Mersenne numbers. Catalan Mersenne primes are special case of double Mersenne primes M_{M_n} (see `http://tinyurl.com/j4tqwch`). Catalan conjecture that Catalan Mersennes are primes up to some limit. After the first non-prime the remaining Catalan Mersenne numbers are necessarily composite. The known double Mersennes are given by M_{M_p}: $p = 2, 3, 5, 7$. No other cases are known. These primes are good candidates for labelling scaled up variants of say hadron physics. To my opinion Catalan criterion is more plausible.

6. Classical number fields are in key role in TGD [K70, K63, K27] and have dimensions $D = 1, 2, 4, 8$. Also CH involves these dimensions. $D(n-1) = M(n-1)+1$ giving dimensions $2, 4, 8$ for M_2, M_3, M_7. For M_{127} one would obtain $D = 128$, which does not correspond to any division algebra. This might relate to the above observation.

2.3.2 CH as a prediction of quantum TGD

In the following the interpretation of Boolean map in ZEO is proposed. Also it is shown that M_7 level allows a natural realization in terms of spin-isospin states of fermions and that M_{127} level is obtained in second quantization meaning going from the level of embedding space to the level of WCW.

Interpretation of the lower level Boolean map in terms of ZEO

One can ask, why one should have this kind of map? One interpretation is that the space of Boolean statements at given level is imbeddable to the space of quantum Boolean maps at previous level. Quantum Boolean maps would represent Boolean rules A→ B, "theorems" or "laws of physics".

1. In TGD framework the interpretation of CH would be as a hierarchy of statements about statements about... The number of statements about N statements is indeed 2^N. One statement corresponding to all bits equal to 0 (in set theoretic realization empty set) is thrown away so that one has $2^N - 1$ statements instead of 2^N.

2. ZEO means that physical states are pairs of states with opposite conserved quantum numbers: they correspond to physical events, which replace states as fundamental entities in ZEO. The fermionic parts of positive and negative energy parts of states would be pairs of many-fermion states allowing interpretation as elements of quantum Boolean algebra. Zero energy states themselves would correspond to pairs of these fermionic states and thus to "theorems" A→ B or maps from Boolean algebra to itself. The allowed statement pairs would satisfy fermion number conservation and conservation of various quantum numbers and would indeed represent laws of physics.

3. A possible interpretation of the map would be that the statements at given level $M(n+1)$ must be representable as theorems at previous level $M(n)$. For $M(n) > M_7 = 127$ this would not hold true anymore. Could this have some deep mathematical meaning as the wild association with Goedel's theorem suggests?

   In the model of genetic code and its generalizations [K30] I have proposed that each level of CH defines a maximal number of set of statements forming a set theoretic inclusion hierarchy and logical implication hierarchy: the number is 2^{n-1} for 2^n n-bit statements. For $M_7 = 127$ the number is 64, the number of DNA codons, which would thus have interpretation as axioms or "fundamental truths". In this case the representability would still hold and map would be bijection. At the next level one would have "memetic code" with 2^{126} codons representable as sequences of 21 DNA codons with stop codon included ($126 = 21 \times 6$). By the proposed criterion, at memetic level only vanishingly small subset of truths would be representable as theorems at genetic level.

Representation of M_7 level in TGD framework

Could the saturation for M_7 have some physical meaning? The maps would be from 8-D space to itself.

1. Bits can be represented in terms of spin and electroweak spin giving $2 \times 2 = 4$ states and embedding space-spinors ($H = M^4 \times CP_2$) of given H-chirality (quark or lepton like), given fermion number (fermion or antifermion) and physical helicity. If also unphysical helicities with fixed fermion number are allowed one would have $4 + 4 = 8$ states. The condition that helicity is physical would reduce the number of states by one half. This applies to both quarks and leptons since color is not spin like quantum number in TGD (colored states correspond to partial waves in CP_2).

2. What could be the interpretation for $2^7 - 1 = 127$ states containing as subset $n = 2^6$ states. Could $n = 2^6$ correspond to the number of states in the tensor product formed by pairs of 8 leptons and 8 antileptons allowed to have also unphysical polarizations? Same would apply to quarks. Allowing both quark-antiquark and lepton-antilepton type states one would have 128 states. The physicality condition for boson polarizations could drop the number of states

to 64. What the dropping of one state would correspond: to the dropping of $\nu_R - \overline{\nu}_R$ pair having no electroweak and color couplings perhaps?

One can imagine two alternative identifications for the two tensor factors.

(a) In TGD framework fundamental bosons correspond to fermion antifermion pairs with members at opposite throats of wormhole contact connecting two space-time sheets. Could the genetic code correspond to 64 elementary bosons with physical polarizations and the maps to those assigning to 8 fermions 8 antifermions?

(b) An alternative identification is suggested by ZEO. The tensor product of fermionic Boolean algebras at opposite boundaries of causal diamond (CD) would replace that at opposite wormhole throats. This would in accordance with the interpretation of zero energy states as statements $A \to B$ represented as Boolean maps.

Representation of M_{127} level in TGD framework

What about the physical interpretation of M_{127} level in TGD framework?

1. The first thing to observe is that physically $p = M_{127}$ corresponds in TGD to the p-adic prime p characterizing electron in p-adic mass calculations: Compton length is proportional to the p-adic length scale and thus proportional to $\sqrt{p}$. The remaining Mersenne primes correspond to completely super-astrophysical Compton lengths. Hence M_{127} has a very special role. The Mersenne primes $3, 7, 31, 127$ giving rise to double Mersenne primes correspond to extremely short p-adic length scales.

   Recall that the ratio of m_{CP_2}/m_e is approximately $m_{CP_2}/m_e = 2^{127/2}/\sqrt{5+x}$, where $x \in [0,1]$ characterizes the second order contribution to electron mass from p-adic mass calculations [K39]. The ratio of Planck mass to proton mass equals to $m_{Pl}/m_p = 1.307 \times 10^{19}$. For $x = 0$ this gives $m_{Pl}/m_{CP_2} = (m_p/m_e) \times 3.96 = 7.271 \times 10^3$, which is not far from $2^{13} \simeq 8.912 \times 10^3$. The value of 2^{13} is very attractive number theoretically and would be obtained for $x = .5$, again power of 2.

2. The states at this level should correspond to statements about statements at the lower level represented in terms of quark lepton state space as many-fermion states assignable to wormhole throat or several wormhole throats (elementary corresponds to two wormhole contants and 4 wormhole throats). The construction of infinite primes can be interpreted as a process of forming repeatedly statements about statements and the physical analog is repeated second quantization [K69].

   In the recent situation second quantization would correspond to the formation of many-fermion states at partonic 2-surfaces defined by the throats of wormhole contacts. This would automatically give rise to M_{127} states if one has 127 single fermion states to begin with.

   Physically this step would correspond to a step from the spinor modes of embedding space to the spinor modes of WCW identifiable as fermionic Fock states assignable to partonic 2-surfaces so that indeed a huge abstraction is in question. I have proposed that anyonic states could be this kind of states for large value of $h_{eff} = n \times h$ implying that the size of wormhole throat becomes nano-scopic [K54].

3. One has 127 boson states but how to obtain 127 (or $128 = 2^7$) single fermion states? Counting only spin and weak isospin gives $n = 8 + 8 = 2^4$ ($n = 4 + 4 = 2^3$) single fermion states if one allows (does not allow) also unphysical polarizations. The simplest option is that each single fermion state has 2^3 (2^4) additional states. The location of fermion at one of the 4 wormhole throat could give 4 additional degrees of freedom. This would leave 2 (4) additional states per fermion state still missing.

4. A good guess is that quark color realized as color partial waves comes in rescue and gives the needed states. Light quarks must move in color triplet states and leptons in singlet states. Thefore quarks have $3 \times 8 = 24$ modes and leptons 8 modes giving altogether 32 modes altogether. There are 4 wormhole throats so that $4 \times 32 = 128$ modes are obtained

and if right-handed neutrino is thrown out one has 127 states as required if no constraints on polarizations are posed. It therefore seems that TGD physics codes CH naturally at elementary particle level!

There is indeed a rich set of "vibrational" degrees of freedom giving also rise to color degrees of freedom. The symplectic group of $\Delta M^4_{\pm}$ assignable to either boundary of causal diamond (CD) defined as the intersection of future and past directed light-cones of M^4 with points replaced with CP_2 gives rise to products of S^2 and CP_2 partial waves. Besides this there is a conformal weight labelling the states correlating with $S^2 \times CP_2$ partial wave Light quarks massless before massivation by p-adic thermodynamics move in color partial waves and color triplets are obtained as the color excitations for them corresponding to higher conformal weights and having CP_2 mass as mass scale.

I have already earlier ended up with the proposal that genetic code is realized at the level of dark nuclear physics. Either the states of dark proton or sequence of 3 protons could be organized naturally states corresponding to 64 DNAs, 64 RNAs, 20 aminoacids, and 40 tRNAs and vertebrate genetic code follows from very simple assumption that opposite spins are paired [L2, K31] [L22] (see `http://tinyurl.com/jgfjlbe`). These findings suggest that genetic code and memetic code are also realized at the elementary particle level.

Acknowledgements: I am gratetul for James Bowery for raising the question about the possible relevance of CH for TGD.

2.4 Number theoretical models for genetic codes

The naïve thinking would suggest that the DNA-amino-acid correspondence is unique and same in the alien biology as in our biology. This is not the case. The notion N-particle leads to a model how N-hydrogen atoms define names for molecules and how molecules with conjugate names form especially stable bound states and how the same mechanism explains lock and key mechanism of bio-catalysis. The lock and key mechanism depends only weakly on chemistry and it is quite possible that several genetic codes are realized.

Hence the tRNA molecules mediating DNA-amino-acid correspondence could be different for various life-forms. The stability of various possible tRNA type molecules determining the code would be determined by the electromagnetic environment. Therefore one must take genetic code as a result of selection. The findings about the alien codes, if taken seriously, suggest also guesses about the origin of the genetic code.

The basic new result inspired by the attempt to identify the alien genetic code is the finding that both our and alien genetic codes factorize in a good approximation to a product codes associated with DNA doublets and singlets. This raises the question whether the factorization occurs also at the level of amino-acids. Could DNAs triplets have resulted as a symbiosis of singlets and doublets whereas amino-acids might have been developed via a symbiosis of 2 (3) molecules coded by 4 DNA singlets and 10 (7) molecules coded by 16 DNA doublets?

2.4.1 Three kinds of number theoretical models for the genetic code

TGD has led to three different number theoretic approaches concerning the understanding of the genetic code.

1. In [K30] the model of the genetic code based on the notion of Combinatorial Hierarchy is discussed. This approaches predicts at least one additional code that I have christened memetic code.

2. In [K18] a universal number theoretical code giving genetic code as a special case and based on the maximization of a number theoretic information measure was developed.

3. The model based on the assumption that genetic code has evolved from a product code is the one to be discussed in this chapter (see also the discussion in [**?**]).

Genetic codes as deformations of product codes

In this section number theoretical models based on the approximate factorization of the genetic code into product code formed by doublet and singlet codes are discussed. Product code as such predicts degeneracies approximately but fails at the level of detailed predictions for DNA-amino-acid correspondences. A volume preserving flow in discrete DNA space is needed to produce realistic DNA-amino-acid correspondences. This flow has the general tendency to cluster amino-acids to connected vertical stripes inside the 4-columns appearing as elements of the 4×4 code table, whose elements are labelled by the first two bases of DNA triplet. One can invent an information maximization principle providing a quantitative formulation for this tendency.

Genetic codes based on the maximization of number theoretic information measure

In the chapter [K18] an alternative number theoretic model for the ordinary genetic code and its variants is discussed. This model is based on very general number theoretic notions, in particular, number theoretical generalization of Shannon entropy, and must be regarded as the most convincing one of the three number theoretic models constructed hitherto. This model allows to identify ordinary genetic code and its variants as codes maximizing a unique number theoretic information measure. The model is also consistent with the idea that genetic code has evolved from a product of singlet and doublet codes.

The model predicts the number for "amino-acids" once the number n of "DNAs" is known as $N(n) + 2$, where $N(n)$ is the number of primes not larger than n. For 80 DNA triplets the prediction would be $24 = 3 \times 8$ rather than 23 amino-acids. Hence the two models for the genetic code would not be consistent.

Before making any hasty conclusions one should recall that the interpretation of the Crabwood circle as ASCII text involves considerable uncertainties. A modification of single special symbol or small letter to a symbol not appearing in the proposed interpretation of the Crabwood message would give 24 "amino-acids". For instance, the ASCII symbols for dot *resp.* comma are 00110100 *resp.* 01110100 and differ only by a single bit so that misinterpretation cannot be excluded.

This model of genetic code emerged much later than the model for alien genetic codes and is not discussed in this chapter.

2.4.2 Does amino-acid structure reflect the product structure of the code?

The exact A-G symmetry and the almost exact T-C symmetry of our genetic code supports approximate 2×10 structure such that 16 DNA doublets and 4 DNA singlets code for 10 *resp.* 2 "pre-amino-acids" which combine to form the real amino-acids. The 3×7 decomposition of the number 21 of amino-acids plus stopping sign suggests 3×7 decomposition of the genetic code. This decomposition is however not favored by the symmetries of the genetic code.

The coding of amino-acids involves tRNA binding with amino-acids and this means that the structure of amino-acids need not reflect the product structure of the genetic code and it might be that only the structure of tRNA reflects the product structure. Indeed, the identification of pre-amino-acids as DNA singlets or doublets dictated by RNA-DNA translation mechanism is strongly favored by the physical model for the evolution of the genetic code. With this identification triplet pre-amino-acids (DNA triplets) are simply composites of doublet and singlet pre-amino-acids (DNA doublets and singlets).

Despite this interpretation, the study of the amino-acid geometric structure is in order. It does not reveal any obvious structural 3×7-ness or 2×10-ness. One can however wonder whether this kind of structures might be present at more abstract level and present only in the interactions of tRNA and amino-acids.

1. 2×10 *product structure at amino-acid level*

2×10 decomposition for real amino-acids might approximately correspond to hydrophobic-hydrophilic dichotomy which plays a key role in the amino-acid chemistry. This correspondence

cannot be very precise since the number of the hydrophobic (-philic) amino-acids is 8 (12) rather than 10 (10). Of course, this is what one expects since the product symmetry is broken.

2. 3×7 *product structure at amino-acid level*

Aminocids can be classified into three groups. The first class contains 8 hydrophobic non-polar amino-acids: ala, val, leu, ile, pro, met, phe, trp, Second class consists of 7 hydrophilic polar amino-acids gly, ser, thr, cys, asp, glu, tyr. The third class consists of polar hydrophilic acidic amino-acids asp, glu and hydrophilic basic amino-acids lys, arg, his: 5 altogether.

Could these three classes correspond to the 3×7-ness?

1. First of all, the non-varying group contains almost(!) as a rule both the acidic carboxy group $COOH$ which tends to ionize to COO^- and basic aminegroup NH_3 which tends to ionize to NH_3^+. When carboxy or amine group is associated with the side group, the 2+3=5 acidic or basic polar amino-acids result. Thus the three-ness in standard sense corresponds to the difference for the total numbers of acidic and basic groups of the side chains: amino-acid side chain is either neutral and non-polar, neutral and polar, or charged. This leads to 8+7+5 decomposition and a slight breaking of three-ness.

2. One could however consider a modified definition in which one counts the numbers N_+ of basic and N_- of acidic groups of the *entire* amino-acid and uses the difference $N_+ - N_-$ to tell the net charge of the amino-acid. If this criterion is used, the first group contains one alien, proline. Proline differs from all other amino-acids in that the neutral group $H_3N^+ - COO^- - C - H$ group is replaced by a charged $HN - COO^- - C - H$ group. But this means nothing but replacing the basic group NH_3^+ with a non-basic NH. This implies also a net charge for proline. If net charge is taken as the characterizing property of the third group of amino-acids, proline belongs to it. Therefore first and second would group contain 7 amino-acids and the third group would contain 3 positively charged and 3 negatively charged amino-acids.

3. If one thinks that stopping sign formally corresponds to one additional amino-acid in the third group, one indeed has 7+7+7 decomposition. For some rare life-forms to be discussed later stopping sign codon ATC can code for both stopping sign and non-standard amino-acid pyrrolysine depending on context [I10]. Pyrrolysine, being a derivative of lysine, is basic so that in this case one would have 7+7+7 decomposition even without counting stopping sign formally as an amino-acid.

The 7-ness index labelling the amino-acids with the three groups should be some abstract property and it is impossible to make any conclusions on basis of the chemical formulae alone.

3. Is the product structure at the level of amino-acids really needed?

It has become clear that the product structure for amino-acids is not necessary.

1. The number theoretic model of the genetic code discussed in [K18] neither predicts nor requires the product structure for amino-acids but is consistent with the approximate product structure for codons.

2. In [**?**] a model for the evolution of the genetic code from a product code mapping RNAs to a subset of RNAs is studied. In this model the product structure at the level of coded RNAs is natural but there is no reason for it at the level of amino-acids which, according to the model, originally only catalyzed RNA→ RNA mapping but later replaced the coded RNAs in a kind of palace revolution.

2.4.3 Number theoretical model for the terrestrial genetic code

The study of the terrestrial genetic code allows to deduce the process leading to the breaking of the product symmetry and T-C symmetry. This process turns out to work as such also in case of alien codes.

Approximate reduction to a product code

The dependence of the amino-acid coded by DNA on the third codon of DNA triplet is weak and Crabwood message suggests that both doublet and triplet codes are realized. This inspires the guess that triplet code might have evolved as a fusion of doublet code and singlet codes.

This should be reflected in its structure. There are two options.

1. The decomposition $20 = 2 \times 10$ for real amino-acids suggest that singlet code maps four bases to 2 "pre-amino-acids" such that A and G resp. T and C are mapped to same pre-amino-acid, and 16 doublets to 10 "pre-amino-acids". The exact A-G symmetry and almost exact T-C symmetry of our genetic code support this interpretation.

2. The decomposition $21 = 3 \times 7$ for amino-acids plus stopping sign suggests that singlet code maps four bases to 3 "pre-amino-acids" and 16 doublets to 7 "pre-amino-acids". In the first approximation the triplet code would decompose to a product of doublet code and singlet code in the sense that 4 singlets are mapped to Z_3 and 16 doublets are mapped to Z_7 so that 21 different product states result. The decomposition of the statements consistent with some atomic statements suggests itself strongly. In the first approximation the triplet code would decompose to a product of doublet code and singlet code in the sense that 4 singlets are mapped to Z_3 and 16 doublets are mapped to Z_7 so that 21 different product states result. The problem of this option is that it predicts complete breaking of T-C symmetry and the breaking of the product symmetry should produce T-C symmetry. This looks two complicated.

Product code hypothesis is very strong since the degeneracies of the product code are products of the degeneracies for the composite codes so that the number n_{AB} of DNA triplets coding a given amino-acid having the product form "AB", to be referred as the degeneracy of the amino-acid, is given by the product

$$n_{AB} = n_A \times n_B$$

of the degeneracies of the "pre-amino-acids" A and B. Here A and B can refer to $(A, B) = (3, 7)$ or $(A, B) = (2, 10)$ respectively.

The number $N_{AB}(n)$ of amino-acids with given degeneracy n is given by the formula

$$N_{12}(n) = \sum_{n_1 \times n_2 = n} N_1(n_1) N_2(n_2) \ ,$$

where $N_1(n_1)$ resp. $N_2(n_2)$ is the number of pre-amino-acids with the degeneracy n_1 resp. n_2.

For 2×10 case singlet sector allows only single candidate for the code since the genetic code has exact A-G symmetry and almost exact T-C symmetry with respect to the last base. Thus A and G code for the first pre-amino-acid and T and C the second one. A breaking of the T-C symmetry is needed to obtain realistic code.

In 3×7 case singlet code would have following interpretation. Z_3 is identified as negations of 4 selected statements with 00 excluded. Statement and its negation are projected to this Z_3 representing negations with 00 excluded so that 11 must be projected to some other statement. The degeneracies of the code are unique: 2, 1, 1 since any change of the code changing this degeneracy spectrum implies that one degeneracy vanishes.

Same applies to Z_7 and 16 DNA doublets. Now 1111 is mapped to some statement in the set of negations. In this case the simplest coding is obtained by mapping 7 statements to their conjugates and the two remaining statements to different conjugate statements in the set of 7 statements. The resulting degeneracy structure is 2222233 and entropy is maximal for this code.

Our genetic code as result of symmetry breaking for 2×10 product code

As found, there are two cases to be considered: 3×7 T-C asymmetric and 2×10 T-C symmetric product code. The approximate T-C symmetry favors strongly 2×10 option and 3×7 will be considered only briefly in a separate subsection. On basis of degeneracies alone it is not possible to distinguish between these codes and 3×7 code was in fact the first guess for the product code.

n	1	2	3	4	6
N(prod)	0	12	0	4	4
N(real)	2	9	2	5	3

Table 2.6: The numbers $N(n)$ of amino-acids coded by n DNAs for unperturbed 2×10 product code and for the real genetic code for 2×10 option.

In case of 2×10 code the decomposition of 16 DNA doublets giving almost the degeneracies of our genetic code is (3322 111 111).

$$(2 \oplus 2) \times (3 \oplus 3 \oplus 2 \oplus 2 \oplus 6 \times 1)$$

This gives

It is important to notice that the multiplets appear as doubled pairs corresponding to A-G and T-C symmetries. One generalized amino-acid (which cannot correspond to stopping sign) is lacking and must result by a symmetry breaking in which one amino-acid in the code table is transformed to a new one not existing there. Alternatively three amino-acids are transformed to stopping signs.

It is easy to find the deformation yielding correct degeneracies by removing DNAs from the DNA-boxes defined by various values of degeneracies to other boxes and adding them to other boxes. The rule is simple: taking m DNAs from a box containing n DNAs creates a box with $n - m$ DNAs and annihilates one n-box:

$$N(n) \to N(n) - 1 \ , \quad and \ N(n-m) \to N(n-m) + 1 \ .$$

If one adds k of these DNAs to r-box one has

$$N(r) \to N(r) - 1 \ , \ \ N(r+k) \to N(r+k) + 1 \ .$$

The operation which is not allowed is taking the entire content of a DNA box defined by amino-acid and adding it to other boxes since this would mean that the amino-acid in question would not be coded by any DNA. Thus the number of boxes can only grow in this process.

Realistic degeneracies are obtained by a rather simple operation.

1. Take from one 6-plet two amino-acid and move the first of them to 2-plet to get $N(6) = 3$, $N(4) = 5$, $N(3) = 1 < 2$, $N(2) = 11 > 9$ and move the second one to hitherto non-existing singlet to get $N(1) = 1$.

2. Move one DNA from some doublet to second doublet to get triplet and singlet to get $N(1) = 2$, $N(2) = 9$ and $N(3) = 2$. This operation gives correct degeneracies only and it turns out that correct symmetry structure requires additional operations.

Failures of the product structure and the symmetry breaking as volume preserving flow in DNA space

A slightly broken product structure allows to understand the degeneracies of our genetic code relatively easily. It however leads also to wrong predictions at the level of DNA-amino-acid correspondence.

1. Exact product structure predicts that all 4-columns XYU, $U = A, G, T, C$ appearing as elements of the code table labeled by first and second bases of DNA triplet should have similar amino-acid structure. For 3×7 code the 4-column should have $AABC$ structure. This is not case. Almost all 4-columns have $AABB$ structure and there are also many $AAAA$ type 4-columns. For 2×10 code the prediction is that all 4-columns should have $AABB$ structure and this prediction breaks down only for $AAAA$ type 4-columns.

2. For 3×7 code a given amino-acid should be coded by DNA pairs of form (XYA, XYG), or DNA of form XYC or XYT. For 2×10 code a given amino-acid should be coded either by DNA pairs of form (XYA, XYG) or of form (XYC, XYT). This is not the case. A given amino-acid tends to appear as connected vertical stripes inside the elements of the 4×4 table (4-columns). For instance, all 4-columns of form $AAAA$ (A=leu, val, ser, pro, thr, ala, arg, gly) and 3-column ile break the prediction of the product code.

3. For 3×7 each 2n-plet formed by degenerate (XYA, XYG)-pairs is accompanied by n-plets of type XYT and XYC. In case of 2×10 2n-plet formed by (XYA, XYG)-pairs is accompanied always by an 2n-plet formed by (XYT, XYC) pairs. By studying the degeneracies of the codes one can get idea about how good these predictions are.

It seems that the breaking of the product symmetry tends to form connected vertical clusters of amino-acids inside a given element of the 4×4 code table but that one cannot regard stripes longer than 4 elements as connected structures. The 2×10 structure is favored by approximate T-C symmetry, and one can imagine that relatively simple flow in DNA space could yield the desired condensation of the amino-acids to form connected vertical stripes. The most general flow is just a permutation of DNAs and obviously preserves the degeneracies of various amino-acids. There are 64! different permutations but A-G and T-C symmetries reduce their number to 32!.

The idea about discrete volume preserving flow in DNA space can be made more precise. A-G and T-C gauge symmetries suggest the presence of a discrete symplectic structure. Perhaps one could regard 16×4 DNAs as 16 points of 4-dimensional discrete symplectic space so that the canonical symmetries of this space (volume preserving flows) acting now as permutations would be responsible for the exact A-G gauge invariance and approximate T-C gauge invariance. This brings in mind the canonical symmetries of CP_2 acting as $U(1)$ gauge transformations and acting as almost gauge symmetries of the Kähler action.

A natural guess is that the DNAs coding same amino-acid tend to be located at the same column of the 4×4 code table before the breaking of the product symmetry. If this is the case then only vertical flows need to be considered and A-G and T-C symmetries imply that their number is $8!^4$ corresponding to the four columns of the table.

The **Table 2.9** summarizes our genetic code. It is convenient to denote the rows consisting of A-G resp. T-C doublets by X_1 and X_2. For instance, A_1 corresponds to the highest row phe-phe, ser-ser, tr-tyr, cys-cys and G_2 to the row leu-leu, pro-pro, gln-gln, arg-arg.

1. The simplest hypothesis is 2×10 option is realized and that the flow permutes entire rows of the code table consisting of A-G and T-C doublets. From **Table 2.7** it is clear that there is a G-C symmetry with respect to the first nucleotide broken only in the third row. This kind of primordial self-conjugacy symmetry would not be totally surprising since first and third nucleotides are in a somewhat similar position.

2. There are 3 6-plets leu, ser, and arg, and it is easy to see that one cannot transform them to the required form in which all 6-plets are on A-G or T-C row alone using this kind of transformation. For instance, one could require that leu doublets correspond to T-C doublets before the symmetry breaking. This is achieved by permuting the G_1 row with the C_2 row. Since A_2 contains also ser-doublet, also ser must correspond to T-C type 6-plet, and since arg is contained by G_2 row, also arg must correspond to T-C type 6-plet. Thus there would be 4 T-C type 6-plets but the product code gives only 2 of them.

3. The only manner to proceed is to allow mixing of suitable 6-plet of A-G type and 4-plet of T-C type in the sense that A-G doublet from 6 is moved to T-C doublet inside 4-plet and T-C doublet in 4-plet is moved to A-G doublet inside 6-plet. The exchange of AG_2 (ser doublet) and TG_1 (trh-doublet) represents this kind of permutation.

The tables below summarize the three stages of the construction.

At the last stage the T-C symmetry breaking giving rise to bla-trp and ile-met doublets occurs.

1. thr 6-plet is transformed to 4-plet by replacing thr-thr in AC_2 by bla-trp. trp is the missing amino-acid.

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	thr	stop	thr	T
	leu	thr	stop	thr	C
G	val	ala	glu	gly	T
	val	ala	glu	gly	C
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	ser	asn	ser	A
	ile	ser	asn	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	leu	pro	his	arg	A
	leu	pro	his	arg	G

Table 2.7: Code table before the flow inducing the breaking of the product symmetry.

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	thr	T
	leu	ser	stop	thr	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

Table 2.8: The code table after the action of the flow inducing the breaking of product symmetry.

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	stop	T
	leu	ser	stop	trp	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	ile	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

Table 2.9: The code table after the T-C symmetry breaking

2. TA_2 met-doublet is transformed to ile-met so that the realistic genetic code results.

One might argue that symmetry breaking permutations $G_1 - C_2$ and $AG_2 - TG_1$ should permute amino-acids with a similar chemical character. A similar constraint applies to T-C symmetry breaking. By studying the chemical structure of the amino-acids, one finds that this is satisfied to a high degree.

1. The permutations val-leu and ala-pro exchange amino-acids with non-polar (hydrophobic) sidegroups. The permutations glu-his and gly-arg exchange polar (hydrophilic) amino-acid with a polar amino-acid which is also basic. Ser and thr are both non-polar amino-acids.

2. ile and met are both non-polar so that ile$\rightarrow$ met replacement satisfies the condition.

3. The objection is that the side group for trp is non-polar but polar for thr. Interestingly, the code table decomposes to two connected regions corresponding to non-polar/polar side groups at the left/right such that the non-polar trp located inside the polar region is the only black sheep whereas thr naturally belongs to the polar region. As will be found trp is also otherwise singular case.

A working hypothesis worth of studying is that the symmetry breaking mechanism is universal and applies also to the capital letter code and even to the small letter + special symbol code in an appropriately generalized form. This hypothesis is highly predictive, and the fact that one can produce these codes using the product ansatz, the same "volume preserving flow", and T-C symmetry breaking, encourages to think that the picture has some truth in it.

The information maximization principle determining the "volume preserving flow"

The interaction between the DNA singlets and doublets is the physical explanation for the breaking of the product symmetry. This interaction involves two parts: the flow and T-C symmetry breaking. The flow is analogous to the formation of connected vertical stripes of amino-acids in DNA space: kind of condensation process in which different phases represented by amino-acids tend to condense to form regions consisting of at most 4-units of type XYU, $U = A, G, T, C$. Obviously this means continuity and thus also symmetry analogous to that emerging when (amino-acid) gases condense to a liquid state: the breaking of the product symmetry is the price paid for this additional symmetry. It turns out to be possible to formulate a variational principle consistent with the proposed flow in the direction of the columns of the code table and defining the dynamics of the condensation.

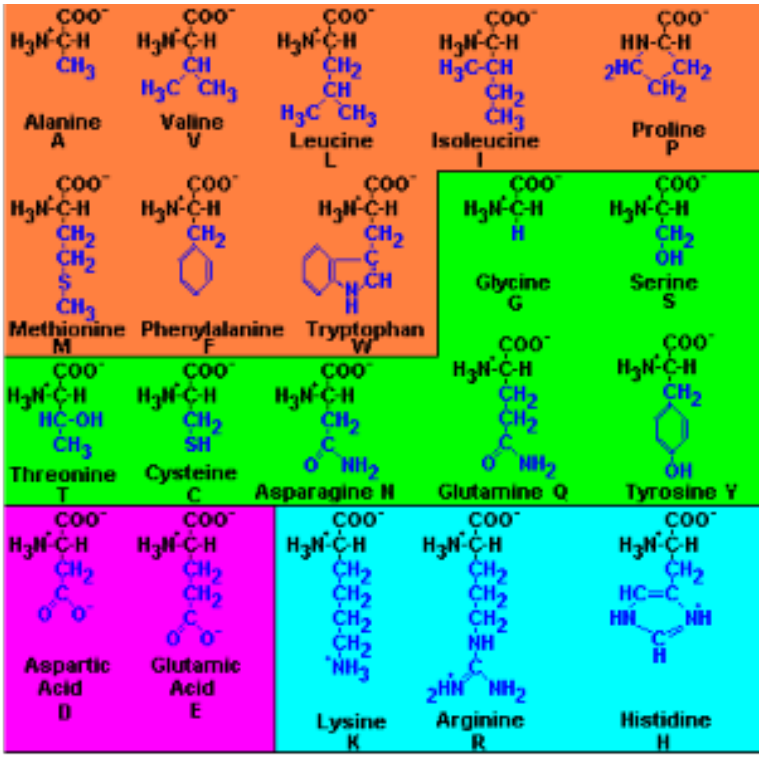


Figure 2.3: The chemical structure of amino-acids. The first group (ala, ...) corresponds to non-polar amino-acid side groups, the remaining amino-acids to polar side groups. The two lowest groups correspond to acidic (asp, glu) and basic side groups.

What this means that one can assign an information measure to the code table such that the volume preserving flow in question maximizes this information measure.

1. Information measure is assumed to be local in the sense that it decomposes into a sum of information measures associated with the elements C_{AB}, $A, B \in \{A, G, T, C\}$, of the 4×4 code table (elements are 4-element columns). In the physical analogy this means that the condensed droplets of various amino-acids can have at most the size of single 4-element column.

2. Consider the element C_{AB}. Let the multiplet associated with the amino-acid a_k contain $n(k, AB)$ amino-acids and let $i(k, AB)$ tell the number of the disjoint parts to which the amino-acidss a_k in the 4-plet AB split. The number of these disjoint multiplets can be $0, 1, 2$.

   Let the i: th region contain $n(k, AB, i)$ amino-acids a_k. The meaning of the equations

$$\sum_{i=1}^{i(k,AB)} n(a_k, AB, i) = n_k(AB) \quad ,$$

$$\sum_{AB} n_k(AB) = n_k \quad ,$$

$$\sum_k n_k = 64$$

   is obvious.

Assign to the i: th connected region containing $n(k, i, AB)$ identical amino-acids a_k probability

$$p(k,i,AB) = \frac{n(k,i,AB)}{64} \ ,$$

to the element AB the total probability

$$p(k,AB) = \sum_{i=1}^{i(k,A,B)} p(k,i,AB) \ ,$$

and to the entire table the probability

$$p_k = \sum_{AB} p(k,AB) = \frac{n(k,AB)}{64} \ .$$

The sum of the probabilities associated with various amino-acids satisfies

$$\sum_k p_k = 1 \ .$$

The information measure associated with amino-acid a_k element AB is defined as

$$I(k,AB) = \sum_{i=1}^{i(k,A,B)} p(k,i,AB) \times log[p(k,i,AB)] \ ,$$

Note that this number is non-positive always. The total information associated with the amino-acid a_k in code table is defined as

$$I(k) = \sum_{AB} I(k,AB) \ .$$

The total information of the code table is defined as the sum of the information measures associated with various amino-acids:

$$I = \sum_k I(k) \ .$$

This information measure is maximized (which means the minimization of the absolute value of the measure since one can speak of the minimization of entropy) by the vertical flow satisfying the previous constraints, and thus satisfying the constraints that the numbers a_k of various amino-acids are fixed and $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries are respected. There is a direct analogy with thermodynamical equilibrium with fixed particle numbers and symmetry. The equilibrium is characterized by the chemical potentials associated with the amino-acids. There is no temperature type parameter now.

The variational principle indeed favors the formation of vertically connected regions consisting of $n = 2, 3$ or 4 amino-acids. By construction the variational principle does not tell anything about larger regions. In particular, it is more favorable for 4 amino-acids in a given column (say ser in the second column of the table) to be contained by single element than by 2 elements since the information measure would be $-1/16log(1/16)$ for two disjoint doublets and $-1/16log(1/8)$ for singlet 4-plet in same element and thus smaller in absolute value. In the similar manner the AAAB decomposition of singlet element instead of say AABA is favored.

The deviations from the standard code as tests for the basic symmetries of the model

The deviations of the terrestrial genetic code from the standard code [I10] provide a testing ground for the postulated symmetries of the genetic code and might also help to deduce the alien codes.

The deviations from universality of the Start codon (coding for met) and stop codons are very rare. With two exceptions all known deviations from the standard code are located in the first and fourth columns of the code table. For the first exceptional case the codon is ATC in the third column and codes for both stopping sign and pyrrolysine, which is an exotic amino-acid. It is somewhat a matter of taste whether one should say that the universality of the third column is broken or not since, depending on context, ATC codes stopping sign or pyrrolysine.

Second exceptional case corresponds to the use of two stop codons to code amino-acids and this necessarily breaks the universality of the third column in T-C 2-subcolumns. The construction of the small letter code indeed forces to assume this kind of breaking of universality. No violations of the predicted A-G symmetry and the universality of the second column of the code table are known.

The deviations from the standard code [I10] provide valuable hints when one tries to deduce information about the alien codes.

1. Consider first the mitochondrial genes.
   i) Mitochondrial codon ACT from animals and micro–organisms (but not from plants) codes trp instead of stopping sign.
   ii) Most animal mitochondria use TAT to code met instead of ile.
   iii) Yeast mitochondria use GAX codons to code for thr instead of leu. This suggests that also in the case of the capital letter code the amino-acid coded 8 times is thr. In case of the small letter + special sign code the 13-fold degerate amino-acid could be thr.

2. The violations of the universality are very rare for nuclear genes. A few unicellular eukaryotes have been found that use one or two of three stop codons to code amino-acids instead. The use of two stop codons to code amino-acids necessarily violates the universality of the third column but need not break the universality for the embedding of amino-acid space to DNA space.

3. There are also two non-standard amino-acids: selenocysteine and pyrrolysine.

   (a) Selenocysteine is encoded by ACT (fourth column) coding stopping sign normally. Interestingly, ACT codes also stopping sign and the translation machinery is somehow able to discriminate when selenocysteine is coded instead of stop. This codon usage has been found in certain Archaea, eubacteria, and animals. This deviation means that the number of amino-acids is 21 or 20 depending on context. This conforms with the view that number 21 indeed has a deep number theoretical meaning and that one can regard stopping sign formally as amino-acid.

   (b) In one gene found in a member of the Archaea, exotic amino-acid pyrrolysine is coded by ATC, which corresponds to the lower stopping sign in the code table. This case represents the only deviation from universality of the third column of the code table but even in this case also stopping sign is coded. How the translation machinery knows whether to code pyrrolysine or to stop translation is not yet known. TGD would suggest that electromagnetic signalling mechanisms ("topological light rays") might be involved.

   The small variants of the letters K and V are lacking from small letter+special sign code. This might signal that the corresponding amino-acids are replaced by selenocystein and pyrrolysine represented by h and \ in the small letter code.

2.4.4 Capital letter code as a product code with broken T-C symmetry

What about capital letter code: does it also have approximate product structure? Product structure predicts that many degeneracies, in particular the largest degeneracies should be divisible by two. In case of 2×10 code all degeneracies are predicted to be divisible by two. This is not the case now as **Table 2.9** shows. One can however try to find a product code which is as near as possible to the real one.

The degeneracies 1111111234 for the doublet 2×10 representation differs from our genetic code in that 1111112233 is modified to 1111111234. These degeneracies would be the degeneracies most naturally associated with the 16 DNA doublet code with 10 "pre-amino-acids" possibly associated with plasmoid like life forms serving as messengers of the aliens.

The simplest option would be that this correspond to taking one doublet from second 2 and adding it to second 3 so that one additional singlet results. Unfortunately, the fact that stopping sign has degeneracy 7(8) excludes this option.

The 1111111234 decomposition predicts the following numbers for DNAs with various degeneracies. Also the corresponding numbers for capital letter code are included.

n	1	2	3	4	6
N(prod)	0	12	0	4	4
N(real)	2	9	2	5	3

Table 2.10: The numbers $N(n)$ of amino-acids coded by n DNAs for unperturbed 2×10 product code and for the real genetic code for 2×10 option.

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	thr	stop	stop	T
	leu	thr	stop	stop	C
G	val	ala	glu	gly	T
	val	ala	glu	gly	C
	thr	stop	gln	arg	T
	thr	stop	gln	arg	C
T	ile	ser	asn	ser	A
	ile	ser	asn	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ser	asp	gly	A
	val	ser	asp	gly	G
	thr	pro	his	arg	A
	thr	pro	his	arg	G

Table 2.11: Capital letter code table before the flow

The following process gives the degeneracies of the OPpose code.

1. Take one DNA from second 8-plet and add it to 6-plet to get two 7-plets so that one has $N(7) = 2$ and $N(6) = 1 > 0$.

2. Change one DNA in 6-plet to the DNA which does not exist in the table to get $N(6) = 0$, $N(5) = 1$, $N(1) = 1$. The non-existing DNA is generated in essentially the same manner also in case of our code.

3. One can transform 7 2-plets into 2 3-plets, 4-plet and 4 singlets as follows. Take from two doublets one DNA and move them to third doublet to get $N(1) = 3 < 5$, $N(2) = 11 > 7$, and $N(4) = 3$. There are four superfluous doublets remaining and forming pairs. For each pair take DNA from one doublet and move it to second one to get $N(1) = 5$, $N(2) = 7$ and $N(3) = 2$.

Assuming that the decomposition of DNA doublets is obtained from that for our code in the proposed manner and that the same flow induces T-C symmetric part of the breaking of the product symmetry, one can fix the DNA-amino-acid correspondence highly uniquely for the capital latter code. The unbroken code contains two octets. Since for yeast mitochondria both GA and TA columns code for thr, the guess is that the second octet corresponds to thr. The second octet must be ser from the product symmetry. The requirement that the code table resembles as much as possible the code table of our genetic code leads to the following working hypothesis for the code table before symmetry breaking.

T-C symmetry breaking can be understood as follows.

1. Take one DNA from second 8-plet (ser or thr and add it to 6-plet representing stopping sign

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	stop	T
	leu	ser	stop	stop	C
G	thr	pro	his	arg	A
	thr	pro	his	arg	G
	thr	stop	gln	arg	T
	thr	stop	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ser	asp	gly	A
	val	ser	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

Table 2.12: Capital letter code table after the flow

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	phe	ser	stop	stop	T
	leu	ser	stop	trp	C
G	thr	pro	his	arg	A
	thr	pro	his	arg	G
	thr	stop	gln	arg	T
	thr	stop	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	ile	thr	lys	arg	T
	met	stop	lys	stop	C
C	val	ser	asp	gly	A
	val	ser	asp	gly	G
	val	asp	asp	gly	T
	val	ala	glu	gly	C

Table 2.13: Capital letter code table after the T-C symmetry breaking

to get two 7-plets so that one has $N(7) = 2$ and $N(6) = 1 > 0$. Thr is chosen in the sequel for definiteness and corresponds to TGC.

2. Change one DNA in thr 6-plet to the DNA which does not exist in the table to get $N(6) = 0$, $N(5) = 1$, $N(1) = 1$. The non-existing DNA is generated in essentially the same manner also in case of our code. stop at ACT is transformed to trp as so that trp is in the same position as in our genetic code.

3. What one must do is to transform 7 2-plets into 2 3-plets, 4-plet and 4 singlets. This is achieved in the following manner.

   (a) Take from two T-C doublets one DNA and move them to a third doublet to get $N(1) = 3 < 5$, $N(2) = 11 > 7$, and $N(4) = 3$. For instance, this is achieved by transforming glu and ala to asp. The value of information measure decreases by $log(64/27)$ in this process. There are also many other ways to do this.

   (b) There are four superfluous doublets remaining and forming pairs. For each pair take DNA from one doublet and move it to second one to get $N(1) = 5$, $N(2) = 7$ and $N(3) = 2$. More concretely $(AA)_2$ leu doublet is transformed to phe-leu, and $(TA)_2$ met-doublet is transformed to ile-met so that correct degeneracies result and the information measure increases in these processes by $2 \times log(27/16)$ which is larger than $log(64/27)$ so that the net increase of the information measure is positive in the entire process.

The process is not obviously completely unique but the proposed choice is favored because the small latter+special sign code can be obtained as a small deformation of this code.

2.4.5 T-C symmetric models for small letter plus special symbol code

One can apply T-C symmetric product model with symmetry breaking also to the code candidates involving small letters. There are three candidates for these codes.

1. The 4×17 code with 18 amino-acids involving only small letters with h interpreted as stoppping sign: this code makes sense for Oppose option only and since the expressive power is not maximal, it will not be discussed in the sequel.

2. $4 \times (16 + 4)$ code with 23 generalized amino-acids (\, h, and special symbols $!, \&, .$ are interpreted as belonging to the extended family of amino-acids).

3. The $4 \times (16 + 4)$ code with 20 amino-acids (\ and h are interpreted now as amino-acids). This code results from the code with 23 generalized amino-acids by assuming that the DNAs coding for $!, \&$ and period code for the stopping sign.

The candidates 2) and 3) appear as Oppose and OPpose options.

The nature of silicon modification

The product model for the genetic codes suggests an interpretation of the small letter codes. The Chilbolton message tells that also silicon is fundamental for the alien life at DNA level so that one can consider the possibility that one of the DNA and RNA doublets is modified by an addition of something containing silicon to give an additional doublet.

For $(4+16) \times 4$ code four additional doublets must be present. If some base of DNA suffers a modification, it suffers the modification also if it appears in RNA triplet at the same position, and this in turn implies that also the conjugate of the DNA base suffers modification so that 32 additional triplets are generated. Thus the modified base of DNA cannot appear in RNA and vice versa. DNA bases (A, G, T, C) correspond to RNA bases (U, C, A, G). Since the T of DNA corresponds to the U of RNA, there is only one possibility. The modified base is T for DNA and U for RNA, and the T_S of DNA must correspond to U_S of RNA rather than A_S. The simplest possibility is that the doublets of form XT have doubled by the silicon modification of the second T to XT_S. Also $T_S X$ type modification is in principle possible but the construction of the code favors the XT_S option (in this case code the table gets a fifth column whereas for $T_S X$ gives rise to a fifth row).

n	1	2	3	4	5	6	8	9	10	12	13
N	0	16	0	4	0	2	0	0	2	0	0
N	10(9)	4(5)	0	3	2(3)	3(2)	0	1	0	0	1

Table 2.14: The numbers $N(n)$ of amino-acids coded by n DNAs for code containing small letters and special symbols for 2×12 option. Both OPpose and Oppose options are included.

2×12 product model for the small letter plus special symbol code with 80 generalized DNAs and 23 amino-acids

The optimal candidate for the code involving 64+16 generalized DNAs involves 20+3 generalized amino-acids. There are two options corresponding to the decompositions $24 = 3 \times 8$ and $24 = 2 \times 12$. The assumption that small letter plus special sign code follows from the capital letter code as extension favors 2×12 option. 2×12 option for the small letter + special sign code allows highly unique model since one can assume that the code results as a simple extension of the capital letter code and is obtained by the same symmetry breaking procedure as the capital letter code and terrestrial genetic codes. The discussion below is restricted to OPpose option.

The first step is to deduce the composition in the set of $4 + 16$ DNA doublets defining the product code. The only working option has the decomposition 111111112235, which corresponds to the decomposition

$$20 \times (2 \oplus 2) = (5 \oplus 3 \oplus 2 \oplus 2 \oplus 8 \times 1) \times (2 \oplus 2) \quad .$$

This gives **Table 2.14** for the degeneracies.

The breaking of the product symmetry looks large but it turns out that the code can be obtained as a relatively small deformation and extension of the capital letter code.

The first things to observe about the code are following.

1. Comparing the decomposition 111111112235 with the corresponding decomposition 1111111234 for the capital letter code, one can guess that the small letter code is obtained from the capital letter code by the following process in the set of 4 exotic RNA-doublets. Decompose the four exotic RNAs to $(2 \oplus 1 \oplus 1) \times (2 \oplus 2)$ such that $2 \times (2 \oplus 2)$ codes for exotic and ordinary amino-acid quartet. Since trp is lacking from capital letter code before symmetry breaking, one can assume that trp is the ordinary amino-acid. Since the exotic amino-acid "period" appears five times, the second 4-plet must code for "period". The two doublets must code for exotic doublets & and ! which reduce to singlets after symmetry breaking. Two exotic doublets fuse with the two octets of the capital letter code to code for two decouplets and must therefore code for the ordinary amino-acids ser and thr. Thus the code table without symmetry breaking looks very much like capital letter code table.

2. The modification $XT \to XT_S$ implies that code table gets fifth column. Only this option allows to generalize in non-trivial manner the flow and allows to see trp 4-plets as being consistent with product code.

3. Terrestrial codes contain two exotic amino-acids scys and plys. The fact that the small letter + special sign code contains the symbols h and \ with ASCII number larger than 64 not appearing in the capital letter code is taken as a suggestion that the corresponding amino-acids are exotic. A natural working hypothesis is cys is replaced with scys and lys with plys. Needless to add, this hypothesis must be taken with a grain of salt.

1. Product code before flow

The code table before the action of the flow and T-C symmetry breaking looks like follows. The code table obviously resembles capital letter code table to a very high degree and satisfies all the constraints resulting from the A-G and T-C symmetries and product structure of the code.

2. The action of the flow

	A	G	T	C	T_S	
A	phe	ser	tyr	scys	.	A
	phe	ser	tyr	scys	.	G
	leu	thr	stop	stop	thr	T
	leu	thr	stop	stop	thr	C
G	val	ala	glu	gly	!	T
	val	ala	glu	gly	!	C
	thr	stop	gln	arg	trp	T
	thr	stop	gln	arg	trp	C
T	ile	ser	asn	ser	.	A
	ile	ser	asn	ser	.	G
	met	thr	plys	arg	&	T
	met	thr	plys	arg	&	C
C	val	ser	asp	scys	ser	A
	val	ser	asp	scys	ser	G
	thr	pro	his	arg	trp	A
	thr	pro	his	arg	trp	G

Table 2.15: Small letter special sign product code before flow and T-C symmetry breaking.

	A	G	T	C	T_S	
A	phe	ser	tyr	scys	.	A
	phe	ser	tyr	scys	.	G
	leu	ser	stop	stop	thr	T
	leu	ser	stop	stop	thr	C
G	thr	pro	his	arg	trp	A
	thr	pro	his	arg	trp	G
	thr	stop	gln	arg	trp	T
	thr	stop	gln	arg	trp	C
T	ile	thr	asn	ser	.	A
	ile	thr	asn	ser	.	G
	met	thr	plys	arg	&	T
	met	thr	plys	arg	&	C
C	val	ser	asp	scys	ser	A
	val	ser	asp	scys	ser	G
	val	ala	glu	gly	!	T
	val	ala	glu	gly	!	C

Table 2.16: Small-letter special sign genetic code after the flow and before T-C symmetry breaking.

	A	G	T	C	T_S	
A	phe	ser	tyr	cys→ scys	.	A
	phe	ser	tyr	cys→scys	.	G
	phe	ser	stop	stop→trp	thr	T
	leu	ser	stop	trp	thr	C
G	thr	pro	his	arg	trp	A
	thr	pro	his	arg	trp	G
	thr	stop	gln→phe	arg	trp	T
	thr	stop	gln	arg	trp	C
T	ile	thr	asn	ser	.	A
	ile	thr	asn	ser	.	G
	ile	thr	lys→ ile	arg	.	T
	met	stop	lys→ plys	arg	&	C
C	val→ ser	ser	asp	gly→scys	ser	A
	val→ser	ser	asp	gly→scys	ser	G
	val→ ser	asp	asp	gly→asp	asp	T
	val	ala	glu	gly	!	C

Table 2.17: Small letter special sign genetic code resulting from T-C symmetry breaking. The replacements $X \to Y$ tell how the code in the sector of ordinary DNAs is obtained from the capital letter code.

3. T-C symmetry breaking

The basic assumptions are that the G-column of the code is universal for the alien code just as it is universal for the terrestrial codes, and that the code table resembles maximally to our code table and capital letter code table.

1. One must transform the two 10s (thr and ser) to 13 and 9. The clue to the symmetry breaking mechanism comes from the finding that one must be able to generate as many as 10 singlets. Hard trial and error work teaches that one cannot get these singlets unless one allows $10 + 4 \to 13 + 1$ mechanism for producing one of the singlets. The transformation of val-val-val-val to ser-ser-ser-val is the only candidate for this transformation and gives $N(4) = 3$ (scys, period, trp) and $N(1) = 1$.

   The thr is the second 10-plet and the transformation of TTC-thr to stop is the only possibility if the universality of the G column in alien sector is assumed. The transformation of $(AC)_2$ stop-stop column to trp-trp implies maximal resemblance with our genetic code, and one obtains $N(13) = N(9) = 1$ (thr, ser), $N(6) = 2$ (arg, trp), $N(5) = 1 < 5$ (stop) and $N(4) = 2 < 3$ (scys, period).

2. The remaining transformations must produce $N(1) = 10 > 1$, $N(2) = 4$, $N(4) = 3 > 2$, $N(5) = 2 > 1$, $N(6) = 3 > 2$ by acting on the T-C type doublets only and thus generating a breaking of T-C symmetry. The first step is to replace & in the $(TT_S)_2$ by "period" to get $N(5) = 2$, $N(4) = 1$, $N(1) = 2$. What one must create by the splitting all the remaining T-C doublets so that 2 4-plets and 1 6-plet as extension of A-G type doublets results. The choice of the A-G type doublets is not unique but the requirement that the code table resembles maximally the code table of the capital letter code fixes the choice of A-G type doublets extended to 4-plets to be AA_1 (phe), $(TT)_1$ (ile) and the A-G type doublet extend to 6-plet to be CT_1 (asp). **Table 2.17** summarizes one possible code table satisfying these constraints. For comparison also the table for capital letter code is given.

Product model for the small letter code with 20 amino-acids and 80 generalized DNAs

The number theoretical model generalizes for the codes defined by 64 ordinary DNAs + 16 DNAs of form XT_SY and assuming that besides 20 amino-acids there are 3 additional modified amino-

acids. A small letter-special symbol code with 80 DNAs and 20 amino-acids is obtained from 23-amino-acid code by assuming that the exotic DNAs coding for special signs !, & and period code for stopping sign and the previous construction for 2×12 code works as such. Oppose option with 64 DNAs (special signs being not interpreted as belonging to the code) and 18 amino-acids is in conflict with the requirement of a maximal expressive power. My personal conviction is that this option can be safely forgotten.

Why the numbers 64 and 80?

The dark matter hierarchy based on the hierarchy of increasing values of Planck constant predicts that the entire universe is a macroscopic quantum system and elementary particles have a hierarchy of zoomed up variants with arbitrarily large Compton length (proportional to $\hbar$) [K26]. Dark matter should be especially important for living matter and life should therefore involve fundamental physics in an essential manner rather than emerge at some very high level of complexity. Hence one can ask whether the numbers 64 and 80 for the codons of the two codes could reflect basic facts about fundamental physics in TGD Universe. The following numerological argument based on detailed counting of particle states encourages to take this idea half-seriously at least.

1. Gravitons and more general stringy states are not counted since they correspond to bound states of fermions and bosons connected by flux tubes. Color is counted neither since it corresponds to CP_2 partial wave and is not spin like degree of freedom in TGD framework. Family replication phenomenon has a topological explanation and is counted neither. This leaves only spinorial degrees of freedom which according to TGD inspired theory of consciousness are responsible for Boolean representations using fermionic Fock states. The natural guess is that these fermionic degrees of freedom might relate to the genetic code or genetic code might represent them.

2. TGD predicts in purely spinorial degrees of freedom 8 lepton states (lepton and anti-lepton both having 4 states due to spin and electro-weak isospin). Also phase conjugates of these states are predicted so that 8+8=16 states are obtained. The number of spinor states is same in the quark sector. This gives 16+16=32 states altogether.

3. Bosons are identifiable as tiny wormhole contacts carrying fermion and anti-fermion numbers at the light-like wormhole throats. Essentially lepto-antilepton and quark-antiquark pairs or their superpositions are in question. $(2 + 1) \times (3 + 1) = 12$ leptonic and 12 quark like bosons with spin and electro-weak isospin equal to 1 or 0 (only two massless spin states are possible). Together with phase conjugates this makes 24+24= 48 states. 24 of them correspond to ordinary electro-weak gauge bosons and Higgs and the remaining 24 are exotic bosons with charge matrices orthogonal to the charge matrices of electro-weak gauge bosons. For exotic counterparts of W bosons and Higgs the sign of the coupling to quarks is opposite. For photon and Z^0 also the relative magnitudes of the couplings to quarks much change. The total number of bosonic states is 48 and the number of all particle states in this sense is 48+16+16=80. If quarks are dropped from consideration the number is 64.

4. The numerological question is whether the 64 ordinary genetic codons are in some deeper sense in one-one correspondence with 48 color singlet gauge bosons and 16 lepton states and the 80 codons of the extended code in one-one correspondence with all states constructed in this manner.

2.4.6 Embedding of the amino-acid space into DNA space and the universal part of the genetic code

The concrete geometric formulation for the symmetries is based on the embedding of 20+1 generalized amino-acids to the space of 64 DNAs. Obviously, the amino-acids are coded by the DNAs to which they are mapped by this embedding. There is indeed an embedding of 20 amino-acids plus stopping sign with 2×10 structure to the set of 64 DNA triplets which have 4×16 structure. 2 is imbedded into 4 which corresponds to the 4 last bases of DNA and 10 into 16 which corresponds to 16 pairs of first two bases of DNA. The lacking amino-acid is embedded as a kind of outsider

for 64 DNA codes. In case of 80 DNA-24 generalized amino-acid code this embedding is replaced with the embedding of 2 amino-acids to 4 and 12 to $16 + 2$ structure.

This kind of embedding would be regarded in the language of mathematician as a a discrete bundle structure which is also singular in the sense that the fiber above a given base point does not always have the same number of points. The 10×2 and 16×4 compositions suggest the interpretation as the embedding of the space formed by 10 points of 2-D space-time to the space formed formed by 16 points of 4-D space-time. Analogous interpretation applies also in the case of the extended codes.

The interpretation conforms with the general idea that DNA represents a plan and involves intentionality and time dimension somehow. The amino-acids coded by several DNAs correspond to surfaces for several time values correspond to the same spatial point represented by amino-acid. The set of DNAs coding single amino-acid brings in mind the notion of "association sequence" defined as a disjoint union of space-like 3-surfaces with time-like separations and possible by the classical non-determinism of the Kähler action absolutely crucial for understanding consciousness in TGD framework [K41]. The number of DNAs coding the amino-acid would measure the degree of intentionality involved with it: each DNA associated with the amino-acid would symbolize one step in a plan. Some of alien amino-acids would be highly intentional: the degeneracies can be as high as 13 to be compared to the maximal degeneracy of 6 for our code!

Consider now in more detail this structure.

1. Exact A-G gauge symmetry implies that the pairs (XYA, XYG) form fibers and one can choose freely XYA or XYG to represent the amino-acid. In case of T-C symmetry symmetry breaking can select either XYT or XYC uniquely as a representative of the amino-acid.

2. For amino-acid coded by two DNAs only the identification of the amino-acid is unique apart from the possible gauge symmetry. For $n > 2$-plets the identification involves non-uniqueness.

3. The requirement that the embedding of amino-acids to DNA space is universal allows to fix identification uniquely in case of $n > 2$-plets. It turns out that one can assume universal embedding to make sense for both terrestrial and alien codes (if the replacements cys$\rightarrow$ scys and lys $\rightarrow$ plys possibly occurring for the small letter + special sign code are appropriately interpreted). This assumption fixes the embedding highly uniquely and the only uncertainties relate to the T-C symmetry breaking. The possibility to choose the universal part of the code table to be the same for all codes, suggests that the proposed model catches something essential. It is also difficult to imagine that a randomly generated ASCII message could allow interpretation in terms of genetic codes having so high symmetry properties and common construction principles. **Table 2.18** summarizes the universal part of the genetic code resulting from the embedding of the amino-acid space to DNA space. Also small letter code is included.

2.4.7 Summary

To sum up, both the terrestrial and hypothetic alien genetic codes can be constructed from the A-G and T-C symmetric product codes by assuming a breaking of both product– and T-C symmetries. Product structure and symmetries suggests strongly that genetic codes have evolved as a fusion of much simpler doublet and singlet codes. Hydrophilic-hydrophobic dichotomy is a good candidate for the dichotomy implied by the 2×10 product structure. The assumption that the breaking of the product symmetry induced by the "volume preserving flow" in DNA space tending to cluster amino-acids in the vertical direction of the code table is universal, and the hypothesis that the embedding of the amino-acid space to the DNA space is universal, together fix the identification of the codes highly uniquely.

The small letter-special symbol code with 80 DNAs and 23 amino-acids is favored because it maximizes both the information content and the expressive power of the code. The degenerate code with 80 DNAs and 20 amino-acids is obtained from the 23-amino-acid code by assuming that the exotic DNAs coding for special signs !, & and period code for stopping sign. To my own opinion

	A	G	T	C	T_S	
A	phe	ser	tyr	cys (scys)	.	A
						G
						T
	leu		stop	trp		C
G		pro	his	arg		A
						G
						T
			gln			C
T	ile	thr	asn			A
						G
						T
	met	thr	lys (plys)		&	C
C			asp			A
						G
						T
	val	ala	glu	gly	!	C

Table 2.18: A possible embedding of the amino-acid space to the DNA space. The gauge choice XYA allowed by A-G gauge invariance of the last codon is made. The identification is same for both our code, capital letter code, and small letter plus special sign code. There is some uncertainty related to the T-C symmetry breaking.

the OPpose option for the small letter code with 80 DNAs and 23 amino-acids is the most plausible alternative.

Acknowledgements

I want to express my gratitude for several persons. In particular, for Tapani Koivula for encouraging me to take seriously UFOs and ETs and for interesting suggestions (in particular, for stimulating the idea that tectonic energy could serve as a "food" of plasmoid like life forms), Martin Keitel for helping me to realize that crop circles are real and telling about the Chilbolton and Crabwood crop circles as well as for concrete help, and for Toni Siira for providing material related to UFOs and for interesting email exchanges. I want also to thank for Jukka Kinnunen for two champaign bottles (the first one for the capital letter code and the second one for the small letter code): I hope that I will sooner or later invent the means of establishing communications with aliens (the third bottle of champaign). I would also want to thank the ITs responsible for these charming Chilbolton and Crabwood crop formations. If I only knew their names! As an underground intellectual myself, I hope that amplitude modulated micro-waves or whatever from my computer could mediate my deep gratitude and warm greetings to this underground intelligentsia.

2.5 Genes, Memes, And Universal Language

In TGD framework the notion of magnetic body plays a key role in the understanding of bio-systems and communications between magnetic and material body could be based on memetic code words. Magnetic body is the fundamental intentional agent is in the same relation to the material body as memetic code to the genetic code and computer software to the hardware or the manual to the electronic instrument. Hence there is a strong temptation to believe that memetic codewords represented as field patterns of duration.1 seconds is associated with the communications between magnetic body and brain.

For instance, the fact that 10 Hz is basic hippocampal frequency suggests that declarative memories could be based on time mirror mechanism (see **Fig.** `http://tgdtheory.fi/appfigures/timemirror.jpg` or **Fig. ??** in the appendix of this book) with negative energy sig-

nal from the magnetic body of the geometric future reflected from the brain of the geometric past as a positive energy signal back to the magnetic body of the geometric future. Classical communications could utilize memetic code using pulse or frequency coding. These field patterns could also define shared mental images. For instance, sequences of the memes represented as field patterns could activate intronic memes, which in turn would activate genes.

2.5.1 Genes-Memes, Biology-Culture, Hardware-Software?

The reports of the Public Consortium about human genome in Nature, Feb 15, 2001 [I15] and of Celera Genomics in Science of Feb 16th, 2001, [I34] demonstrated that the amount of human genome differs relatively little from those of lower organisms: we have only about 30, 000 genes, little more than twice the number 13, 601 of genes for fruit fly. This paradoxical finding strongly supports the view that our genome is not solely responsible for what we are and that the intronic portion of DNA (only about 1 per cent codes of human DNA codes or amino-acid sequences), is not " junk DNA", but contains important biological information and expresses it non-chemically.

In TGD Universe introns would express memes as the classical field patterns associated with MEs ("topological light rays") responsible for the basic expressions of language understood in an extremely general sense. This language includes body language and even cellular signalling, and could quite well make possible (not necessarily conscious) interspecies communications based on the memes and genes expressed by both communicating species and forming a common portion of grammar and vocabulary. All eukaryotes (cells with nuclei), even bacteria, would possess part of the memes of this universal language. The memetic code word is predicted to consist of a sequence of 21 DNA triplets and carries 126 bits of information instead of 6 bits of genetic code. Of course, also genes could be expressed in terms of MEs and could define a lower level language possessed also by prokaryotes.

The actual role of DNA could be understood using a computer analogy. Memes represent the program modules written using the programming language defined by the memetic code and realized in terms of the field patterns associated with MEs. Genes represent the lower level programs coding for the necessary hardware. System builds only the hardware needed, that is cell expresses only a small fraction of the genome. For neurons this fraction is known to be highest. DNA engineering requires besides the addition of the new programs (memes, introns) also the insertion of the necessary hardware (new genes). Memes and corresponding genes should have very intimate relationship. In this conceptual framework the standard view is wrong since it identifies the build-up of a new hardware as the sole activity at the DNA level. This would be like identifying the addition of a net card to a computer as the fundamental activity related with computers.

2.5.2 Pulse And Frequency Representations Of The Genetic And Memetic Code Words

The most general form of p-adic length scale hypothesis implies that each p-adic prime $p \simeq 2^k$, k integer, defines a hierarchy of physically favored p-adic time scales given by $T_p(n) = p^{(n-1)/2}T_p \equiv T(n,k)$, $T_p = \sqrt{p}T_{CP_2}$, where T_{CP_2} is the so called CP_2 time scale about 10^4 Planck times. The most general assumption assigns to any prime $p \simeq 2^k$, k integer, a hierarchy of cognitive codes with codeword having a duration equal to n-ary p-adic time scale $T_p(n)$ such that the number of bits is factor k_1 of k.

Code words could be realized either as k_1 first harmonics of the fundamental frequency $f_p(n) = 1/T_p(n)$ or as temporal sequences of k_1 bits of duration $\tau = T_p(n)/k_1$ represented as pulses of maximal duration τ. These representations will be referred to as frequency and pulse representations respectively. EEG represents a good candidate for frequency representation.

1. Pulse representations, scalar wave pulses, and transformation of intentions to actions

Pulse representations could be realized in terms of scalar wave pulses predicted by TGD and claimed to exist already by Tesla [K25]. Scalar wave pulses can be visualized as capacitors moving with light velocity and carrying longitudinal essentially constant electric field. If charged particles of matter end up temporarily to the space-time sheets of the scalar wave pulse, they are accelerated without dissipation and generate negative energy "acceleration radiation" rather than brehmstrahlung at harmonics of the frequency determined by the duration of the scalar wave pulse.

Under obvious conditions on the duration of the scalar wave pulse the negative energy radiation can be amplified to positive energy radiation by time mirror mechanism.

Quite generally, the generation of scalar wave pulses seems to provide a basic mechanism generating negative energy radiation (phase conjugate radiation) and nerve pulses are probably accompanied by scalar wave pulses. The transformation of the p-adic counterpart of the space-time sheet of the scalar wave pulse to a real one, a kind of switch-on process, could provide a generic realization of intention besides a direct generation of the p-adic counterpart of the negative energy topological light ray. The hierarchy of magnetic bodies could use this process as a generic manner to realize cascades of intentions proceeding from magnetic body down to the level of DNA.

Denoting by $f(\omega)$ the Fourier transform of single pulse in the interval $T(n,k)$, one can write the Fourier transform of the pulse sequence as

$$F(\omega_n) = \sum_k \delta_k exp(ik\tau_b\omega_n) f(\omega_n) \quad , \quad \omega_n = \frac{n2\pi}{T(n,k)} \quad ,$$

where τ_b is the duration of the bit and δ_k is equal to 1 or 0 depending on whether k^{th} bit corresponds to a pulse or not. The duration of the pulse can be anything in the range $(0, \tau_b)$. If $f_b = 1/\tau_b$ corresponds to a frequency of some oscillation a resonant coupling occurs. Magnetic transition frequencies and the frequencies corresponding to the increments of zero point kinetic energies are especially interesting as far as the transformation of the pulse representation to a conscious experience or controlled action is considered. For instance, pulses could correspond to magnetic pulses used in the transcranial magnetic stimulation and known to induce altered states of consciousness [J16].

2. Genetic and memetic codes as cognitive codes associated with spoken and written language

Genetic and memetic codes are the most obvious candidates for the codes associated with spoken and written language. Genetic code would correspond to $k = 2^7 - 1 = 127$ and one must distinguish between 6-bit(64 DNA triplets) and almost-7-bit representations. These codewords can be realized dynamically as temporal field patterns. For genetic code primes $p \simeq 2^k$, $k = 6 \times n$ define candidates for the duration of the genetic code word if all factors of k are assumed to define a possible number of bits of the code word. The time scales come as powers of 8 so that they cover the entire range of biologically relevant time scales and genetic code could appear as fractally scaled versions unlike memetic code. What is interesting is that the possible durations of code word range down to about 11 CP_2 times. Therefore one cannot exclude the possibility that the biological realization of the genetic code is only a particular example of its realizations and that genetic code makes possible communications even between living and so called non-living matter.

Representations of the genetic code

$k = 2 \times 126 = 2 \times 6 \times 21 = 252$ allows the representation of both 126-bit memetic codeword, 6-bit genetic codeword, and 7-bit code word. For pulse representation corresponding to $k = 252+6n$ the genetic codon the duration of the code word and bit are $\tau = 2^{-3n} \times 50$ ms and $\tau_b = 2^{-3n} \times 8.3$ ms respectively. The realization using nerve pulse patterns certainly possible for $n \geq 0$, $n = 1$ would $\tau_b = 1.04$ ms which seems to be somewhat too short. Frequency representation would be realized using the 6 first harmonics of the fundamental frequency $f_1 = 2^{3n} \times 20$ Hz. In the following only 6-bit representations are discussed.

1. Representations of 6-bit code in the range of audible frequencies

20 Hz corresponds to the lowest end of audible frequencies ($20 - 2 \times 10^4$ Hz). Audible range allows 3 representations of the genetic code corresponding to the fundamental frequencies f_1 equal to 20 Hz, 160 Hz and 1280 Hz. 1 kHz frequency is between the frequency ranges associated with the latter two representations. Above (below) 1 kHz the wavelengths of incoming sound waves are shorter (longer) than head size so that the mechanisms determining the direction of the sound source are different above and below this frequency. Speech might correspond naturally to pulse representations whereas music could correspond to frequency representations. Also nerve pulse-EEG dichotomy could correspond to talking-singing dichotomy (left brain speaks and right brain sings).

2. EEG and nerve pulse representations of 6-bit code

1. Cortical EEG frequency range favors the realization using $f_1 = 2.5$ Hz: all harmonics in the range 2.5-15 Hz are important EEG resonance frequencies. For 20 Hz representation 120 Hz would represent the highest harmonic and it is questionable whether cortical EEG contains it with a sufficient intensity. Cerebellar EEG however allows much higher frequencies than cortical EEG.

2. The cyclotron frequency of Si^{++} ion is 21.4 Hz so that it could define a frequency representation of the genetic code in Earth's magnetic field, at least if its value is subject to a homeostatic control.

3. Ca^{++} has cyclotron frequency of 15 Hz in Earth's magnetic field with value $B_E = .5$ Gauss. A pulse representation of the genetic code with $\tau_B \simeq 66.7$ ms ($f_b = 15$ Hz) would excite harmonics of Ca_{++} cyclotron frequency and thus couple the representation to the Bose-Einstein condensate of Ca_{++} ions. Nerve pulses could realize this representation. Blackman [J7] has found that the harmonics of $f_b = 15$ Hz frequency have effects in living matter, and Ca^{++} waves are known to play an exceptional role in biology [J15] (for TGD based model see [K34]. Hence the Bose-Einstein condensate of Ca^{++} ions might provide a fundamental pulse representation of the genetic code.

4. The presence of fractally scaled-up versions of the Earth's magnetic field the sheets of the many-sheeted DNA would allow also scaled versions of Ca^{++} representation with durations $\tau = 8^{-n} \times .05$ ms of the code word. Depending on whether magnetic flux quanta are tubes or sheets the p-adic primes of space-time sheets of magnetic flux tubes comes as $k = 169 - 3n$ or $k = 169 - 6n$. For sheets one would have $k = (169 = 13^2, 163, 157, 151)$: these primes define important p-adically scale up electronic Compton scales relevant to DNA in the range 10 nm-5 μm and three of these primes define Gaussian Mersennes. Sheet option is favored by the explanation of the findings of Peter Gariaev about radio emission induced by irradiation of DNA by laser light [I23]. All these representations except $k = 169$ are realizable also using audible frequencies, which suggests a direct connection between the sheets of the many-sheeted DNA and the representations of the genetic code at audible frequencies.

Representations of the memetic code

For the memetic code one must distinguish between almost-127-bit representations and 126-bit representations. In both cases there is a very limited number of representations, which suggests that the emergence of memetic code might relate to the emergence of explosive cultural evolution. The first representations corresponds to the time scales $T(126)$ and $T(127)$: the latter defines the Compton time of electron. Next representations corresponds to the time scale of about .05 seconds and.1 seconds respectively.

1. 126-bit representations

1. 126-bit memetic code word can be represented using the same representation as for the genetic code, namely $k = 2 \times 126 = 252$ with $\tau = .05$ ms and $\tau_b = .4$ ms and $f = 20$ Hz and $f_b = 2520$ Hz. Audible frequencies could realize both representations and music experience might involve both frequency and pulse representation of 126-bit memetic code corresponding to the left brain (rhythm) and right brain (melody) aspects of music.

2. 126-bit representation using nerve pulses as such is not possible. The analog of the intronic representation of the memetic code using sequences of 21 DNA triplets could be however possible. $k = 252$ allows 21-bit representation for which bit is replaced by 6-bit with duration $\tau_6 = 50/21 = 2.38$ ms, which corresponds to a typical duration of nerve pulse. Each of the 21 nerve pulses should generate a genetic codon of duration $\tau = 50/64 = .78$ ms presumably communicated to the neuronal nucleus and/or vice versa. 6-bit fine structure could be perhaps expressed at the microtubular level as has been originally proposed by Koruga [I16], [J10]. One would have $\tau_b/\tau_6 = 21/64$, the ratio of the number of amino-adics (stopping sign counted as effective amino-acid) to the number of DNA codewords. τ_b/τ_6

represents a reduction of information: this loss of information is not due to the degeneracy of the code but due to the fact that only one third of the total duration of the bit of 21-bit code is used to represent information.

One could imagine that the 6 bits represented as negative energy topological light rays activate the corresponding DNA triplet by coupling 3 switches on so that supra-current can flow through it. Sequence of 21 pulses would switch a unique memetic codon and sequences of these pulses in turn would switch on meme forming by definition a closed supra current circuit with return current flowing along conjugate strand. Switches could correspond to join along boundaries bonds connecting atomic space-time sheet to some larger space-time sheet, where the supra-current can flow. Each pair of bits would switch on one nucleotide of the triplet. This would occur in correct order if the three nucleotides are ordered by pulse length associated with bit (which can indeed vary) and 4 different bit pairs switch on A, T, C, and G. Bit could be represented by the polarization direction associated with the negative energy topological light ray.

The generation of nerve pulses using 64 bit sequence to code additional information at microtubular level could be based on frequency representation. Pairs of em MEs with opposite polarizations could represent a bit pair corresponding to a single nucleotide. These waves would induce microtubular excitation representing the DNA triplet.

2. 127-bit representations

For 127-bit representation the duration of the memetic codeword would be $T(2, M_{127}) = .1$ seconds. This time scale might be identified as the minimal duration of cortical mental images, and the so called features introduced by Walter Freeman [E2] could define a pulse representation of memetic code words of almost-127 bits. $\tau_b = .8$ ms is definitely too short a time scale to be realized by the neuronal dynamics alone. Frequency representation is realized utilizing 127 first harmonics of $f_1 = 10$ Hz, which defines the average frequency of alpha band and is fundamental hippocampal frequency. $f_b = 1270$ Hz could define the frequency responsible for synchronous neuronal firing known to be about 1 kHz. Note that the code word containing only f_1 would not generate any conscious experience (10 Hz is not audible frequency) so that the highest bit is not quite fully represented.

1. One can imagine at least two electromagnetic realizations (for the spectrum of magnetic transition frequencies see [K61]).
   i) Living matter contains both Co and Fe ions and the harmonics of Co_{++} and Fe_{++} cyclotron frequencies are 10 Hz for the nominal value $B_E = .5$ of the Earth's magnetic field. Thus pulse both pulse representations and frequency representations of memetic code coupling to these magnetic transitions are in principle possible.
   ii) For $B = 127/90 \times B_E$, $B_E = .5$ Gauss, both the third harmonic of proton cyclotron frequency and electron's spin-flip-cyclotron transition frequencies are 1270 Hz so that the bits of the memetic codon would couple to the Bose-Einstein condensate of the Cooper pairs of electrons and protons in the pulse representation.

2. Also classical Z^0 fields make possible realizations of the memetic code (for the spectrum of Z^0 magnetic transition frequencies see [K61]).

   (a) Z^0 cyclotron frequencies of nuclei are proportional to $(A - Z)/A$ and around 10 Hz if one assumes the earlier hypothesis that Earth's Z^0 magnetic field corresponds to the space-time sheet $k = 173$ [K60]. The value $(A - Z)/A = 1/2$ characterizing surprisingly many biologically important ions (C, N, O, S and Si [**?**]) is ideal in this respect. Thus it would seem that Z^0 cyclotron transitions might provide a rich repertoire of frequency representations of the memetic code. Note that neutron could define a cyclotron representation of the genetic code with 20 Hz fundamental frequency.

   (b) The temporal field patterns associated Z^0 topological light rays provide one possible pulse representation of the memetic code [K61].

   (c) Temporal sequences for the changes Z^0 magnetization directions for a block of cognitive antineutrinos at cell membrane space-time sheet provide a conscious pulse representation of the memetic codeword [K60]. Conscious experience would result, when the Z^0

magnetization directions flip back to the direction of external Z^0 magnetic field in spin flipping cyclotron transition. $M_{127} = 2^{127} - 1$ different conscious experiences results since nothing happens if all cognitive antineutrinos are in the direction of the external Z^0 magnetic field. Z^0 magnetization direction could be altered by the Z^0 magnetic pulse associated with the Z^0 ME inducing cell membrane oscillations of nerve pulse pattern.

2.5.3 Mapping Of The Memetic Code To Microtubular Code

The importance of microtubuli for long term memory is evident [J17, J10]. Microtubule decomposes into a sequence of cylinders containing 13×13 tubulins such that the helical twist is 2π along each of the 13 helical strands consisting of 13 tubulins. Therefore the code with $k = 13^2 = 169$ bits with bit realized as a tubulin conformation is a natural microtubular cognitive code [K48].

$k = 169$ defines the p-adic time scale associated with the Earth's magnetic field and next to the p-adic length scales $k = 151, 157, 163, 167$ associated with DNA so that microtubular level would naturally correspond to the level next to DNA in evolution, and have therefore some sort of self-reflective character. Microtubular representation of long term memories would certainly be consistent with this self-reflective character. This suggests that 169-bit microtubular code words represent the log file of neuron as a temporal list of activated 126-bit memetic code words with remaining bits representing parity bits making possible error correction at both microtubular and DNA level.

In the following some arguments for why microtubular code words should represent memetic code words are developed, and a mechanism for how to achieve this is proposed. Needless to say, this is only one possible scenario and it is easy to imagine variants of this scenario.

Microtubuli and long term memory

In spin glass phase tubulin conformations are spatially uncorrelated but temporally stable (the excellent articles of Dimitri Nanopoulos [J17, J10] provides a model for microtubule as spin glass). Therefore microtubuli in spin glass phase are ideal for the representation of memories coded to bits represented by tubulin conformations [K48], [J10]. The two tubulin conformations have different electric dipole moments and conscious bits would result as "spin-flips" when the microtubule is in a strong longitudinal electric field forcing tubulins to the same conformational state. Essentially ferro-electric polarization is in question. The fundamental quale would be the change of the tubulin conformation. The patterns for the changes of tubulin conformations would generate mental images, and could also give rise to conscious memories by sharing of mental images. They could also give rise to signals communicated classically to the geometric future where they could induce reverse transition generating copies of the microtubular code words.

Time mirror mechanism for the realization of intentions proceeding as a process initiated from the magnetic body allows to consider two possible options for the role of the microtubuli. The options are not of course mutually exclusive.

1. Microtubuli as log files and communication lines

For this option intentional action does not involve microtubuli and they would be specialized to represent memories and serve as communication lines. The intentional action from higher than microtubular level would affect intronic DNAs directly, and patterns of tubulin conformations would provide a log file listing the memetic codons activated during the history of the neuron. Since the hierarchy of the magnetic bodies must have been there for all the time, one an indeed argue that neuronal microtubules have emerged later and do not participate in the intentional actions at intermediate level. Intentional action and the memory about it would be decoupled from each other completely.

Microtubuli allow besides ferro-electric and spin glass phase also phase which is optimal for signal transfer. The proposed realization of memetic code words as sequences of 21 nerve pulses with each pulse accompanied by genetic codon would suggest that microtubuli also mediate propagation of memetic codon, which can represent the desire to activate corresponding memetic codon in the post-synaptic neuron. Here the error correcting code $K_2(13, 64, 5)$ originally proposed by Koruga [I16], [J10] could be involved.

2. Why microtubuli cannot serve as intentional agents?

One must also consider the option for which microtubuli would represent the last step before DNA level in the hierarchy of desires propagating downwards in the self hierarchy. One can however represent heavy criticism against this alternative.

1. One can wonder whether the microtubular memes are generated intentionally or in a random manner in a phase transition leading to spin glass phase with basically un-predictable meme sequence. In the latter case, intentional action would be reduced to a selection to activate or not to activate the existing memes.

2. In this case it would be possible to have long term memories about events that never occurred, which seems strange. Random generation of the memes would also be in conflict with the notion that there are at least 42 parity bits making possible error correction. Thus it would seem that microtubular codewords can be activated only from the DNA level. In the case that microtubuli act as signal pathways this would indeed be the case.

3. Not all memetic code word sequences representable at microtubular level need to have counterpart at DNA level. This would lead to a situations in which meme could not be expressed at all.

These arguments favor the view that microtubuli are passive historians making possible self-reflection by providing a log file about activated memetic codons and possibly serve also as communication lines allowing the propagation of memetic codons between neuronal nuclei as sequences of 21 nerve pulses accompanied by genetic codon each. Only this option will be discussed in the sequel.

3. How to generate and read microtubular code words?

The coding of the intronic memetic code word to a microtubular code word would involve switching-on mechanism in spin glass phase of the microtubule for which initial state consists of "0": s. The tubulins corresponding to bit "1" would make transition to the conformation representing bit "1". The activation of intronic meme should automatically generate the positive energy photons at frequency corresponding to the energy difference between two conformations of tubulin. Intronic memes should have kind of hardwired connection to a fixed ordered sequence of microtubular code words. Note that in TGD framework there is no need to static microtubular memory since memories can be communicated from geometric past. Therefore memory capacity would be unlimited in this sense.

The conscious reading of the microtubular code word using strong enough longitudinal electric field would generate positive energy photons, which could be communicated to the geometric future and generate declarative memory mental images. Also a direct sharing of mental images yielding episodal memories is possible.

Representation of the memetic code words as microtubular code words

The challenge is to understand how 126-bit genetic code word or (possibly 127-bit codeword) is mapped to 169-bit microtubular codeword. There are several hints how this mapping could be realized.

1. Number theoretical decomposition of the microtubular code word to memetic code word and 43 parity bits

It is possible to represent microtubular 169-bit codewords as $13 \times 13 = 169$ square lattice of bits.

1. One can write the number of microtubular bits as

$$169 = 126 + 43 = 3 \times 42 + 42 + 1 \ ,$$

and there is a temptation to assume that the first 126 bits correspond to the memetic codon and 42+1 bits represent parity bits making possible error detection. From the geometric

representation it is clear that the bit in the middle of the 13×13 square is an excellent candidate for "1" in $42 + 1$.

2. 126-bit memetic code word allows a natural identification of the parity bits. The $126 = 3 \times 42$ decomposition allows also 42-bit code word, whose bits are obtained by decomposing 126-bit code word to a sequence of 42 3-bits, and defining each bit B of 42-bit as some Boolean function $B = f(b_1, b_2, b_3)$, say as a product $B = b_1 b_2 b_3$ of the bits of the corresponding 3-bit by representing bits as 1 and -1: the result is -1 (bit "0")if the number of bits "0" is odd and 1 otherwise. The comparison of codewords with a reference codeword assumed to be the correct one would allow to locate errors leading to internal inconsistency of the code word. The comparison of 42-bit codeword with the original one would allow to locate single bit changes of the memetic code word with a resolution of 3-bits.

3. A possible interpretation of the 43^{th} bit results from the requirement that each memetic code word gives rise to a conscious experience. This is guaranteed if the bit in the middle of the square is always "1" so that in the phase transition it changes the direction always and conscious experience results even when all the remaining bits are "0": s: the interpretation in this case would be as a mental image representing "nothing happened". An alternative possibility is that this bit represents parity bit. For instance, the product of all memetic bits or of all 42 parity bits. This bit could also be "1" only if there are no erratic bits. This bit could also represent 127^{th} bit of the 127-bit memetic code word.

2. How intronic DNA could represent parity bits?

If microtubule represents passively the information communicated to it, intronic memes should be accompanied by 42-bit parity code words. The minimal portion of DNA helix containing an integer number of DNA triplets consists of 10 triplets and corresponds to a length of $L(151) = 10$ nm (cell membrane thickness). 20 triplets would correspond to 2 full 2π twists. This encourages to consider the possibility that memetic codons correspond to 3 2π twists (length of 30 nm) along DNA so that memetic code words are followed by by a sequence of 9 DNA triplets serving some control function. Since 10 nm corresponds to electron Compton scale $L_e(151)$, the idea that dark electrons with this Compton length are relevant.

These 9 DNA triplets represent 54 bits. 7 of these codons could represent the 42 parity bits of the memetic codon preceding it. The remaining two genetic codons (12 bits) should represent further control information. The factorization $Z_{126} = Z_2 \times Z_3^{a)} \times Z_3^{b)} \times Z_7$ allows to identify two coset groups $Z_{126}/Z_{21} = Z_6$ as $Z_6^{a)} = Z_2 \times Z_3^{a)}$ and $Z_6^{b)} = Z_2 \times Z_3^{b)}$ corresponding to the identifications $Z_{21}^{a)} = Z_3^{a)} \times Z_7$ and $Z_{21}^{b)} = Z_3^{b)} \times Z_7$. This would mean the possibility to define two non-equivalent 6-bit parity code words as products $B = b_1 \times ....b_{21}$ of 21 memetic bits corresponding to the two sub-groups Z_{21}. The two DNA triplets could represent these parity 6-bits. Needless to say, these prediction are very strong and immediately testable by studying the intronic DNA.

3. The helical structure of the microtubule and the representation of the memetic code word and of parity bits

The tubulins representing parity bits should differ physically from those representing memetic bits. Time mirror mechanism suggests that the energy difference between two tubulin conformations differs considerably from that for the memetic tubulins. A weaker symmetry breaking induced by the helical electric field should order the bits of helical genetic code words and also order the 7 genetic code words to a sequence of vertical pairs running from left to right. Genetic code words should correspond to connected regions, most naturally helical stripes. Also the memetic code word and parity bits should correspond to a connected regions. There should be a clear signature telling where the microtubular code word ends.

The breaking of the rotational and translational symmetries is necessary and the helical structure of microtubuli could induce it. Denote by a the vertical distance between tubulins and by $\Delta\phi = 2\pi/13$ the angular distance between two tubulins along horizontal circle.

1. Genetic codons would be arranged to the helical stripes rotating making full 2π around the vertical section section of the microtubule defined by 13×13 tubulins. The 10 helices span a helical region spanning the angle range $\Delta\phi = 10 \times 2\pi/13$. Each helix would represent

2 memetic codons whereas the 13^{th} tubulins at $z/a = 13$ would represent parity bit. This would give 20 genetic codons. The 21^{th} genetic codon would correspond to the 6 lowest tubulins of the 11^{th} helical stripe. Therefore the pairs of 2 sub-sequent genetic code words would correspond to helices beginning at

$$(\tfrac{z}{a} = 1, \phi = k \times \Delta\phi) \ , \quad (\tfrac{z}{a} = 7, \phi = k \times \Delta\phi + \pi) \ ,$$

$$\Delta\phi = \tfrac{2\pi}{13} \ , \qquad k \in \{1, 2, ..5\} \cup \{9, 10, ..13\} \ .$$

The 21^{th} code word would correspond to $z = na$, $n = 1, ..., 6$, $k = 11$. The region representing parity bits would be connected and consist of vertical part and the 13^{th} horizontal stripe. It turns out that this guess is probably quite not correct: it seems that the first pair of helices representing genetic codons starts at $(z/a = 2, k = 2)$ so that the horizontal line at $z/a = 13$ contains 12 tubulins (2 genetic code words).

2. Perhaps the simplest mechanism guaranteeing the desired symmetry breaking is based on a static helical electric field, which is non-rotational and thus representable as a gradient of a scalar potential V. Electric field could be constant in the memetic section of the microtubule since tubulins are charged and Coulombic interaction energy would grow linearly with the azimutal angle ϕ and longitudinal coordinate z along the helical strands. In this case the potential would be of form

$$V(z, \phi) = k_1 \times \frac{z}{a} + k_2 \times \frac{\phi}{2\pi}$$

in the region populated by the genetic code words.

The value of the potential should fall rapidly down at $z = 13 \times a$ defining the upper edge of the microtubular codon and the vertical stripes defining the parity bits. The strong gradient of the electric field in the parity bit region could give rise to a strong dipole interaction and change the energy difference between microtubular conformations dramatically both at $z/a = 13$ and inside the

   (a) lower helical stripe S_{low} having having height of 6 units and width of 2 units starting at $(z/a = 1, \phi = k \times \Delta\phi)$, $k = 12, 13$ and

   (b) upper helical stripe S_{up} having height of 6 units and width of 3 units and starting at $(z/a = 7, \phi = k \times \Delta\phi) + \pi)$, $k = 11, 12, 13$.

This behavior of electric field dictated by its non-rotational character would differentiate between memetic and parity bits.

3. Genetic codons are ordered to a sequence of pairs of codons if the value of the potential increases with constant steps along the helical stripe, and also in the transition from the top of k^{th} helical stripe to the bottom of $(k+1)^{th}$ helical stripe. This gives

$$k_1 = -\frac{k_2}{13} \ ,$$

which fixes the potential apart from overall scaling:

$$V(z, \phi) = V_0 \times (\tfrac{z}{a} - 13 \times \tfrac{\phi}{2\pi}) \ ,$$

giving

$$V(z = n \times a, \ \ \phi = s \times \tfrac{2\pi}{13}) = V_0 \times (n - 13 \times s) \ .$$

The length of a single tubulin in the vertical direction is $a \simeq 8$ nm and the outer radius of microtubule is $R \simeq 12.5$ nm [J17]. This gives $\Delta z/R\Delta\phi \simeq 1.32$ whereas $\Delta V_z/\Delta V_\phi = -1$ rather than $-1/1.32$ required by the orthogonality with respect to the helical strands. Thus the electric field can be regarded as a superposition of a field orthogonal to helical strands with a weaker field parallel to the z-axis.

4. The requirement that the 5+5+1 (5+5) microtubular codons are represented at the lower (upper) half of codon can be satisfied if the the value of the potential becomes in some sense too large at the point $(z/a = 7, \phi/2\pi = 11/13)$ and that this forces V to rapidly raise up from the minimum value

$$V_{min} = -137V_0 \ .$$

The maximum of the potential at $(n = 1, s = 1)$ given by

$$V_{max} = -12V_0 \ .$$

$(n = 1, s = 1)$ bit is non-memetic bit and shifted by one unit upwards from the horizontal $n = 13$ row of 13 bits: this distinguishes it as a natural candidate for the 43^{th} bit. With this identification the first helical stripe containing two genetic codons would start at $(n = 2, s = 2)$ and $n = 13$ horizontal line would contain only 12 points corresponding to two genetic codons. Vertical stripes of parity bits would contain 5 genetic codons represented as helical stripes. Thus all genetic codons would correspond to helical or horizontal stripes. Horizontal and helical genetic codons should differ somehow but the origin of difference remains unclear.

Symmetries of the genetic code and the error detection

The ratio of the number of the number of parity bits to memetic bits is $R = 42/126 = 1/3$ and almost equals to the ratio 21/64 of the number of genetic code words to the number amino-acids. If parity bits represent directly the "memetic amino-acids" the action of all memetic code words with given 42 parity bits is identical and the comparison of parity bits would be enough to check that everything is in good shape at the level of the memetic expression. Obviously, this option is trivial.

If the memetic code is directly induced by the genetic code, the ratio R would be $R = log_2(21)/6 \simeq .73$. For both options the number of the "memetic amino-acids" would be considerably smaller than $(2^{126} - 1)/63$ suggested by the direct generalization from the case of the genetic code, and corresponding to $R \simeq 20/21$.

If the memetic code is induced by the genetic code which is same for both chemical and field pattern expressions, intronic memetic codons possess the A-G symmetry and almost exact T-C symmetry of the genetic code in the sense that memetic code words related by these symmetries would activate the same genes. This would allow to improve further the error detection.

1. A-G and almost T-C symmetries imply that the last 2 bits of 6-bit defining genetic code word in good approximation reduce to single bit, say the last bit. Therefore the second parity bits could be taken to be the product b_4b_5. This improves considerably the effectiveness of error detection at the level of expression.

2. Also the first bit of the genetic code word is less significant since the genetic code table contains many 4-sub columns (codons of form XYZ, with Y fixed) for which all 4 amino-acids are same and quite a many 2-sub-columns (codons of form XYZ, X= A, G or X= T, C) are identical. Therefore a relatively safe choice is to take the first parity bit for the genetic codon to be the product b_2b_3. This choice would localize with a reasonable reliability the errors with 2-bit accuracy at the level of expression.

Could error correction mechanism be used to detect mutations of memes?

The first question to be answered concerns the purpose of the error correction process. Is error correction used

1. to remove the internal inconsistencies of the memetic code words at intronic level due to mutations or,

2. to stabilize long term memories represented at microtubular level?

Only the first option would be needed if the refreshment of the memetic code words by activated intronic DNA occurs all the subjective time in the geometric past. Both types of error correction could rely on the following mechanism.

The comparison of the microtubular code word with that of the geometric past by time mirror mechanism, assumed to yield resonant interaction if the compared code words are identical, could reveal the emergence of those mutations at DNA level which alter some parity bits and memetic bits in such a way that the parity bit pattern ceases to be consistent with the memetic bit pattern. There would be simply no internally consistent microtubular code words in the geometric past identical with this pattern. Large number of temporal copies of the codeword in geometric past would make the mechanism reliable.

The internally inconsistent change of the microtubular codeword and even a change in general could be detected by this mechanism. In absence of resonance a process trying to fix up the meme at DNA level by trial and error could be initiated and could yield an internally consistent or even original meme. Note that this comparison mechanism would be conscious and even the correction mechanism might be conscious intentional process.

To sum up, the model for the mapping of memetic code to microtubular code is dictated by the general ideas about realization of intentions and p-adic cognitive codes. When combined with general number theoretical arguments and physical considerations the model becomes highly unique. The prediction for the intronic representation of the memetic codon is readily testable, and also the prediction for the microtubular electric field is in principle testable.

2.5.4 Genes, Memes, And Language

The idea about intronic memes as computer programs running in the hardware coded by genes together with quantitative facts lead to a view about how memes and genes could relate to language. It must be emphasized that the idea about correspondence between genes and language is not new. The article [I22] gives a nice summary about various findings supporting the view that language and DNA are closely related.

Zipf's law

One of the basic resemblances between genes and language is Zipf's law relating the rank r of the event with its frequency f of occurrence [J11]. The rank of a given event is defined by ordering the events in sequence using as a criterion the frequency of occurrence: the event occurring most often has rank 1, etc.. Zipf's law states $f = C/r^a$, where a is a constant near one, and C is a constant depending on the size of the sample. In linguistics the event could correspond to the occurrence of a given word or character, and in genetics to the occurrence of a given DNA triplet.

Zipf's law holds also for many systems regarded as non-living, such as masses of stars in a constellation of stars. Interestingly, the sum of the frequencies for an infinite number of events is proportional to Riemann Zeta function $\zeta(a) = \sum_n 1/n^a$ at point $a \simeq 1$, which can be regarded as a product of thermal partition functions associated with primes regarded as bosons: $\zeta(a) = \prod_p 1/(1-p^a)$, $log(p)$ plays here the role of energy and a to the role of inverse temperature. Interestingly, the line $a = 1$ defines a critical line such that $\zeta(a)$ converges for $Re(a) > 1$. $a = 1$ corresponds to the temperature at which Bose-Einstein condensation occurs and the system becomes macroscopic quantum system. Thus Zipf's law might relate to p-adicity and macro-temporal quantum coherence in some deep manner.

There is also evidence in favor of a typological relationship between the words of human speech and DNA "words" (see the references in [I22]). The word formation appears to obey laws similar to those of formal genetics so that one can speak of dominant and recessive features, mutations, etc.. In [I22] graphical representations character sequences defined by written texts and nucleotide (A, T, C, G) sequences are studied (amino-acid sequences of long proteins would be more appropriate for comparison with character sequences). The fractal dimensions of the resulting planar fractals are in the range $0 < D < 1$. A random sequence of characters corresponds to $D = 0$ and repetition of single character to $D = 1$, whereas written texts correspond to $D = .7 - .8$.

Could the phonemes of language be expressions of DNA triplets?

The previous construction of representations of genetic and memetic codes, in particular the facts that the frequency $f \sim 10$ Hz represents the fundamental frequency associated with speech organs and that 20 Hz frequency represents the lower limit for audible frequencies and the rate of mRNA-amino-acid translation, suggest that memetic code might be involved with speech and speed recognition. Since the duration of a phoneme in speech is $\sim .05 - .1$ seconds, one must seriously consider the possibility that phonemes might somehow relate to genetic or memetic codewords.

The number of phonemes of native origin in Finnish language the same as the number of characters and equals to 21, the number of amino-acids plus stopping codon counted as an effective amino-acid. In English language the number of phonemes it is not so easy to estimate the number of phonemes since written language differs so much from spoken but the number is not too far from 21. In Russian the number of different characters is 32, half of the number of DNA codons. Certainly one cannot expect precise correspondence between the numbers of phonemes/letters and amino-acids and it might well be that DNA→phoneme coding differs from the DNA→amino-acid coding.

These findings together with the observation force to consider the possibility that phonemes might play a role similar to that of amino-acids, and be interpreted as resulting in the translation of DNA triplets to field patterns to neural activity to the motor activity of speech organs. Words in turn would represent analogs of protein sequences coded by sequences of DNA triplets. The fact that memetic code represents statements about statements would suggest that memes represented by introns correspond to higher level structures of language, kind of main computer program producing meaningful expressions of language while running. Words represented by genes could be the hardware of language or lower level language and DNA triplets would represent the basic material of the hardware expressed as phonemes. This would of course require expression of genes and memes in terms of field patterns inducing the generation of nerve pulse patterns.

Consonants carry more information than vowels (early form or written language used symbols only for consonants). This picture is consistent with the fact that the property of being consonant is determined by the very brief time interval in the beginning of the pulse sequence defining the phoneme so that the occurrence of high frequencies make it consonant. There are 8 (7) vowels in Finnish (English) language, which suggests that the first 3 bits of the generic codeword in the frequency representation and representing lowest frequencies are responsible for the basic vowels and the remaining 3 bits corresponding to the higher frequencies add to the beginning of the phoneme something making it consonant.

The frequencies for the occurrence of various phonemes should be the same as for the occurrence of the DNA triplets coding them. The simplest working hypothesis that the DNA-phoneme code is same as DNA-amino-acid code does not work in case of say Russian language (32 characters) but deserves a testing in the case of Finnish language. Of course, one could consider the possibility of context dependent coding of phonemes: also ordinary genetic code can be context dependent in some situations (the same codon codes for stopping sign or amino-acid depending on context). The prediction would be that the frequencies for the occurrence of phonemes would equal to those of amino-acids.

It is not possible to assign a definite duration to the intronic representation of the memetic codeword. Speech is indeed extremely flexible: the rate of speech can vary, vowels can be represented multiply, etc.. This variation would be made possible by flexibility at the DNA level or at level higher than this (magnetic body would control introns). If speech represents genetic code, 50 ms would however be a good guess for the minimal duration of phoneme and 20 Hz for the lower end of consciously experienced frequencies (as it indeed is). Rather remarkably, the rate for the translation of mRNA triplets to amino-acids is 20 nucleotides per second so that one codon corresponds to the duration of the genetic codon in $k = 252$ representation of the genetic code.

On the other hand, the memetic code words generated while listening speech or reading text could correspond to the mental images representing the meaning of a word, and could quite well have a duration of.1 seconds whereas the minimal duration of phoneme would be about 50 milliseconds. If time mirror mechanism is involved time is not problem: the understanding of speech would occur at the level of DNA in the geometric past. Same applies also to the production of speech: the desire to produce an expression of language would generate DNA activity in the geometric past.

The overall conclusion is that memes and genes of DNA would define language independent universal grammar introduced by [J18] [J18]. Languages would differ from each other only in the different association of phonemes to the DNA triplets. Also languages based on electromagnetic realization and not directly conscious to us are possible and even probable.

How memes could control genes in the production of language?

Language is not expected to be the only function controlled by memes. Memes could be responsible for a high level control of genes also in their ordinary activities. Memes would represent a higher level control structure utilizing the existing program like structures defined by genes activating genes. In case of language the fundamental expression would be in terms of field patterns inducing nerve pulse patterns inducing in turn speech motor activities.

Computer metaphor suggests that memetic programs correspond to sequences of memetic codewords with each memetic codeword defining a main program as a sequence of sub-program calls. Production of speech would mean activating these programs from magnetic body by time mirror mechanism. Genetic program calls would be realized as addresses pointing to genes defining the subprograms: 2^{126} different addresses is much more than needed to point to any desired gene. Also genes could use this addressing to point to other genes. The pointed gene could generate field pattern giving rise to a word or sequence of words or it could point to another gene. In this manner meme could generate entire sequence of words by inducing a sequence of subprogram calls (computer language LISP suggests a possible model for what occurs). Genes have a hierarchical structure, and one expects that higher levels of this hierarchy could fix the parameters determining the rate of speech, durations of phonemes, accents, emotional content, etc....

Pointing could be achieved by electromagnetic field patterns utilizing time mirror mechanism so that address would be expressed by negative energy topological light rays (phase conjugate laser waves). Pointing could be based on avoidance of starvation. Negative energy photons at the frequency serving as the name of the pointed system would induce the dropping of charged particles to a larger space-time sheet.

In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant h_{eff} so that cyclotron energy would be liberated.

The pointed system would lose energy and would generate negative energy topological light rays at characteristic frequencies to compensate the lost energy. If the frequency is higher, the pointed system would point to a lower level in the hierarchy of sub-programs. One cannot of course exclude the possibility that pointed gene points back to the pointing gene or meme. This could give rise to recursive self-referential program structures. At the lowest level of hierarchy there would be gene which act as a population inverted many-sheeted laser generating a cascade of positive energy photons at various frequencies and in this manner yielding the desired response.

2.5.5 Does Memetic Code Make Possible Communications Between Different Species?

The observations of Cleve Backster [J6] give scientific support for the view that plants react to human emotions. The TGD based interpretation would be as sharing as mental images. One can however ask whether sharing of mental images might make possible the development of more evolved communications involving signalling by codes. For instance, people in hypnosis report that they can share the experiences of plants and shamans claim that they can experience what it is to be an animal and communicate with plants. According to what the shamans of the South America tell, their refined medical knowledge is told to them by plants [J14]. In principle common intronic memes could make possible this kind of communications even between different species: these communications would not of course be conscious to us under normal circumstances.

Interspecies communications by sharing of mental images

Sharing of mental images does not require neither target nor receiver to be able to communicate symbolically. Therefore the target and receiver could be any living system: animal, plant, even bacterium. In TGD Universe one cannot exclude even "non-living" systems as targets and even sharers of mental images. The remote viewing of non-living targets is indeed possible and in this case either mental images of target or some system perceiving target are shared. Since emotions represent holistic summaries about contents of consciousness, they are good candidates for universal mental images and the sharing of emotions could occur even between different species.

Support for the extreme generality of the sharing of the mental images as a basic mechanism of remote viewing comes the fascinating experimental discoveries made by Cleve Backster [J3, J6]. These findings have led Backster to introduce the notion of primary perception, which seems to have a natural identification as sharing of mental images.

1. Plants, eggs, and even bacteria are able to have primary perceptions. Backster tells in the interview that even yoghurt got wild when he took a chicken out of refrigerator and began pulling off strips of meat. Plants respond electrically to strong negative emotions and to the violence or death suffered by other living organisms. That primary perception correlates with the strength of emotions conforms with the view that entropy gradients with respect to subjective time, which are indeed identifiable as emotions, measure the strength of perception.

2. Distance does not seem to matter much. Sperm separated by a large distance from its donor reacted when the donor inhaled amyl nitrate. White cells were found to remotely react to the emotions of their donors. Same was found to apply to plants and their owners.

3. Plants and even bacteria seem to have a defence mechanism resembling shock. If bacteria share the mental images of suffering organisms by receiving negative energy MEs sent by them, the shock could be interpreted as resulting from the depletion of positive energy resources (all excited states of population inverted many-sheeted lasers decay to the ground state) or be a mechanism preventing this depletion.

An interesting question is whether humans have lost this ability or is this reaction usually unconscious at our level of self hierarchy and whether human skin could exhibit galvanic skin response to say death of other life-forms.

Interspecies classical communications using common memes and genes

The assumption that even classical communications between different species are possible is much stronger hypothesis than the assumption that mere sharing of mental images occurs. The general model for interspecies communications using symbolic representations for the communicated information rather than mere sharing of mental images relies on the pan-psychic view about life and consciousness ("Everything is consciousness and consciousness can be only lost"). Also the hypothesis that speech and written language are only one particular realization of language involving at fundamental level memes controlling genes expressing themselves in one of the many possible ways, supports this view.

1. General model

1. If the intronic portion of the DNA corresponds to memone defining basic linguistic repertoire expressed using genes defining the vocabulary. Even plants could possess language possibly realized using MEs ("topological light rays"). Introns could control genes in terms of electromagnetic MEs and genes could could express themselves by MEs. Genes would define the words of the language. One could say that interspecies communications reduce actually to intercellular communications between cells of different species.

2. Successful communication requires that the languages of communicators have common portion in their vocabularies. Cells possessing common expressed memes defining basic expressions and genes defining the vocabulary could communicate with each other. Meme level

communications would be possible between any two eukariotes (organisms having cell nucleus): bacteria, plants, fungi, animals. Also communications between plants and humans would be possible.

3. Communications could occur by sharing of DNA level mental images induced by activated memes: negative energy MEs would make possible the needed quantum entanglement. Communications could occur also classically. The simplest form of classical communication would involve the coding of the meme to the field pattern of em or Z^0 ME to a name of meme using memetic code in turn activating the same meme in the receiving organism. Memes could express themselves by controlling genes in turn generating various types of expressions for the meme This could in principle allow even translation of memes to speech in altered states of consciousness in which back projection to ears would transform the internal speech to sounds.

4. The general model for sensory representations and motor actions based on time mirror mechanism involves both quantum and classical communications. There is a great temptation to assume that the same model applies also in the case of inter-species communications. Both the psychokinetic aspect corresponding to the remote motor action aspect, and the remote sensing aspect corresponding to the remote sensory perception would be present and would be essentially geometric time reversals of each other. Psychokinetic aspect of course represents more than mere communications.

5. Unless the code is universal so that the classical signal induces directly a standard mental image, most plausibly emotion, irrespective of species, a code assigning symbols to mental images must be established by sharing of mental images. There are good justifications to argue that the establishment of a code requires sufficiently intelligent communicators. On the other hand, even if the signals from say plant do not have any "meaning" for a human receiver, they could generate effects analogous to synesthesia.

6. Organisms living in symbiosis (say some insects and flowers) could have common memes and genes allowing them to communicate. Common memes and genes would be the analogs of common genes causing the coloring of the flower and insect to be similar. This kind of communication could also explain the refined medicine of South American shamans. Shamans tell that plants have taught this medicine to them. In the book "The cosmic Serpent" [J14], Jeremy Narby proposes that shamans communicate directly with the DNA of the plant and that bio-photons might be essential for these communications.

2. Are "skin senses" in preferred role in inter-species communications

The general model of sensory organs [K28] provides further pieces to the model. The basic hypothesis is that sensory organs are the seats of primary qualia and that the experiencing self corresponds to the magnetic body of size much larger than the material body. The feedback via brain to the sensory organs is assumed to make possible the active processing of the sensory input to sensory percept.

The model introduced also a division of sense to "brain" and "skin" senses motivated by the following observation. During the development of vertebrate embryo three basic types of cells are formed: ectoderm giving rise to skin and central nervous system, endoterm giving rise to many internal organs, and mesoderm giving rise to muscles, skeleton, connective tissue, ... What is remarkable is that the ectoderm giving rise to brain, spinal cord, eye, .. suffers an inversion during the formation of the neural tube. The wall of the neural tube is inverted so that inside becomes outside and vice versa. This explains the strange finding that the eyes of vertebrates are inversion of the eyes of invertebrates and apparently look very awkward from engineering view point.

This leads to the distinction between "brain senses" and "skin senses".

1. For "brain senses" (vision, olfaction) the back projection by the telepathic sharing of mental images from brain to sensory organs allows to build sensory percept as a caricature.

2. For "skin senses" (with hearing included) the entanglement of the sensory organ with brain is replaced with the entanglement with external world, and can thus give rise to remote sensing

based on the sharing of mental images using time mirror mechanism. This remote viewing need not be conscious-to-us except in special situations, say during hypnosis.

If this distinction is sensible, skin senses would be in a special role as far interspecies communications are considered.

A model for insect-plant communications

Callahan has made very important discoveries related to the olfaction of insects and insect-plant interaction. Callahan's work [I44, I11] demonstrates that the insect olfaction is based on infrared light generated by the odorant molecules interacting with the antennae of the insects. This might be true for our olfaction too. Callahan has also shown plants communicate with insects by generating infrared light [I11]. This finding conforms with the findings of Albrecht-Buehler [I32] showing that all cells contain microtubular structures acting as receiving antennae for infrared light. Furthermore, plants suffering from de-nutrition are found more easily by insects than healthy plants.

These findings encourage to consider the following mechanism for insect-plant communications. This mechanism could apply also to the plant-human interactions.

1. Insects generate infrared MEs propagating like massless particles inside low frequency negative energy MEs acting as bridges quantum entangling the plant and the insect. Both classical communications by positive energy IR MEs and quantum communications by negative energy IR MEs are in principle possible.

2. In the case that plant suffers from de-nutrition, it can gain metabolic energy by sending negative energy MEs received by insect. This gives for plant metabolic energy and at the same time generates the quantum entanglement bridge making it possible for the insect to find the plant. The same mechanism explains also the episodal memory feats of synesthetes: due to the over-activity of subcortical parts of brain the neurons of the left cortex suffer starvation and generate negative energy MEs providing them metabolic energy and simultaneously entangling them with the geometric past so that episodal memories result. Also the life review of NDE experiences could be a by-product of the neuronal starvation.

Are human-plant communications possible?

Concerning the ideas about human plant-communications, I am grateful for Peter Hageman [I1] for inspiring discussions. Hageman claims to be able to express "plant language" by "dancing" in meditative state, and has made detailed maps of motor expressions of plant mental images and proposed a detailed taxonomy about plant language, and also developed refined ideas such as the notion of dialect. It is easy to debunk Hageman's views since the interpretations necessarily involve a lot of subjective elements. One could imagine a scientific testing of Hageman's claims by checking whether the vocabulary defined by the bodily expressions is invariant of a given plant. Similar testing is used in the case of motor synesthesia.

The common portions of the memone and genome of plant and human would in principle make possible this communication. Thus the memes and genes, which plant can communicate to humans are those which are expressed also by some cells of the human body. Since plants do not have a central nervous system, it seems that the communicable memes and genes should correspond to rather primitive expressions common to us and animals. Obviously, the memes and genes responsible for the body language is a good first guess in this respect. Note however that genes could define lower level language and could also be communicated in this manner.

This body language representation brings in mind motor synesthesia in which sensory input from some sensory modality is expressed as motor activity. The memes and genes expressible by body language could of course be expressed also by using ordinary language. The universality of the memetic and genetic codes is indeed consistent even with the transformation of communications to linguistic expressions.

2.5.6 Intronic Portions Of Genome Code For RNA: For What Purpose?

The last issue of [I13] contains an article about the discovery that only roughly one half of DNA expresses itself as amino-acid sequences. A detailed summary of the results has been published

in Nature [I5]. The Encyclopedia of DNA Elements (ENCODE) project has quantified RNA transcription patterns and found that while the "standard" RNA copy of a gene gets translated into a protein as expected, for each copy of a gene cells also make RNA copies of many other sections of DNA. In particular, intron portions ("junk DNA", the portion of which increases as one climbs up in evolutionary hierarchy) are transcribed to RNA in large amounts. What is also interesting that the RNA fragments correspond to pieces from several genes which raises the question whether there is some fundamental unit smaller than gene.

None of the extra RNA fragments gets translated into proteins, so the race is on to discover just what their function is. TGD proposal is that the RNA gets braided and performs a lot of topological quantum computation [K4]. Topologically quantum computing RNA fits nicely with replicating number theoretic braids associated with light-like orbits of partonic 2-surfaces and with their spatial "printed text" representations as linked and knotted partonic 2-surfaces giving braids as a special case. An interesting question is how printing and reading could take place. Is it something comparable to what occurs when we read consciously? Is the biological portion of our conscious life identifiable with this reading process accompanied by copying by cell replication and as secondary printing using amino-acid sequences?

This picture conforms with TGD view about pre-biotic evolution. Plasmoids [I39], which are known to share many basic characteristics assigned with life, came first: high temperatures are not a problem in TGD Universe since given frequency corresponds to energy above thermal energy for large enough value of $\hbar$ [K26]. Plasmoids were followed by RNA, and DNA and amino-acid sequences emerged only after the fusion of 1- and 2-letter codes fusing to the recent 3-letter code. The cross like structure of tRNA molecules carries clear signatures supporting this vision. RNA would be still responsible for roughly half of intracellular life and perhaps for the core of "intelligent life".

I have also proposed that this expression uses memetic code which would correspond to Mersenne $M_{127} = 2^{127} - 1$ with 2^{126} codons whereas ordinary genetic code would correspond to $M_7 = 2^7 - 1$ with 2^6 codons. Memetic codons in DNA representations would consist of sequences of 21 ordinary codons. Also representations in terms of field patterns with duration of.1 seconds (secondary p-adic time scale associated with M_{127} defining a fundamental bio-rhythm) can be considered.

A hypothesis worth of killing would be that the DNA coding for RNA has memetic codons scattered around genome as basic units. It is interesting to see whether the structure of DNA could give any hints that memetic codon appears as a basic unit.

1. In a "relaxed" double-helical segment of DNA, the two strands twist [I9] around the helical axis once every 10.4 base pairs of sequence. 21 genetic codons correspond 63 base pairs whereas 6 full twists would correspond to 62.4 base pairs.

2. Nucleosomes [I7] are fundamental repeating units in eukaryotic chromatin [I2] possessing what is known as 10 nm beads-on-string structure. They repeat roughly every 200 base pairs: integer number of genetic codons would suggest 201 base pairs. 3 memetic codons makes 189 base pairs. Could this mean that only a fraction $p \sim 12/201$, which happens to be of same order of magnitude as the portion of introns in human genome, consists of ordinary codons? Inside nucleosomes the distance between neighboring contacts between histone and DNA is about 10 nm, the scale $L_e(151)$ associated with the Gaussian Mersenne $(1+i)^{151} - 1$ characterizing also cell membrane thickness and the size of nucleosomes. This length corresponds to 10 codons so that there would be two contacts per single memetic codon in a reasonable approximation. In the example of Wikipedia [I7] nucleosome corresponds to about 146=126+20 base pairs: 147 base pairs would make 2 memetic codons and 7 genetic codons. The remaining 54 base pairs between histone units + 3 ordinary codons from histone unit would make single memetic codon. That only single memetic codon is between histone units and part of the memetic codon overlaps with histone containing unit conforms with the finding that chromatin accessibility and histone modification patterns are highly predictive of both the presence and activity of transcription start sites. This would leave 4 genetic codons and 201 base pairs could decompose as memetic codon+2 genetic codons+memetic codon+2 genetic codons. The simplest possibility is however that memetic codons are between histone units and histone units consist of genetic codons. Note that

memetic codons could be transcribed without the straightening of histone unit occurring during the transcription leading to protein coding.

2.6 Corals And Men

The comparison of the human genome with that of invertebrates during great genome project yielded some surprises [I15, I34]. In particular, it was found that human genome possesses 223 genes which are lacking from the genome of the model invertebrates. Even more, a considerable fraction of these genes seems to be lacking even from the genome of other vertebrates and should have thus appeared relatively recently to the human genome. This led to the TGD inspired proposal that human genome has been subject to genetic engineering relatively lately with an even more crazy sounding proposal that intelligent intra-terrestrial life forms are responsible for this engineering (see [K22, K23]). Needless to say, this hypothesis is absolute non-sense unless one takes completely seriously the notion of many-sheeted space-time and related ideas (see **Fig.** `http://tgdtheory.fi/appfigures/manysheeted.jpg` or **Fig.** 9 in the appendix of this book).

Towards the end of year 2003 a new sensational result was published [I25]. The genome of certain coral, Cnidarian Acropora millepora, was compared with the genomes of fly (Drosophila melanogaster), nematode worm (Caenorhabditis elegans) and human genome. For simplicity, I shall refer to these animals as corals, flies, and worms in the sequel.

Before going to results, it deserves to mention that the phylum Cnidaria [I3] is a major group of invertebrates that includes the sea anemones, corals, jellyfishes, hydroids. Radial symmetry is characteristic for these animals whereas more advance animals have bilateral symmetry. All cnidarians are carnivors. The name cnidaria comes from "cnida", stinging capsules used to deliver toxin, to stick to a prey, or to entangle with an object. Cnidarians are believed to branch from the evolutionary tree much before flies, worms and vertebrates, and the expectation was that its genome should give information about the genome of the common precedessor of metazoans ("animals"). Obviously, coral genome should possess genome having much stronger resemblance to fly and worm genomes than that of vertebrates.

The astonishing result was that the genome of coral resembles human genome to a surprisingly high degree but much less the genomes of the fly D. melanogaster and nematode worm C. elegans. The conclusion of the authors is that the genes usually regarded as vertebrate inventions have been possessed by the believed-to-exist common precedessor of all animals, and that invertebrates have lost most of the genes common to human and coral during their evolution.

These strange conclusions are based on the existing wisdom about the evolution of animals and about the role of genome, and thus also challenge this wisdom.

1. The mutation rate of flies and nematode worms is high but it is not known whether genes can disappear. One can of course criticize the conclusion. Is the loss of genes, kind of "de-evolution", really a good survival strategy? Could it be that the gene loss hypothesis is dictated by some hidden assumptions? One can imagine several assumptions of this kind.

   (a) It makes sense to speak about continuously growing evolutionary tree from which corals branch before the emergence of the flat worms believed to be common precedessors of vertebrates, flies, worms, and other invertebrate phyla.

   (b) There are no of interventions from outside to the genetic evolution (genetic engineering by some more advanced life forms).

   (c) There is no horizontal gene transfer between corals and vertebrates (say fishes) living belonging to the ecosystems containing corals.

2. Corals possess relatively few tissue types. Coral is in fact the the most primitive animal possessing neurons. The neurons are organized into a homogenous neural net like structure. Therefore the presence of genes of vertebrates with highly developed nervous systems in the coral genome looks paradoxical. Could genes have some unknown functions besides those related to the coding of "hardware" ?

2.6.1 Why Corals And Vertebrates Should Have Common Genes?

The fact that corals and higher vertebrates have a lot of common genes, must have some sensible explanation. If flies and worms have never possessed genes common to vertebrates and corals, there must be something common to corals and vertebrates but not to higher vertebrates and flies, worms, perhaps all other invertebrates than corals.

1. Corals (polyps) are simple multi-cellulars consisting of two cell layers, epidermis and gastrodermis. The non-tissue layer between them is called the mesoglea. Corals are in a complex interaction with an ecosystem involving also vertebrates. Interestingly, corals are the only animals living in symbiosis with plants (dino-flagellates, which are simple mono-cellulars) providing them metabolic energy produced in photosynthesis. Social life requires communications and language of some kind, and this might explain why corals possess so complex genome.

2. Corals form large populations, coral reefs. One could regard coral reef as a super-organism, with corals taking the role of the cell in ordinary organisms. Some corals could even define super-neurons of the super-neural system of this super-organism. This could resolve the paradox caused by the simplicity of the nervous system of the coral itself viz. the complexity of the coral genome: complexity would reside in the connections and communications of the super-neural system.

3. Rather remarkably, both vertebrates and corals possess skeletons having calcium as a basic building brick. Coral skeleton consists of calcium carbonate $CaCO_3$ or limestone (calcium carbonate plus sediment). Usually the basic function of skeleton is thought to be that of a mere supporter but it might have also other functions as following arguments suggest.

   The function in question could be that of antenna.

1. Ca_{++} waves are known to play key role in the functioning of the nervous system [J15]. The finding, which led to the notion of magnetic body crucial for the functioning of living systems in TGD Universe, was that irradiation of living matter at the harmonics of Ca_{++} cyclotron frequency in Earth's magnetic field has effects in living matter [J7] and that these effects can be best understood if living cells are macroscopic quantum systems.

2. What makes Ca_{++} (and Mg_{++}) ions so special that they are bosons and can therefore form super-conducting Bose-Einstein condensates at the magnetic flux tubes of (say) Earth's magnetic field. The dropping of Ca_{++} ions from smaller space-time sheets to the magnetic flux tubes generates cyclotron radiation at the harmonics of the cyclotron frequency, and this mechanism is crucial for the generation of EEG.

   In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant h_{eff} so that cyclotron energy would be liberated.

3. The fact that EEG is associated with vertebrate neural systems and corals representing the simplest life forms having neurons, suggests that communications could be on Ca_{++} cyclotron radiation and be between neural systems of corals and vertebrates living around it. The calcium containing skeletons possessed by both vertebrates and corals could serve as antennae allowing to generate field patterns representing the communicated signals strong enough to make possible communications with say fishes.

   These observations can be combined with the earlier vision about the role of genome.

1. TGD based view for genetic code predicts that genes are not expressed only chemically but also in terms of field patterns representing one particular expression of the universal language

defined by genes and memes, the latter being represented by the intronic portions of the genome. The hypothesis is that common memes and genes make possible even inter-species communications. Thus DNA would not characterized so much species than communications in the ecosystem in which the species.

2. The proposed electromagnetic realization of the language defined by DNA and utilizing genetic code is as transitions at the harmonics of cyclotron frequency of Ca_{++} ions. The time $\tau_c = 1/f_c$ defined by cyclotron frequency $f_c = 15$ Hz of Ca_{++} ion in the magnetic field of $B_e = .5$ Gauss, defines the duration of the code word consisting of 6 bits. Bit "1" can be realized as a pulse of duration about $\tau_c/6$. Second realization if the codeword is as superpositions 6 lowest harmonics of cyclotron frequency generated when Ca_{++} ions drop to larger space-time sheets (bit "1" corresponds to harmonic with Fourier amplitude above critical intensity).

The combination of these ideas leads to the following vision about why corals and vertebrates possess common genes.

1. Linguistic communications based on electromagnetic field patterns are crucial for the functioning of the complex ecosystem formed by corals and various species belonging to it. In particular, fishes are vertebrates so that it would be advantageous for the coral to possess a considerable fraction of vertebrate genome responsible for the universal language.

2. The basic difference between humans and corals is due to the intronic portion of the genome, which dominates human genome and defines higher level linguistic structure based on menetic codewords with duration of.1 seconds and having 126 (or 127) bits. One could test whether fishes and other vertebrates living in the coral environment share identical genes with the coral.

2.6.2 Did Corals And Vertebrates Receive Their Common Genes Via Horizontal Transfer?

One can imagine several alternative models for how corals and vertebrates received their common genes. These "language genes" could have been "invented" by either corals or vertebrates and transferred horizontally from corals to vertebrates or vice versa. The most general view is that the system inventing the "language genes" was the entire system coral + vertebrates (possessing magnetic body), and the transfer of genes occurred in both directions.

Many-sheeted space-time allows to consider the possibility that the genes were transferred along magnetic flux tubes connecting the many-sheeted DNAs of corals and vertebrates involved (recall that many-sheeted DNA involves hierarchy of magnetic flux tubes with magnetic field strengths scaled by powers of two). The large sized magnetic body of the coral might have played essential role in this transfer. If one sees the magnetic body associated with corals and associated life-forms as a single conscious organism, this hypothesis looks natural.

Horizontal transfer of genes from vertebrates to corals?

Perhaps the simplest hypothesis is that the genes of vertebrates not possessed by invertebrates like flies and worms, appeared in the genome of corals, only after they were needed, that is during the co-existence with vertebrates as parts of same ecosystem.

The simplest possibility is a horizontal gene transfer from vertebrates to corals, so that vertebrate genes could be seen as genuine vertebrate inventions as usually believed. Since corals possess calcium backbone, it is indeed sensible to transfer "language genes" to corals. The transfer of "language genes" could have occurred also to other organisms but, by the absence of Ca containing skeleton, the transferred "language genes" would have been useless for them. The genes coding for the calcium containing skeleton of coral must have been present from the beginning, and for this option must be independent of "language genes".

Horizontal transfer of genes from corals to vertebrates?

The horizontal transfer of genes could have also occurred from corals to vertebrates so that vertebrate genes could be seen as coral inventions. This makes sense if the common genes were primarily involved with the communications between corals and vertebrates so that the co-evolution of vertebrates and corals was basically evolution of communications using genetic code. Also the vertebrate genes responsible for coding Ca_{++} based structures like bones should have counterparts in the genome of the coral. If corals possessed neurons from the beginning, the genes allowing to differentiate the cell to a neuron could have been transferred, not only to vertebrates but also to the invertebrates with nervous system, and corals could have functioned as a kind of organizing centers of evolution.

2.6.3 What Happened In Cambrain Explosion?

The most science fictive hypothesis is that the vertebrate genes were possessed by corals from the beginning. Ironically, this is the hypothesis forced also by the standard view about evolutionary tree. Since these genes had no function at the time when even flat forms preceding flies, worms, and vertebrates were still absent, the only reasonable conclusion seems to be that some advanced life forms intervened the terrestrial evolution somehow.

There are two basic options.

"Language" genes could have appeared to the genome of coral by some kind of genetic engineering. Since corals are the simplest organisms possessing neurons, also the genes responsible for the differentiation of cells to neurons could have emerged during this intervention.

2. Corals themselves could have been these extra- or intra-terrestrial life forms possessing these genes.

Corals would have served as kind of gene banks and "language" genes would have been transferred horizontally to the genomes of vertebrates during the evolution of the ecological coexistence with vertebrates such as fishes. "Neuronal genes" would have been transferred also to other phyla than future vertebrates.

Obviously, this intervention could have have induced profound changes, entirely new phyla could have emerged as a result of these genetic modifications by horizontal gene transfer. Although this scenario sounds un-necessarily science-fictive, it deserves a serious consideration since, as will be found, it could allow to resolve the puzzles related to the Cambrian explosion.

This option can be tested by looking whether corals possess genes possessed by higher vertebrates like humans but not by any of the vertebrates, which have possibly been members of same ecosystem with corals. One could also try to test the hypothesis that coral has possessed "language genes" already at Cambrian period. This could be the case, if "language genes" and genes coding for Ca^{++} body of coral belong to the same gene cluster.

Did Cambrian explosion involve the intervention of intra- or extraterrestrial life forms?

According to the fossil records, multicellular fauna emerged suddenly in the so called Cambrian explosion [I48]. Already Darwin realized that the absence of fossils from pre-Cambrian era posed serious challenges for the idea about gradual evolution in which evolutionary tree develops gradually new branches. The problems are following.

1. Why did the Cambrian explosion occur so late? This problem is discussed in the chapter [**?**].

2. Why no fossils of the pre-Cambrian precedessors of the Cambrian fauna have been found? The obvious explanation is that the faunas of pre-Cambrian era did not contain hard parts and thus yielded no fossils. During last decades two pre-Cambrian faunas have been however found. Edicaria are multi-cellulars with a pan-cake like shape whereas Tommotian fauna consists of simple cup and cap like multi-cellulars [I48]. Contrary to what one might expect, there is however no continuous evolution of these faunas to the Cambrian fauna and it seems that Cambrian explosion suddenly generated the precedessors of the recent day fauna.

3. The third problem which Darwin could not yet face emerged much later. The Burgess Shale fauna found 1909 by Charles Doolittle Wallcott challenged even the very notion of the evolutionary tree (for an excellent popular discussion of implications of Burgess Shale fauna see the book "Wonderful Life" of Stephen Jay Gould [I48]). It was found that several phyla of animal kingdom (kingdoms consist of phyla), which do not exist today, emerged in Cambrian explosion and then disappeared. The usual view about evolution is that it creates complexity from simplicity rather than vice versa. Obviously, just the opposite occurred in Cambrian explosion. Even more remarkably, not a single phylum has appeared to the fauna after the Cambrian explosion.

All these problems would have a nice resolution if Cambrian explosion were due to the intervention of intra- or extra-terrestrial life forms. Suppose that life evolved in intra-terrestrial conditions, in the safe womb of Mother Gaia, one might say. In this frame of mind Cambrian explosion could be seen as a moment when Mother Gaia gave birth to new phyla preceding the recent day fauna. After the moment of birth these children of Mother Gaia had to survive by their own in the harsh Cambrian environment and many of them did not. This would elegantly explain why Cambrian explosion was followed by a strong extinction of phyla.

The metaphor about mother Gaia giving birth to life forms could have at least two meanings.

1. The most concrete meaning is as the emergence of these life-forms from intra-terrestrial conditions to the surface of Earth: many-sheeted space-time might make this Jules Verne like travel possible. Corals might have been these intra-terrestrial life-forms realizing genetic code in terms of field patterns using calcium containing skeletons as antennae, and being the first animals possessing primitive nervous system and ability to realize genetic code electromagnetically in EEG frequency range. After this the horizontal transfer of intra-terrestrial genes would have stimulated the evolution of vertebrates from more primitive life forms and have generated various phyla.

   Although corals are simple life forms, coral populations are not, and they could be seen as super-organisms with cells being replaced by double cell layers, corals. If this interpretation is accepted, coral populations represent "alien" life forms at a higher level in the evolutionary hierarchy. This interpretation would make natural the identification of corals as organizing centers of evolution. The radial geometry of corals would nicely symbolize their role as evolutionary organization centers.

2. A less concrete realization of the metaphor would be as intra-terrestrial genetic engineering involving the insertion of packets of introns and genes (software plus necessary hardware) to the DNAs of already existing life forms. Of course, option

3. could be seen as are representing a special manner to perform this genetic engineering by utilizing a life form possessing the genes possessed also by the highest vertebrates and radiating them horizontally.

Variants about the genetic engineering theme

The idea about genetic engineering performed by intra- and/or extraterrestrials could have been realized in several ways.

1. The first vertebrates got their vertebrate genes from intra- or extraterrestrials, and these genes were horizontally transferred to corals living in symbiosis with them. This genetic intervention should have occurred after the Cambrian explosion if it turns out that the nearest precedessors of vertebrates do not possess the common genes.

2. The transfer of genes was from corals to vertebrates and corals received their vertebrate genes in Cambrian explosion from some highly advanced life form, or corals themselves were this advanced life form. During the gradually evolving co-existence with simpler life forms these genes were gradually horizontally transferred to the precedessors of recent day vertebrates.

3. Corals and the precedessors of the vertebrates living in symbiosis with them got their common vertebrate genes simultaneously from outside. Note however that they could have been inventions made by the entire ecosystem in question.

2.6.4 What Ontogeny Recapitulates Phylogeny Principle Means At The Level Of DNA?

The idea about corals as a gene bank could resolve some other mysteries related to the genome.

1. The revised view about the evolution of organisms possessing nervous systems would not rely so much on mutations but already existing and possibly conserved gene and meme banks inherited from corals. Only a fraction of these genes would be in use and evolutionary pressures would determine which portion of these memes/genes is activated. Mutations might only have a secondary and mostly harmful role in the evolution.

2. Introns are the basic candidate for the gene reservoir. This conforms with the idea that introns code for memes since it is plausible that the activation of memetic programs becomes possible only when genes coding for the needed hardware are activated.

The quite recent finding [J19] that the removal of massive portions of the conserved part of the genome has no apparent effect on the organism's functioning supports the idea about genetic repertoire. It is usually believed that conserved regions of genome have some function. Many of these conserved regions are in the "junk" portion of DNA and do not code for proteins. They could however still have some function and in some cases the conserved regions indeed seem to affect the expression of the nearby genes. To identify the function of the highly conserved intronic regions the team of Edward Rubin at the Lawrence Berkeley National Laboratory deleted two huge regions of intronic DNA from mice containing nearly 1000 highly conserved sequences shared by human and mice. One of the chunks was 1.6 million DNA bases long, the other one was over.8 million bases long. The unexpected result was that the genetically modified mice were virtually indistinguishable from normal mice in every characteristic they measured, including growth, metabolic functions, lifespan and overall development.

The result could be understood if the intronic portion of both mice and men derives from a very early period of evolution, perhaps the evolution leading to corals (where-ever it occurred). These conserved genes would have developed to their stable forms during the evolution leading to corals and represent a repertoire of functions waiting for their activation. One could understand the instantaneous popping up of highly developed biological functions, which is often used as a counter argument against the view that the evolution is made possible by random mutations. The interpretation also conforms with the idea that at least part of introns code for memes. In the case of mouse memone would not be yet of much use since speech organs and culture are lacking. The comparison of the introns of man and apes to see whether memes having some function related to language are active in humans but not in apes could serve as a test of this prediction.

Ontogeny recapitulates phylogeny principle would be realized as a gradual shift of the activated portion of the memone and genome during the development of the embryo. Also the memes and genes still waiting circumstances allowing for their expression would be present in the DNA. It might be possible to create artificially earlier evolutionary forms of a given organism and evolution might be studied in the laboratory. The partial transmutation of the morphologies of two different organisms to each other might be possible if the organisms possess common portions of the conserved genome.

If also the future phylogeny is coded to the recent DNA, both mice and men would possess enormous evolutionary potential (frog to prince effect!). Perhaps the explosive cultural evolution of civilization during last centuries has been accompanied by a corresponding shift in the activated portion of memone. This shift could also occur during the lifespan of individual and the idea about personal growth would have a genetic justification. The evolutionary potential might be some day be utilized by the artificial activation of memone and genome. Of course, the activation of higher memetic programs would be possible only if the genes coding for the needed hardware are also present and activated. Again the computer metaphor would work: I have used only a minor portion of the potential of my text processing program to write this piece of text.

Gene activation by electrostatic fields?

The basic question concerns the method of activation. The discovery of chemists Guido Ebner and Guido Schuerch [B1] , [J2] raises the hope that these ideas might be more than over-active imagination and their work also provides a concrete proposal for the activation mechanism. These

findings are briefly described in the article of Hardmuth Mueller [B1] who proposes quite different explanation for the strange findings. Ebner and Schuerch studied the effect of electrostatic fields on the growth and morphogenesis of various organisms. Germ, seeds, or eggs were placed between conducting plates creating an electric field in the range.5-2 kV/m: note that the Earth's electric field is in the range $.1 - 4$ kV/m and of the same order of magnitude.

The outcome was rather surprising and in the year 1989 their employer Ciba Geigy (now Novaris) applied for a patent "Method of enhanced fish breeding" [J2] for what is called Ciba Geigy effect. The researchers describe how fishes (trouts) develop and grow much better, if their eggs have been conditioned in an electrostatic field. The researchers report [J2] that also the morphology of the fishes was altered to what seems to represent an ancient evolutionary form: this was not mentioned in the patent.

The chemists founded their own Institute of Pharmaceutical Research near Basel, where Guido Ebner applied for another very detailed patent, which was never granted (it is not difficult to guess the reasons why!). In the patent he describes the effect of electrostatic fields on several life forms (cress, wheat, corn, fern, micro-organisms, bacteria) in their early stage of development. A clear change in the morphogenesis was observed. For instance, in one example fern had all sort of leaves in single plant apparently providing a series of snapshots about the evolution of the plant. The evolutionary age of the first leaf appeared to be about 300 million years whereas the last grown-up leaf looked close to its recent form.

If one takes these finding seriously, one must consider the possibility that the exposure to an electrostatic field can activate passive genes and change the gene expression so that older morphologies are expressed. The activation of not yet existing morphologies is probably more difficult since strong consistency conditions must be satisfied (activation of program requires activation of a proper hardware).

It is known that the developing embryo has an electric field along the head-tail axis and that this field plays an important role in the control of growth. These fields are much weaker than the fields used in the experiment. p-Adic length scale hierarchy however predicts an entire hierarchy of electric fields and living matter is indeed known to be full of electret structures. The strength of the electric field in some p-adic length scale related to DNA might somehow serve as the selector of the evolutionary age. The recapitulation of phylogeny during the ontogeny could mean a gradual shift of the activated part of the memone and be controlled by the gradually evolving electric field strength.

The finding that led Ebner to his discovery was that it was possible to "wake up" ancient bacteria by the exposure to an electrostatic field. This would suggest that in the case of primitive life forms like bacteria the electric field strength of Earth controls the state of bacterium whereas in higher life forms endogenous electric fields have taken the role of Earth's electric field.

Electric fields and healing

Wound healing is very much like morphogenesis and already Becker discovered that electric field induces a healing of wounds [J5]. More recent studies of the effects of electric fields on healing and on embryos are discussed [J8] and one can find useful quantitave information from this article. The typical strengths of the electric fields appearing in organisms are in the range.01-.1 kV/m: the upper bound of this field is the lower limit of Earth's recent electric field strength and considerably below the field yielding Ciba Ceigy effect. There are however also much stronger fields present: the voltage over epithelium (double cell layer) is in the range 30-50 mV and would make 6-10 kV if the thickness of epithelium were 5 μm. In the 1950s it was discovered that the direction of external electric field determines whether a flatworm which has been cut in two pieces develops head or tail. A natural voltage gradient exists between the severed worm's tail and the place where its head once was. A naturally occurring electric field of strength 40 V/m has been found to play a vital role in the wound healing in the cornea of rats: it is found that the cells divide in the plane orthogonal to the field and pushing new cells to the wound.

A further finding reported in [J8] was that a voltage of 2 mV over cell diameter (1 kV/m if cell radius is 2 μm and in the same range as the field applied in Ciba Geigy effect) alters the front back orientation of the neuroblast. The proposed interpretation of these findings is that electric field provides only directional information whereas the findings of Ebner suggest that much more profound meme/gene level effects might be involved. For instance, one can ask whether the

exposure to an appropriate external electric field could induce the return of a differentiated cell to the stem cell stage realized as a shift in the activated portions of memone and genome.

Generalized four-wave mechanism and the concrete mechanism of gene activation by static electric fields

Concerning the concrete mechanism behind the activation there are several constraints. The activation mechanism must be localized at the level of DNA. On the other hand, a given region of DNA must activate only in an electric field of a particular strength coding for its evolutionary age. The basic finding of Ebner about "wake-up" of ancient bacteria in a static electric field suggests that the activation must be a kind of "wake-up" process for an appropriate part of DNA. "Wake-up" corresponds to the generation of self-organization pattern getting its metabolic energy by sending negative energy photons absorbed by some system with corresponding excitation energy. This mechanism is indeed non-local since only the strength of the electric field matters. The transfer of an electron in an electric field through a distance not larger than the size of nucleus by absorbing negative energy photon is a good candidate here.

The generalized four-wave mechanism for remote metabolism requires the existence of generalized standing waves taking care of themselves by sending negative energy (phase conjugate) photons at the energy defined by the frequency of wave. The ideal situation corresponds to a dispersion relation for which the frequency of the oscillation does not depend on wave vector at all: plasma oscillations satisfy this conditions. In the chapter [K34] a model for the coherent electric dipole oscillations was constructed. In this case the frequency depends only on the angle between the wave vector and the direction of the electric field. Same applies to magnetostatic oscillations [D2] for which the Larmor frequency of electron gives the maximum value of frequency. The frequency is constant for effectively 2-dimensional oscillation patterns with wave vectors at the surface of a cone and periodically recurring oscillation patterns able to represent simple 2-dimensional self-sustaining mental images become possible.

Quantitative estimate support this model. In a field of.5-2 keV/m the electron gains a kinetic energy of $5-20$ μeV while travelling a distance of 10 nm corresponding to the thickness of cellular membrane. This corresponds to photons with microwave frequencies in the range .12-.48 GHz and wave lengths in the region.6-2.5 m so that the energy can be sucked from quite large spatial volume by inducing transfer of electron through this distance without a gain of kinetic energy. These frequencies corresponds to the nanosecond scale assigned with the coherent electric dipole oscillations whose importance was first realized by Fröhlich [I35]. In the above mentioned model of coherent dipole oscillations as analogs of magnetostatic oscillations these frequencies correspond the p-adic length scale $L(151) = 10$ nm associated with cell membrane thickness which is of central importance in the coiling hierarchy of DNA.

Also magnetostatic waves in a magnetic field associated with some level of the hierarchy of DNA space-time sheets could be in question. In this case the Larmor frequency of electron defines the maximal oscillation frequency. From the assignment of $L(169) \simeq 5$ μm to the Earth's magnetic field, the length scale associated with the needed field varying in the range $.05-.1$ Tesla is in the range.1-.2 μm.

2.6.5 Where Did Those 223 Genes Pop Up?

The reports of the Public Consortium about human genome in Nature, Feb 15, 2001 [I15] and of Celera Genomics in Science of Feb 16th, 2001, [I34] contained two big surprises.

Are we really so near to fruit flies?

The first astonishing discovery was that the amount of human genome differs relatively little from those of lower organisms: we have only about 30, 000 genes, little more than twice the number 13, 601 of genes for fruit fly. This paradoxical finding forces to think that our genome is not solely responsible for what we are and that the intronic portion of DNA (only about 1 per cent codes of human DNA codes or amino-acid sequences), is not "junk DNA", but contains important biological information and expresses it non-chemically.

In TGD Universe introns would express memes as the classical field patterns associated with MEs ("topological light rays") responsible for the basic expressions of language understood in an extremely general sense. This language includes body language and even cellular signalling, and could quite well make possible (not necessarily conscious) interspecies communications based on memes expressed by communicating species and forming a common vocabulary. All eukaryotes (cells with nuclei), even bacteria, would possess part of the vocabulary of this universal language. The memetic code word is predicted to consist of a sequence of 21 DNA triplets and carries 126 bits of information instead of 6 bits of genetic code. Of course, also genes are expressed in terms of MEs and define a lower level language.

In this framework the actual role of DNA can be understood using the computer analogy. Memes represent the program modules written using the programming language defined by the memetic code, and realized in terms of the field patterns associated with MEs. Genes represent the necessary hardware needed to realize these programs. System builds only the hardware needed, that is cell expresses only part of the genome. DNA engineering requires besides the addition of the new programs (memes, introns) also the insertion of the necessary hardware (new genes). Memes and corresponding genes should have very intimate relationship. In this conceptual framework the standard view is wrong since it identifies the build-up of a new hardware as the sole activity at the DNA level. This would be like identifying the addition of a net card to a computer as the fundamental activity related with computers.

The head-scratching discovery

The "head-scratching discovery" by the public consortium, as Science termed it, came when the genome was compared with the genomes of our precedessors. It was found that human genome contains 223 genes not possessed by invertebrates. Contrary to what one might expect, these 223 genes could make an enormous difference. The reason is that this number is more than two thirds of the number of the 300 genes differentiating between humans and chimpanzees so that these genes could be the main determinant of the dramatic difference between humans and chimpanzees in standard genetics.

Of course, in TGD framework the most important differences would probably relate to the intronic portion of the DNA responsible for language. Dramatic differences between our intronic DNA that of our invertebrate and perhaps even vertebrate precedessors, in sharp conflict with the idea of continuous evolution, should be discovered.

Are the enigmatic genes a horizontal gene transfer from bacteria?

Biologists can explain the presence of the enigmatic genes only by a "rather recent horizontal transfer from bacteria". Here "rather recent" refers to the evolutionary time scale.

This explanation can be challenged on various grounds.

1. The simplest working hypothesis is that the transfer from bacteria is a probabilistic process. The problem is however why the horizontal transfer did not occur to the genomes of other vertebrates and invertebrates and gradually through the whole evolution. One could argue that something characteristic to the vertebrate genome should have made this process possible. In TGD framework one could imagine that the intronic portion of the vertebrate genome could have contained something which made the transfer possible: a common part of memone with the bacteria involved and making possible language based communications ("language" understood in a generalized sense) at DNA level perhaps?

2. The enigmatic genes are involved with important physiological functions. In particular, they are responsible for important neurological enzymes which stem from mitochondria having its own genome. According to my non-professional interpretation this statement means that also mitochondrial genome contains these enigmatic genes. Thus both mitochondrial and nuclear genomes would have been altered by this horizontal transfer from bacteria. Simultaneous double horizontal transfer does not however look a probable event.

3. Only 113 of the 223 enigmatic genes are widespread in bacteria: it would be easier to believe in the horizontal transfer if all of them were widespread. These 113 widely occurring genes

are not encountered in invertebrates at all. As a matter fact, this finding suggests that the transfer occurred from the vertebrate genome to the bacterial one and only partially, rather than vice versa. The analysis of proteins expressed by the enigmatic genes demonstrated that out of 35 identified, only 10 had counterparts in other vertebrates. 25 of them were unique to humans. This suggests that a considerable part of the horizontal transfer has occurred relatively recently and together with associated introns might even distinguish us from chimpanzees.

Horizontal transfer as DNA engineering?

The objections against the horizontal transfer from bacteria force to consider seriously the possibility that the horizontal transfer represents an intentional DNA engineering, both memetic and genetic. The most important transfer should have been to the intronic part of the DNA. The addition of memes would be like adding a new program to a computer. The addition of genes would be like adding a new hardware (say net card or data cable) required by the program to run. The comparison of the intronic portions of DNA of humans and lower vertebrates might thus lead to futher "head-scratching" discoveries. The data are consistent with the assumption that genetic/memetic engineering activities have occurred in several steps during the evolution of the vertebrates although a considerable portion of the enigmatic genes and associated introns, perhaps even two thirds, have been "injected as a single dose".

The evolution of the hominides in Africa had a stagnation period of about 1.5 million years as demonstrated by the study of the ancient stone tools. Then, for about 50 thousand years ago, a sudden jump to creativity occurred. The first ornaments appeared meaning that hominides had become artists and started to express their position in the social hierarchy by clothing and ornaments. This signals about development of highly refined social structures. A general belief is that also language began to develop rapidly and made possible a cumulation of knowledge. It seems that modern human was born and started to migrate from Africa to North. Could it be that memetic engineering induced this crucial step in evolution? Could it be that Neanderthals had to leave because they were not subject to this memetic engineering? Also the emergence of the first civilizations for about 10 thousand years ago might have involved memetic engineering. The ancient Sumerian myths about Gods who came from Heaven and made us their images might be memetic fossils reflecting what occurred.

Who performed the (memetic and) genetic engineering?

One can imagine two identifications for the ancient genetic/memetic engineers.

1. The guess that the engineers were extra-terrestrials (ETs) is supported by ancient myths. The Sumerian and Akkadian texts found inscribed on clay tablets, in which the role of the Elohim in Genesis is performed by the Anunnaki, tell about "Those Who From Heaven to Earth Came". These myths would relate to the last step in the sequence of engineering activities.

2. The second guess is that genetic engineering is due to a highly advanced civilization of a remote geometric future, perhaps futuro-terrestrials, and applying highly advanced technology based on time mirror mechanism and possibly utilizing simpler life forms, perhaps plasmoids, as their couriers. Abduction experiences might relate to genetic manipulations using plasmoids to do the hard job. In this case encounters with aliens would be based on sharing of mental images.

3. The third guess is that genetic engineering is self engineering. The work of Yu. Chen Kangeng gives evidence that the transfer of the genetic information by electromagnetic means is possible [J1]. According to [I22], where the method is summarized, the successful transfer of the genetic information from a donor bio-system to an acceptor system was achieved via high-frequency electromagnetic fields feed repeatedly through the optically-active donor bio-system and then delivered over a long period of time to the receiving bio-system in its early developmental stages. The hybrids created through the irradiation of eggs and seeds with such "genetically loaded" fields are claimed to show very specific mixed characteristics that

were transferred to the next generation without need for further irradiation. This idea is discussed in [K76] on basis of a proposed realization of genetic code at the level of dark matter.

It would seem that the donor genome or parts of it are imprinted to the electromagnetic field pattern in the process and that this field pattern is able to modify the target genome.

Nothing precludes the possibility that genes/supergenes/hyper genes at some level of dark matter hierarchy can also code for genetic self engineering since these activities are after all very similar to other genetically coded bio-chemical activities. The computer analogy would be programs writing programs. The engineering genes would be activated by W MEs inducing plasma oscillation patterns. The claimed effects could be understood if the interaction with genetically imprinted electromagnetic field pattern activates genes inducing genetic self engineering yielding the genetic modifications consistent with the pattern represented by the em radiation.

Magnetic body would receive information about the desired outcome as electromagnetic field patterns emitted by other organisms, most naturally members of the same species. If these modifications are successful, the magnetic body is exposed to this information for long enough time to react and activate W MEs inducing the genetic program inducing the genetic program leading to the suggested genetic modification.

Hyper-genes integrating groups of organisms to larger wholes would be naturally involved with the mechanism. This mechanism would guarantee a rapid propagation of successful genetic modifications to the entire population and would be much more effective than the slowly occurring selection of random mutations. The possibly existing genes responsible for the genetic self engineering could be also introns and express themselves by activating nuclear RNA and process like reverse transcription.

Chapter 3

Many-Sheeted DNA

3.1 Introduction

The problems of how genes code information about the morphology of organism and how this information is expressed, belong to the great puzzles of developmental biology. A closely related mystery is the differentiation of cells. The notion of genetic program is far from precise and it is not clear how close the analogy with a computer program is. There are also several problems which challenge the basic dogmas of genetics.

1. Only 1 per cent of DNA of human genome actually codes polypeptides. Eukaryote genes contain intron sequences which are transcribed into hnRNA but snipped off when hnRNA is transformed mRNA in a process called slicing. The higher the evolutionary level of organism, the higher the fraction of introns is. Molecular Darwinists see introns as "junk DNA" but there is evidence that introns are far from junk. For instance, the splicing of the intron contribution from hnRNA to give mRNA can give several different outcomes depending on the stage of the development of the organism and introns are crucial for the effectiveness of the immune system [I14]. Hence one can wonder whether intron mRNA and exon mRNA could both form the real output of gene subprograms serving in some sense as input for other gene subprograms. This interpretation obviously conflicts with "gene-single protein" dogma in its basic form.

2. There are large amounts of highly repetitive DNA which is silent. One can wonder whether there is some fundamental mis-understanding involved. Could it be that this DNA is analogous to control DNA not transcribed to RNA and therefore not at all useless. There is also active repetitive DNA.

3. There is large amount of silent DNA in control sections between genes. Could it be that this silent DNA expresses itself in some non-chemical way? Chemical expression is very slow, translation rate being twenty amino-acids per second, and one can wonder whether life might have invented faster modes of gene expression and control of gene expression. Also the question whether there is a relation to the typical frequency scales of brain consciousness of order 10 Hz, which can be related to the magnetic and Z^0 magnetic transition frequencies, can be raised.

4. Plant genome is often by a factor of hundred longer than human genome. One could argue that the complexity of organism is measured by the length of the shortest program coding the organism. It is however not at all obvious how the genome of plants could be more redundant than human genome since repetitive sequences common to all animals are present. Introns are actually more frequent in human genome. This suggests that some new unidentified degrees of freedom giving rise to complexity might be present and that the chemistry of DNA in the sense of standard physics is perhaps not all that is needed to understand genetic program.

5. Various self-organization process such as self-assembly and de-assembly are very frequent in living systems. The problem how genes give rise to morphology of the organism is poorly

understood. This forces to challenge the dogma of genetic determinism. One should be able to understand what is determined by genes what is determined by self-organization and whether the genes of the standard physics are enough.

The reason why the above mentioned problems have turned out to be so intractable might be due to a wrong view about space-time. Many-sheeted space-time concept of TGD might be absolutely crucial for the expression of genetic code. DNA itself might involve many-sheeted space-time structures coding faithfully the topology of the body parts. This many-sheeted structure of DNA could allow to understand the miraculous looking features of DNA replication and differentiation of cells. TGD based view of evolution as p-adic evolution implied by the basic quantum theory, should be a crucial element of the picture. Together with the p-adic length scale hypothesis it leads to precise quantitative predictions and a general model for genetic program based on the many-sheeted space-time concept. The model explains also why introns are present only in eukaryotic genome. Most importantly, it seems that the statements represented by the dynamical intron-exon decompositions of genes and defining Boolean algebra, could represent our conscious beliefs and thus affect our behavior as conscious beings. Notice the beautiful connection between matter and mind: genes code the information, not only about the material structure of organism, but also about its belief system. Thus without introns, the pariah class in the society of biomolecules regarded as "junk DNA" by always-so-imaginative reductionistic materialists, we would have no world views and belief systems! In this chapter TGD based view about genetic code and its realization are discussed in detail.

3.1.1 Many-Sheeted DNA

The replacement of the DNA of standard physics with many-sheeted DNA suggest surprisingly simple model for how organism's morphology is coded and decoded to DNA.

1. How the morphology of body is coded?
   The most striking feature of DNA is its one-dimensionality. According to work of Mae-Wan Ho, living systems are liquid crystals [D1]. Liquid crystals are effectively one-dimensional since the layers of the liquid crystal consist of homogenous liquid phase determined by macroscopic characteristics such as pH, temperature, ionic concentrations and electric fields. This suggests that the structural information coded into DNA could be essentially information about the macro- properties of the layers of liquid crystal. This would make 1-dimensional coding of the body plan using DNA sequences very natural. Kind of contraction of the body parts to DNA sequences having many-sheeted structure could be in question! This coding would preserve the topological structure of the many-sheeted space-time surface representing the expression domain of the gene. The structure of the expression domains of maternal genes and Hox genes [I47] controlling morphogenesis supports this picture.

2. How DNA is expressed?
   The very naive first guess is that during growth various thin space-time sheets associated with DNA gradually grow and are glued together by the join along boundaries contacts and form the space-time sheets associated with their expression domains. Somewhat exaggerating, many-sheeted DNA would represent only a particular developmental period of organism in which it is contracted to a thin thread. For instance, the cells determined to develop into eye are glued to the space-time sheet representing future eye and replication products belong also to this space-time sheet. Clearly, the gluing to the space-time sheet of the future expression domain would generate the needed long range correlation between cells in the expression domain. It must be emphasized that self-organization should play key role in this process: for instance, liquid crystal nature of the living matter should determine morphology to a high extent.

3. What makes differentiation and control of the morphogenesis possible?
   Differentiation must be explainable as a selective activation of transcription and although a local process, involves also top-down control making possible a precise timing. Concentration gradients for the transcription factors, that is proteins controlling transcription, are

certainly crucial in this respect. When the concentration of the protein falls below a critical value, the truth value of a statement representing input to some gene program modules changes. This leads obviously to spatial patterns of gene expression resulting from branching of gene programs. For instance, the development of organs should result as a combination of genetic control of this kind plus self-organization. Join along boundaries bonds between gene space-time sheets and larger space-time sheets or genes and control regions of chromosome make possible quantum control of genetic expression based on phase gradients of the super conducting order parameters and resonant Josephson frequencies which correspond to magnetic transition frequencies of genes, control regions or related substructures. It could also be that the # contacts (wormhole contacts) from genes to various space-time sheets representing body parts provide the interaction with the classical fields of the macroscopic space-time sheets representing body arts and controlling the activity of a particular gene. In any case, the fact is that the action mechanisms of transcription factor proteins in eukaryotes are not understood. The mechanism is not purely chemical one since transcription factors are often located quite far from the promoter region. Electromagnetic oscillations with resonant frequencies could be in question. In absence/presence of oscillation gene is activated.

3.1.2 Realization Of The Genetic Program

TGD suggests concrete ideas about how organism can act as a conscious computer [**?**] Genome represents possible statements consistent with a fixed atomic statement (single element set in set-theoretic representation of Boolean algebra) represented as sequences of DNA. DNA triplets define basic axioms of the axiom system in question. Active genes which have coded some minimum about of intronic mRNA and protein coded by the exon part of the gene give rise to conscious experience about the truth of the statement represented by the gene. Otherwise the truth value of this statement is ill-defined and not consciously experienced. Truth values of the statements representing conclusion of the statement represented by gene in turn act as premises for the statements represented by some genes and these genes in turn activate and give rise to experience of the truthness of corresponding statements. In this way genetic program proceeds and gives rise to a sequence of experiences about truthness of statements represented by the genome. Note however that the experiences of truthness at DNA level need not correspond to our conscious experiences: entire hierarchy of selves having connection to DNA level is involved.

The beautiful feature of this realization of genetic program is that no cables for signal transmission are needed. The genetic program is also extremely robust and flexible unlike ordinary symbol based programs in which the change of the value of single binary digit can lead to a catastrophe. Furthermore, spatial patterns of gene expression develop naturally: gene in give cell producing transcription factor affects only finite region of space since subcritical concentration of the transcription factor means effectively its total absence. This can lead to intricate structural patterns of gene expression and determination of cells making possible differentiation. The translation of average protein requires 20-60 seconds and the cognitive processes of ours which possibly occur at DNA level must be rather slow. Time scale of emotions is however slow as is also higher level abstract thinking.

Both introns and exons represent statements which are true if the premises of the gene statement are true. Simple model for how introns can be separated from the exon part of the genetic module explains the many mysterious properties of introns elegantly and introns become an absolutely essential element of the genetic program. In particular, addition or subtraction of a marking - "comment sign" - to nucleotide changes the nucleotide from exonic to intronic or vice versa. Thus this marking serves essentially as a binary digit telling whether nucleotide belongs to exon or intron. Unless physical realization of these markings poses any additional constraints, comments signs can be dropped anywhere in gene and this means that same gene can be expressed in 2^N way, where N denotes the number of basic units in the maximal decomposition into exons and introns. Obviously, an interpretation as a representation for the statements of Boolean algebra for statements about N basic statements suggests itself strongly: perhaps each eukaryotic gene represents Boolean algebra! If also intron-exon decomposition is assumed to be dynamical then

the number of exon-intron decompositions in gene consisting of N DNA triplets is

$$M = \sum_{k=1}^{N} \left(\begin{array}{c} 3N \\ 3k \end{array} \right) \quad .$$

The premises of the gene statements are represented in the operator sequences associated with the gene. Intron $\leftrightarrow$ exon transformation induced by the addition or cancellation of "comment signs" associated with nucleotides leads to a generalization of the operon model for the regulation of gene transcription. The protein coded by introns which have become an exon part of gene serves as a repressor of the gene expression for original exons. The shifting back to a mode in which exons are coded to protein means that the coding of the supressor protein stops and the genes whose activation depends on the output of the gene in question are automatically activated.

A cautious proposal is that many-sheeted genes could represent a hierarchy of conscious beliefs: genome would be a collection of Boolean algebras represented by genes. In case of prokaryotes these Boolean algebras contain only one expressed element; in case of eukaryotes number of elements can be much larger but again totally intronic gene is not expressed. Maybe DNA could code thoughts and proteins emotions associated with them.

3.1.3 Are Non-Chemical Transcription Factors And Non-Chemical Gene Expression Possible?

Enhancers and silencers affect gene expression in a non-local way difficult to understand purely chemically. There are also tissue specific transcription factors. The notion of many-sheeted DNA suggests the possibility of non-chemical transcription factors. Classical em and Z^0 fields are especially interesting possibility as far as gene expression and its control in long length scales are considered. The general quantum control and coordination mechanisms based on Josephson currents flowing between gene space-time sheets and larger space-time sheets and making possible comparison circuits, clocks, alarm clocks and novelty detectors, suggest themselves. Indeed, the frequency scale 20 amino-acids per second for the translation process corresponds to a typical scale for the magnetic transition frequencies, which lie at the heart of the TGD based theory of brain consciousness. Classical fields affect various macroscopic quantum phases and one cannot exclude the possibility that gene level is involved with cognition and sensory experiencing even in the time scales shorter than the long time scales associated with the neural transmitter action.

Neural level could control genetic level (this is known to occur chemically) via non-chemical control mechanisms. Nuclear matrix, cytoskeleton and the collagen network associated with connective tissues are liquid crystals and ideal tools for transforming electrical signals to mechanical (say conformational wave s) and vice versa. The massless extremals associated with the microtubules connecting neuronal cell membrane with the nuclear region could make possible the information transfer from neural level to gene level: in fact, the non-dispersive vacuum currents associated with the massless extremals are optimal for communication purposes. This suggests that nerve pulse patterns could be transferred into genome along cellular matrix.

The idea that information from the genetic level would be transferred to neural level and that genetic level could even control neural level chemically is consistent with experimental facts. One could even consider the possibility that genome plays the role of neuronal brain. One can indeed play with idea that possible "this is true" experiences associated with the active genes could be expressed as our emotions. As noticed, the time scale of chemical gene expression is .05 seconds and is much slower than the millisecond time scale of nerve pulse so that direct translation of genes to nerve pulse patterns is not plausible. This is however consistent with the realization of "this is true" experiences as emotions which are characterized by slow time scales. Thus the statements "If A then B" expressed by genes B and the control structures A associated with them could give rise to neural activity translating these experiences to sensory experiences about the internal state of brain accompanied by and often identified with emotions, which in turn could be expressed as internal speech. Music metaphor does not however require any precise coding to nerve pulse patterns. The idea that this communication could occur also non-chemically is much more speculative and not actually supported by the most stringent form of the master slave hierarchy. It is also difficult to imagine how the coding of DNA sequence to, say nerve pulse patterns, could

be achieved. In principle, memetic code could be realized as sequences of 21 DNA triplets. The idea about direct one-to-one mapping of DNA level to memetic level seems however implausible.

The large amount of silent DNA suggest that some non-chemical gene expression mechanisms might be at work. This does not necessitate communication between genomes although also this is possible in principle. The extreme would be that neuronal genomes could form neuronal democracy communicating to each other their "If A then B" opinions with conclusion B depending on what the exon-intron decomposition of gene B is for particular gene. This would make possible neuronal voting. Assume that the sub-selves of self are neuron groups with identical synchronized inputs A. This means that same genes are activated and output depends only on the intron-exon decomposition of the individual gene and that sub-self experiences entire spectrum of opinions about what A implies. Self experiences the neuron group sub-self as the average over the opinions "If A then ..." of individual genome subsub-selves. One can also consider the possibility of Boolean "machines". Gene B receives the premises A of "If A then B" as nerve pulse pattern acting to the control sequence associated with B and generate as output the nerve pulse pattern representing statement B when premises are satisfied.

3.1.4 Model For The Genetic Code

The basic numbers of genetic code are probably not accidental. This led for ten years ago to an attempt to construct a model for abstraction process reproducing the basic numbers of the genetic code. The simplest model for an abstraction process is based to a repeated formation of statements about statements starting from two basic statements. If one drops at each step of construction the statement corresponding to empty set in the set theoretic realization of Boolean algebra, one obtains a hierarchy allowing to understand the basic numbers of genetic code.

What one obtains is so called Combinatorial Hierarchy [**?**]onsisting of the Mersenne numbers $2, M(1) = 3, 7.127, 2^{127} - 1, ..$ constructed using the rule $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$. The explicitly listed ones are known to be primes. Combinatorial Hierarchy emerges from a model of abstraction process as subsequent transitions from level to meta level by forming Boolean statements about Boolean statements of level n and dropping one statement away. Combinatorial Hierarchy results also by constructing the sets of all subsets with empty set excluded starting from two element set. The set of statements at level n can be given a structure of Finite Field $G(M(n), 1)$ if $M(n)$ is prime. The multiplicative groups $Z_{M(n)-1}$ form a nested hierarchy and the coset spaces $Z_{k_n} \equiv Z_{M(n+1)-1}/Z_{M(n)-1}$ are cyclic groups. Combinatorial Hierarchy based model of Genetic Code explains the number of DNA:s and amino-acids and the representation of words of the GC as triplets of 4 different codewords. Aminoacids correspond to $k_{n=3} = 21$ axioms of a formal system defined by $n = 3$ level of Combinatorial Hierarchy having a unique imbedding as the group $Z_{k_n} \subset Z_{M(n)-1} = Z_{126}$ and DNA:s correspond to the set $X_{N(DNA)} \subset Z_{M(n)-1}$ of $N(DNA) = (M(n)+1)/2 = 64$ statements consistent with a given atomic statement at level n regarded as special cases of general theorems. GC corresponds to the mapping $x \to x^{k_{n-1}} = x^6$ in $Z_{M(n)-1}$ mapping DNA type statements to amino-acid type statements. The numbers of DNA:s coding single amino-acid are reproduced in a symmetry breaking mechanism involving the finite groups $Z_{p_{n-1}}$ and Z_{k_n} and symmetry breaking is in a well defined sense minimal. The infinite hierarchy of possible genetic codes suggests the possibility of an infinite hierarchy of increasingly complicated life-forms.

The physical model of the genetic code leads to a beautiful interpretation of the genetic code as mapping the fundamental 64 truths to 20 basic conscious experiences, perhaps the emotion about truthness. The fact that hormones correlate with emotions suggests that this map assigns to a logical statement an emotion and that even our emotions could relate to DNA level. Note however that TGD predicts entire hierarchy of selves. Aminoacid P corresponds to the emotionally experienced truth $G_1(P)$ or $G_2(P)$.. or $G_n(P)$ is true, where G_i code for protein P. 3 stopping sign codewords cannot be experienced emotionally as truths not non-truths (holy trinity!).

3.1.5 The Relationship Between Genetic And Memetic Codes

TGD leads to a model of Boolean mind in terms of the temporal sequences formed by cognitive neutrino pairs with vanishing total energy. As noticed, the model for abstraction process predicts entire hierarchy of genetic codes [**?**] This leads to the idea that our cognition might correspond to

the level next to the genetic code. The hypothesis that memetic code corresponds to the next level of Combinatorial Hierarchy characterized by Mersenne prime $M_{127} = 2^{127} - 1$, when combined with p-adic length scale hypothesis, leads to a prediction of about .1 seconds for the duration of the "wake-up" period of sub-self corresponding to the codeword of the memetic code.

The memetic codeword consists of 126 bits and could be represented by two possible spin directions of fermion corresponding to two values of Boolean statement. This implies that one millisecond should be the duration of single bit: this time scale is indeed fundamental for nerve pulse activity. What the fermions in question are? Ths question must be left open. The original proposal based on cognitive neutrino pairs at opposite throats of wormhole contact discussed in [**?**]ooks highly unrealistic from the point of view of standard model physics. The possibility of scaled variant of weak interaction physics with intermediate boson length scale of order cell size or cell membrane thickness however allows to consider this kind of option. Dark protons is another assignable to the lipid layers of cell membrane is second option [**?**]

This picture suggests the following general framework. Memes and genes correspond to two levels in the hierarchy of conscious intelligence and genetic programs could be perhaps seen as subprograms called by the higher level memetic programs. One could even see higher level life as symbiosis of memes and genes.

This raises several questions. Does genetic code determine the evolution of the organism or is the development of organism some kind of "social process" in which the genetic level interacts with the memetic level? Do genes code the space-time sheets representing the hardware of the memetic level or do higher level organisms represent symbiosis of two almost independent life forms? Does memetic level control genetic level or vice versa or is the interaction between these levels bi-directional? Despite that these questions which remain open, it seems that the three approaches to understand cognition based on the Combinatorial Hierarchy model of abstraction process, to fermionic Boolean algebra as a model of logical mind and to genetic and menetic programs as a model for conscious intelligence seem to combine to form single "holy trinity" of cognition.

3.1.6 Mersenne Hypothesis

The hierarchy of dark matter levels is labeled by the values of Planck constant having quantized but arbitrarily large values TGD inspired quantum biology and number theoretical considerations suggest preferred values for $r = \hbar/\hbar_0$. For the most general option the values of $\hbar$ are products and ratios of two integers n_a and n_b. Ruler and compass integers defined by the products of distinct Fermat primes and power of two are number theoretically favored values for these integers because the phases $exp(i2\pi/n_i)$, $i \in \{a, b\}$, in this case are number theoretically very simple and should have emerged first in the number theoretical evolution via algebraic extensions of p-adics and of rationals. p-Adic length scale hypothesis favors powers of two as values of r.

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1 + i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that all the four scaled up electronic Compton lengths with $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm) define scaled up copies of electroweak and QCD type physics with ordinary value of $\hbar$ and that these physics are induced by dark variants of corresponding lower level physics leads to a prediction for the preferred values of $r = 2^{k_d}$, $k_d = k_i - k_j$, and the resulting picture finds support from the ensuing models for biological evolution and for EEG [**?**] This hypothesis - to be referred to as Mersenne hypothesis - replaces the earlier rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant. The background necessary for understanding what is involved is described in [**?**]

3.1.7 Fractal Hierarchy Of Magnetic Flux Sheets And The Hierarchy Of Genomes

The notion of magnetic body is central in the TGD inspired theory of living matter. Every system possesses magnetic body and there are strong reasons to believe that the magnetic body associated with human body is of order Earth size and that there could be an entire hierarchy of these bodies with even much larger sizes. Therefore the question arises what one can assume about these magnetic bodies. The quantization of magnetic flux suggests an answer to this question.

1. The quantization condition for magnetic flux reads in the most general form as $\oint(p-eA)\cdot dl = n\hbar$. If supra currents flowing at the boundaries of the flux tube are absent one obtains $e\int B\cdot dS = n\hbar$, which requires that the scaling of the Planck constant scales up the flux tube thickness by r^2 and scaling of B by $1/r$. If one assumes that the radii of flux tubes do not depend on the value of r, magnetic flux is compensated by the contribution of the supra current flowing around the flux tube: $\oint(p-eA)\cdot dl = 0$. The supra currents would be present inside living organism but in the faraway region where flux quanta from organism fuse together, the quantization conditions $e\int B\cdot dS = n\hbar$ would be satisfied.

2. From the point of view of EEG especially interesting are the flux sheets which have thickness $L_e(151) = 10$ nm (the thickness of cell membrane) carrying magnetic field having strength of endogenous magnetic field. In absence of supra currents these flux sheets have very large total transversal length proportional to r^2. The condition that the values of cycloctron energies are above thermal energy implies that the value of r is of order 2^{k_d}, $k_d = 44$. Strongly folded flux sheets of this thickness might be associated with living matter and connect their DNAs to single coherent structure. One can of course assume the presence of supra currents but outside the organism the flux sheet should fuse to form very long flux sheets.

3. Suppose that the magnetic flux flows in head to tail direction so that the magnetic flux arrives to the human body through a layer of cortical neurons. Assume that the flux sheets traverse through the uppermost layer of neurons and also lower layers and that DNA of each neuronal nuclei define a transversal sections organized along flux sheet like text lines of a book page. The total length of DNA in single human cell is about one meter. It seems that single organism cannot provide the needed total length of DNA if DNA dominates the contribution. This if of course not at all necessarily since supra currents are possible and outside the organism the flux sheets can fuse together. This implies however correlations between genomes of different cells and even different organisms.

These observations inspire the notion of super- and hyper genes. As a matter fact, entire hierarchy of genomes is predicted. Super genes consist of genes in different cell nuclei arranged to threads along magnetic flux sheets like text lines on the page of book whereas hyper genes traverse through genomes of different organisms. Super and hyper genes provide an enormous representative capacity and together with the dark matter hierarchy allows to resolve the paradox created by the observation that human genome does not differ appreciably in size from that of wheat.

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` [L16].

3.2 Background

The foundations of genetics were discovered by George Mendel in 1866, but remained generally unknown until 1900. During the first half of nineteenth century it was gradually realized that genes play major roles in the functioning and evolution of organisms. The discovery of DNA revealed the principles of heredity and how genes store hereditary information and transmit it from generation to next. Hereditary information is contained within the nucleotide sequence of DNA.

Organization, expression, and evolution of the hereditary information are the main aspects of genetics. Hereditary information is organized into chromosomes consisting of DNA sequences. It is expressed via transcription to mRNA followed by a translation to protein. The evolution of the hereditary information involves basically sexual breeding in one chromosome from the chromosome pairs of both parents combine to form chromosome pair. Also recombination of the members of the chromosome pairs is possible during meiosis. Also other mechanisms, such as fusion or fission of chromosomes and modification of DNA sequences, are possible. There are excellent books about topics [I14] but for the convenience of the reader the basics of genetics are very briefly summarized in the following.

3.2.1 DNA And RNA

DNA add RNA provide a way to store and organize genetic information [I14].

1. Genetic information is stored in nucleic acids, which are long sequences of nucleotide serving as letters of genetic code: three nucleosides form single world of code. There are four different nucleotides so that the number of different words is 64.

2. Nucleotide consists of three basic units joined by covalent bonds: nucleotide= nucleoside+sugar+$5'$-phosphate. The units are sugar, which is deoxiribose in case of DNA and ribose in case of RNA, phosphate and nucleoside (nucleic acid). Nucleosides are the information carrying part of DNA and RNA.

3. DNA and RNA sequences contain 4 different nucleosides. In case of DNA they correspond to C(ytocine), T(ymine), A(denine) and T(ymine). In case of RNA T is replaced by U(racil). U, T and C are purines containing one carbon ring and A and G are pyrimidines containing two carbon rings.

4. DNA molecules/nucleic acids/polynucleotides are formed as very long sequences of nucleotides bound together by phospho-diester bonds.

DNA double helix consists of two DNA strands, which are conjugates of each other, conjugation being defined as $A \leftrightarrow T$, $C \leftrightarrow G$. The helices are bound by hydrogen bonds between A and T and C and G respectively.

Sequences of DNA triplets form genes, which represent basic units of hereditary information revealed as traits of the organism. Each gene involves also additional DNA sequences serving as control structures in the transcription of gene to mRNA. In prokaryotes there is only single chromosome in the form of a circular double strand. In eukaryotes the chromosomes are located in nucleus and appear in homologous pairs. Eukaryotic chromosome is a complicated helical structure resembling beads in thread formed by DNA. DNA is wound around nucleosomes with diameter $d \simeq 10$ nanometers. Nucleosomes consist of octamer formed from 4 different histones. Chromosome structure will be considered in more detail later.

RNA appears both inside nucleus and cell. There are several types of RNA.

1. Messenger RNA (mRNA) is the outcome of transcription of DNA inside nucleus and is translated to proteins outside the nucleus.

2. Transfer RNA (tRNA) is involved in the translation of mRNA to protein: tRNA molecules bind specific amino-acids and glue them to specific mRNA triplets in a way dictated by genetic code. rRNA appears as a building block protein of ribosomes playing the role of reading head in the translation of mRNA to proteins.

3. In case of eukaryotes transcription involves intermediate state in which DNA is transcribed to hnRNA which contains also the transcriptions of introns ("junk DNA"), which are split in so called splicing process cutting away intron RNA to form RNA-protein complexes which remain inside nucleus.

3.2.2 Proteins

Proteins are in a vital role in organisms. The diversity and complexity of life is largely due to the diversity and complexity of proteins. Some proteins act as transcription factors controlling genetic expression. Some proteins are used by cells in chemical communication between cells: hormones serve as signalling proteins; various receptor proteins serve as receptors of chemical signals and hormone-receptor complexes serve as transcription factors. Neural transmitters appear in the synaptic communication between neurons. Some proteins act as enzymes catalyzing biochemical reactions. Other proteins serve as structural building blocks, either by themselves or in association with nucleic acids (nucleoproteins), polysaccharides (glycoproteins) or lipids (lipoproteins). Some proteins, such as myoglobins and hemoglobins are associated with metal-containing organic molecules.

Proteins consists of polypeptides, which are polymers of 20 different amino-acids. Genetic code assigns unique polypeptide to a given gene. With single exception amino-acids share the same basic structure. Hydrogen atom H, carboxyl group COOH and amino group NH_2 and radical R linked to carbon atom. R determines exclusively the chemical properties of protein. 8 amino-acids are nonpolar (hydrophobic) and 12 of them are polar (hydrophilic). Of the twelve polar amino-acids 7 are neutral, 3 are basic (tending to become positively charged) and 2 and acidic (tending to become negatively charged) under physiological conditions. Carboxyl and amino groups tend to become ionized at physiological pH; -COOH group tends to lose its proton and NH_2 group tends to gain a proton.

In polypeptides, which are products of gene translation, amino-acids are linked to each other by peptide bonds formed when NH_2 group of one amino-acid and $COOH$ group of next amino-acid are linked (H_2O molecule is snipped away in this process). Polypeptide chains spontaneously adopt so called secondary structure determined by the nature of the R groups along the backbone. Backbone forms alpha helix, a coil containg 3.6 amino-acid redidues per turn. Another secondary structure is the beta pleated sheet configuration consisting of rows of polypeptide chains hydrogen bonded with each other. Polypeptide can also adopt the form of a random coil. Proline, because of its unique structure, causes a kink in the polypeptide backbone. Polypeptides have also tertiary structure. How the tertiary structure is determined by the chemistry of amino-acids is poorly understood. One of the big problems of biology is to understand who protein is able to fold to such a unique configuration. TGD suggests that tertiary structure might not be determined solely by the standard chemistry and that many-sheeted nature of protein might be crucial in determining the final result of the folding. There is also quaternary structure associated with proteins formed by polypeptide sequences. The formation of higher level structures, such as micro-tubules, micro-filaments, cell membranes and collagen fibers involves self-organization and living matter seems to behave as a liquid crystal whose basic properties depend only on very general properties of protein.

3.2.3 Replication, Transcription, Translation

Information processing in living matter involves three basic processes: replication, transcription and translation. Replication of DNA means replication of DNA double helices and is essentially copying of genetic information. Replication involves unwinding of the parental strands of DNA double helix. They serve as templates on which the growing complementary daughter strands are synthesized. The direction of the synthesis is opposite for the two strands and only the second (leading) strand can be synthetized continuosly whereas the synthesis of the second strand occurs discontinuously and results in disjoint pieces of DNA containing approximately 1000 nucleotide pairs (Okazaki fragments of length about 34 nanometers), which later combine to form connected DNA strand.

DNA can be transcribed to mRNA molecules (messenger RNA) translated to proteins; to tRNA (transfer RNA), which is the RNA molecule affecting the coding of RNA triplets to amino-acids and to rRNA, which is the building block of the machinery affecting the translation. In case of prokaryotes the transcription of DNA to mRNA occurs directly. The rules for the transcription are

$$\begin{aligned} A \to U \ , \quad T \to A \ , \\ C \to G \ , \quad G \to C \ . \end{aligned}$$

In case of eukaryotes the transcription involves two steps since eukaryote genes in general decompose into exons translated to protein plus introns.

First the entire gene is transcribed to hnRNA sequence. After this so called splicing occurs and gives rise to mRNA, which corresponds to the DNA sequence formed by the exons. In the splicing process intron sequences are split off and wind around specific proteins which do not leave the nucleus. There are different pathways for slicing meaning that the decomposition to exons and introns is not unique. Dynamical exon-intron decomposition is essential for the working of immune system.

Transcription is a complicated process involving the action of several enzymes. RNA polymerase I is involved in the transciption of large rRNA molecules, RNA polymerase II with the transcription of hnRNA, RNA polymerase III with transcription of small 5S-rRNA molecules and tRNA molecules. Usually so called heavy strand is transcribed. Light strand can be transcribed

to some tRNA molecules at least. Gene is preceded by AUG triplet. In eukaryote cells RNA polymerase II copies sequences containing 6000-8000, sometimes even 20.000 nucleotides. The average length of mRNA sequence is 1500 nucleotides and the amino-acid corresponds to a sequence of average length of 1200 nucleotides.

RNA II polymerase binds to the promotor region preceding the gene. Promotor region contains at least two binding sites, so called TATA block and CCAT sequence regognized by RNA polymerase. Between promotor site and gene are operator site in which repressor enzymes bind and make translation impossible. TAC sequence denotes the beginning of that part of gene which is translated to protein (apart from introns). At the end of the gene there is rather long $A \cdots AAA$ control sequence preceided by TGA sequence signifying the end of the part of the gene to be translated. Introns which are not translated begin with AC and end with CA.

The translation of mRNA to polypeptide occurs outside the nucleus. Translation involves tRNA molecules, which are about 80 nucleotides long. Each tRNA contains a specific triplet which is anticodeword for the corresponding codeword in mRNA and binds only to this codeword in translation process. Each tRNA molecule binds with a specific amino-acid molecule and each amino-acid has at least one tRNA binding to it. The allowed bindings of tRNA and amino-acid molecules define genetic code. In translation tRNA carrying amino-acid attaches to an mRNA codeword to its own anticodeword and the amino-acid forms a peptide bond with the polypeptide sequence already translated at rRNA.

Genetic code assigns to 64 RNA triplets 20 amino-acids so that there is a considerable degeneracy involved. The largest number of DNA codewords mapped to same amino-acid is six. Three codewords are interpreted as stoppping sign for the translation. Genetic code is universal for the nuclear DNA of all eukaryotes and prokaryotes. The mitochondrial genetic codes of various eukaryotes however differ slightly from the universal genetic code. For instance, 4 DNA triplets can correspond to stopping sign.

Replication, transcription and translation are not the only information transfer processes occurring in living matter.

1. Reverse transcription $RNA \rightarrow DNA$ is known to occur in some cases and is also involved with the homing phenomenon of introns. Reverse transcription might have led from a system of RNA and proteins to system involving DNA sequences and primitive form of genetic code. The simplest starting system of this kind would consist of DNA coding RNA coding a protein which catalyzes both transcription and reverse transcription. This kind of system might have gradually evolved to a more complex DNA sequences.

2. RNA replication can occur in cells infected by viruses. What happens is that viral RNA strand which can be either single or double stranded, is replicated to its complement which in turn serves as a template for the synthesis of progeny RNA molecules.

3. Direct translation of DNA to protein without transcription has been observed only in vitro. This process probably never occurs in living cells.

3.2.4 Introns, Pseudogenes, Repetitive DNA, Silent DNA

The genes in nuclei of the eukaryote cells contain introns, sequences consisting of 10-1000 nuclotides interspersed with the exon parts of DNA which is translated to a protein coded by gene [I6] . Molecular Darwinist could compare introns with the commercials appearing between TV program or simply as selfish DNA. One could see them also unused parts of a computer program separated from the program code by comment signs in front of each line corresponding now to DNA nucleotide. The latter metaphor is consistent with the observation that intron can begin even in the middle of DNA triplet and that the transcription to mRNA is not unique so that same gene can give rise to several proteins. The content of intron sequences seem to be unrelated to the exon sequences: as if two separate interspersed computer codes would be in question.

Only one prokaryote cell, photosynthetic cyanobacterium Fischerella, is known to contain introns [I6]. Usually also the genes of cell organelles (such as mitochondria of human cell) contain only very few introns. Fungi are however an exception in this respect [I14]. The higher the evolutionary level of the eukaryote cell, the higher the fraction of introns in the genome is. For humane genome the fraction of exons is about one per cent. During transcription both introns and

exons are transcribed to hnRNA, intron sections are snipped away in a process called splicing and the resulting mRNA for the protein coded by exons is transferred from the nucleus and translated to a protein coded by the gene. It is possible to snip off the introns from genome but the mRNA coded by these genes is not transferred from nucleus, which suggests that introns have some role in genetic program. The addition of introns does not seem to have any dramatic effects on the genetic program.

Introns are a headache of molecular Darwinism. The nickname "junk DNA" tells the basic attitude towards introns. Introns represent selfish DNA living as parasites of the genome. There are two opposite schools concerning how introns have appeared.

1. The first school claims that introns came early. Somewhat surprisinly, this school sees bacteria as results of a long evolution which has gradually snipped off the introns from a primitive cell in order to achieve maximal rate of DNA transcription. One can of course wonder why the same thing has not happened to the cell nuclei also.

2. Second school tells that introns came late: this view conforms with the observations about the fraction of introns in genome. Introns seem to start from preferred sites and exons seem often to correspond to a modular decomposition of the protein they code. On basis of this it has been also proposed that introns separate modular parts of proteins from each other. The facts that introns can appear in the middle of protein module and even split single DNA triplet are not however consistent with this interpretation.

One can criticize the identification of introns as junk DNA.

1. It is difficult to see how human genome containing so high per cent of junk DNA could work with such a fantastic precision while viruses, second form of junk DNA, are often lethal. There are several pathways for slicing. Exon-intron transformation has been found to occur: exon and intron parts of gene simply change their roles [I6, I29] ! This suggest that exon-intron property is additional dynamical degree of freedom in genone and might have deep meaning. Exon↔exon transformation is indeed crucial for the working of immune system.

2. mRNA produced by intronless gene does not get out of nucleus. It seems that the presence of introns somehow initiates a module of genetic program taking care that protein mRNA gets out of the nucleus. Introns seem thus to be necessary for the functioning of the cell and could be in some sense regarded as an output of gene interpreted as a genetic subprogram. Note however that intron mRNA which winds around spherical proteins in the process of splicing, have not been reported to serve as transcription factors.

3. The positions of the intron sequences in similar genes are not same for various species. There are wandering introns which can move even from cell to another one. There is a phenomenon called homing [I6, I30]: the RNA coded by intron inserts itself into DNA sequence and builds by inverse transcription its complement in complementary DNA strand. In retrohoming intron transforms to RNA installed to DNA sequence by reverse splicing [I17] . This suggests that introns might provide a new mechanism for the evolution of the genome and provide a mechanism for modifying the program code of genetic programs. It is also known that there are long range correlations (in scale of one micro-meter) in genes containing introns [I36]. This suggests that introns are essential element in the organization of DNA to larger structures.

All these properties of introns suggest that their role in genetic program is badly misunderstood in the framework provided by molecular Darwinism and the basic dogmas of genetics.

Besides introns there are pseudogenes of various types, which by definition code no proteins. For instance, eukaryote genes from which introns have been snipped off, behave as pseudogenes. Pseudogenes can also contain "programming errors": for instance, the DNA triplet signifying the beginning of gene has changed. Genetic program metaphor suggests interpretation of pseudogenes as unused program modules. The idea about two interspersed program codes could explain the program errors as only apparent program errors. Of course, every experienced computer programmer would suggests the possibility of also genuine program errors! Also the interpretation as control structure affecting transcription via long range interactions rather than via chemical

contact interactions might make sense. It is indeed known that so called enhancers and silencers act as transcription factors in this manner.

Genetic code contains large amounts of repetitive DNA.

1. Five per cent of genome of the eukaryotes consists of highly repetitive DNA consisting of 5-300 nucleotides (even 10^6 copies are possible). In particular satellite DNA, containing less than 10 nucleotides belongs to this class. This DNA are active during mitosis and meiosis [I14].

2. 30 per cent of DNA is moderately repetitive. The first class corresponds to rRNA, 5SRNA, tRNA and histogenes (10-100 copies). These genes are concentrated in certain chromosomes. In case of genes coding rRNA, tRNA the repetition of genes is understandable since translation making possible large number of amino-acid copies does not occur. The fact is however that also genes coding proteins appear as very many copies and there is no obvious explanation for this. So called SINE segments have length not longer than 10^3 np and are interspersed through the entire genome as $10^4 - 10^5$ copies. LINE-segements consist about 3×10^3 np: there are about 10^4 copies are interspersed through the entire genome. Part of these sequences are transposons (see below).

3. 65 per cent of DNA are present in only few (1-15) copies. Both exons and introns belong to this group of DNA and exons form only one percent of human genome.

4. The control regions between genes are rather long and seem to contain DNA with no obvious function. Also second strand of DNA can be regarded as silent DNA since its presence is not absolutely necessary for the storage of genetic information. The question is whether this silent DNA has some hitherto unidentified function.

The genome of both prokaryotes and eukaryotes contains transposons, which are movable DNA sequences able to insert themselves to DNA with the help of insertion sequences. Insertion sequences are short (less than 2000 nucleotides) and do not code proteins. Insertion sequences can carry also promotor and repressor sequences with them. Transposons could be important for evolution.

3.2.5 Is Central Dogma An Absolute Truth?

The Central Dogma of molecular biology states that each gene corresponds to a unique polypeptid. There are several observations challenging Central Dogma.

1. It is known that many alternate pathways of transcript splicing are possible and give rise to different protein outcomes called isoforms. This would suggest that transformation of some introns to exons and vice versa occurs routinely in gene expression. Using computer program analogy, this transformation would mean that the program part represented by introns becomes active and the part represented by exons becomes passive.

2. The phenomenon of superimposed genes [I14]. There are genes nested inside genes and translation can start also in the middle of gene producing shorter protein than the gene usually. These phenomena were first observed for bacteriophage $\phi X174$, whose genome is known in its entirety. It is known that gene is transcribed as a whole and that different proteins result from frame shift. Gene can also overlap the DNA sequences formed by two subsequent genes as first observed in bacteriophage $G4$. These observations suggest that the standard notion of gene fails somehow.

3. It is known that also the "nonsense" strand of DNA can serve as template for transcription [I14].

3.2.6 Is Life Nothing But Biochemistry?

It is not at all obvious whether the hypothesis "life is nothing but biochemistry" holds true.

Organism	Human	Mus musculus	Amoeba	Marbled lungfish
$N(DNA)/10^9$	3	3	670	139
Organism	Salamander	Onion	Trumpet lily	
$N(DNA)/10^9$	81	18	90	

Table 3.1: The amount of total genome measured as the number of DNA triplets.

1. It is not known whether protein folding is coded into the chemistry of DNA. The problem is mathematically unattractable due to the occurrence of combinatorial explosion. It seems more probable that folding might be self-organization type phenomenon and thus affected by the conditions of environment: protein development can be regarded as hopping in spin glass type energy landscape leading to some deep valley of free energy valley. TGD suggest that folding is the quantum analog of this kind of process. In particular, p-adic length scale hierarchy and many-sheeted space-time concept (see **Fig.** `http://tgdtheory.fi/appfigures/manysheeted.jpg` or **Fig.** 9 in the appendix of this book) suggest that one cannot understand protein folding in terms of DNA chemistry alone.

2. DNA is essentially one-dimensional structure. This suggests that gene codes only one-dimensional skeleton of its expression domain and that self-organization by quantum jumps could take care of the rest. Indeed, the work of Mae-Wan Ho [I40] shows that living organisms are liquid crystals which can be regarded as one-dimensional crystals and two-dimensional liquids, whose properties can be characterized by some global parameters. Perhaps genes code the properties of various layers of the liquid crystal. One of the basic characteristics of liquid crystals is self-assembly and de-assembly. Depending on pH, ionic concentrations, temperature, electric fields, ... liquid crystals organize to micelle like structures (cell membranes, collagen fibers, ...) and effectively one-dimensional layered structures [D1].

3. One can wonder how morphology is coded in DNA and how it is decoded from DNA. It is not at all obvious that DNA chemistry, which is purely local, is enough to code morphology.

4. So called enhancers and silencers are transcription factors, which encourage or disencourage gene expression in eukaryotes. The position of these proteins or orientation in DNA does not seem to be important [I14]. For instance, they can bind to introns and the distance of the binding site from gene promotor regions can be thousands of nucleotide pairs. This would suggest that the mechanisms of enhancing and silencing are not purely chemical if chemical at all. This would suggest the generalization of the notions of gene expression and transcription factor. Chemical expression takes place very slowly. Non-chemical expression modes yielding non-chemical transcription factors could make possible very fast running of genetic programs and there could be even connection between many-sheeted genome and nerve pulse activity.

5. The naïve expectation is that the size of the genome should correlate with the evolutionary stage of the species. Eukaryotes indeed have genome which is typically 10^3 times longer than prokaroyote genome. The **Table 3.1** however shows that the total length of genome does not correlate with the complexity of the organism faithfully. The genome of plants is typically 10-100 times longer than human genome. The genome of amoeba is by two orders of magnitude longer than that of human! The genomes of monkeys and men are almost identical. This suggests that there might be some unindentified degree of freedom associated with DNA which explains these differences.

3.3 Many-Sheeted DNA

The notion of many-sheeted DNA suggest a profoundly new manner to understand how the morphology of the organism is coded to and decoded from DNA. p-Adic length scale hypothesis leads

to precise quantitative predictions for the number of levels of genetic program as function of a suitably defined size of the organ. The proposed model for introns leads to the interpretation of gene as a representation for Boolean algebra and to the proposal that genes realize not necessarily conscious-to-us Boolean mind at the basic level. What is especially nice is that connection with the realization of Boolean mind in terms of cognitive neutrino pairs is consistent with this picture. Many -sheeted DNA suggests also new forms of gene expression and of control of gene expression. For instance, nerve pulse patterns could affect also genetic program of postsynaptic cell via the classical em and Z^0 field patterns associated with them and genes could affect cell membrane via conformational waves propagating along micro-tubules connecting nucleus to cell membrane.

3.3.1 Many-Sheeted DNA As Hierarchy Of Genetic Programs

Many-sheeted DNA allows to realize genetic subprogram hierarchy in an elegant manner. Many-sheeted DNA and proteins are like a hierarchy of ordinary DNA and proteins effectively living in different space-times corresponding to body parts. One can consider the possibility that subprograms correspond to p-adic space-time sheets and subprogram hierarchy corresponds to the hierarchy of p-adic space-time sheets. The gene program in a given length scale would selectively activate programs in shorter length scale, etc.. DNA sequences with the same chemical structure correspond to different genetic programs since the many-sheeted structure of DNA affects its functioning. Analogous conclusion is true about proteins.

One can assign to gene a unique p-adic prime as the prime characterizing the largest p-adic sheet at which gene has # contacts. The number of levels in subprogram hierarchy could be deduced from the size of the organism. Gene can have # contacts to several space-time sheets characterized by p-adic primes $p \simeq 2^k$, k power of prime. Denote by k_G the largest value of k associated with gene. k_G characterizes the position of gene in subprogram hierarchy. Gene can have # contacts with space-time sheets $k < k_G$ also. Gene can be characterized by the p-adic k_G labelling the largest space-time sheet to which it has # contacts. "Comment sign" marking each nucleotide of intron could correspond to a direction of classical field at some space-time sheet characterized by p-adic prime $p \simeq 2^k$, $k = k_I$. The only sensible assumption seems to be $k_I = k_G$.

The other # contacts of gene must be assumed to be on space-time sheets with $k < k_G = k_I$. This implies that given program can call only programs which are in the lower level of the hierarchy. This would suggest that programs belonging at the lower level of hierarchy cannot call program at higher level. Does this imply that growth process in which larger and larger space-time sheets are activated can only occur by self-organization? This would mean that DNA space-time sheets with increasing value of k_G expand in phase transition like manner and fuse to form space-time sheets corresponding to various body parts. On the other hand, it is not at all obvious that growth process could not start from higher level and lead to gradual differentiation at lower levels. In fact, embryogenesis seems to occur in this manner [I14].

Also proteins can be classified by the number k_P characterizing the largest space-time sheet to which protein has # contacts. Proteins must mediate program calls to gene modules G_1 with various values of $k_{G_1} < k_G$. This suggests that protein activating gene characterized by k_{G_1} must have same $k_P = k_{G_1}$. This would automatically guarantee that chemically identical proteins activate only the genes belonging to the level of the fractal hierarchy they represent.

The notion of many-sheeted DNA has immediate applications.

1. Many-sheeted DNA provides a possible explanation for why DNA triplets act as codewords of the genetic code. If members of each DNA triplet are glued to space-time sheet containing only # contacts from the nucleotides of the triplet, codewords have a clear geometrical meaning.

2. The notions of many-sheeted DNA and many-sheeted protein suggests also an explanation for how enhancers and silencers are able to regulate gene expression. Interaction with classical em or Z^0 fields via wormhole contacts provides a non-chemical interaction mechanism. Second mechanism is based on Josephson currents running along join along boundaries contacts. Since interaction with much larger length scale is involved, these interaction mechanisms are not too sensitive to the position of the transcription factor and the distance of the binding site from gene promotor regions can be thousands of nucleotide pairs. This mechanism explains

also the observe issue specificity of some transcription factors. Proteins with same chemical structure can be quite different transcription factors if they have contacts to different space-time sheets.

3.3.2 Possible Answers To The Basic Questions

Many-sheeted DNA suggests stupifyingly simple coding of body's morphology. The genes would be obtained by simply contracting the many-sheeted space-time representing expression domains of genes to one-dimensional structure. Decoding of the morphology means the growth of this structures to their original size. Of course. this hypothesis is oversimplified but its extreme simplicity makes it worth of testing.

How the structure of expression domain of the gene is coded in the structure of gene?

The p-adic length scale of the gene correlates trivially with the p-adic length scale of the protein coded by it. Already protein folding implies that the correlation with the size of the structure coded by DNA is not so straightforward. Furthermore, proteins are not mere building blocks but can have quite abstract functions like regulating gene expression of genes.

Consider now various aspects of the idea that expression the domain of gene is coded into the structure of gene and this that correspondence could be also realized at functional level.

1. The first thing that comes into mind is that the p-adic length scale of the gene correlates with the p-adic prime of the space-time sheet which corresponds to the expression domain of the gene during early phases of the embryogenesis. Gene clusters, say Hox cluster, would represent kind of a miniature of the body and every gene of Hox cluster would give rise to a space-time sheet which would be a scaled down model of the expression domain of the gene. Thus the expression domains of various genes in the genome could correspond to the extended space-time sheets at the level of the genome and the topology of these genome level expression domains, in particular, their ordering, would be consistent with that for the actual expression domains. Expression domain corresponds most naturally to a join along boundaries condensate generated by the formation of the join along boundaries bonds between the extended space-time sheets associated with the genes. This means that the p-adic prime of the expression domain can be much smaller than one could conclude it to be on basis of its size.

2. One could test the hypothesis that the total length of the region occupied by gene and by the DNA controlling its activity in the genome could correlate with the size of its expression domain at the stage of the development when the gene is expressed. Note that many genes affecting morphogenesis are expressed in a very early stage: many of them in the embryonic stage when no cell formation has yet occurred. This stage corresponds to the p-adic length scale of a fertilized cell about 10^{-4} meters. Of course, the correlation between the content of the gene program and the size of its expression domain, is not necessary and might be even un-desirable.

3. Fractality suggests that the communication by expression factor proteins at the level of genome might mimic the hormonal communication occurring at the level of the entire organism. This could mean that the hormonal communication between the expression domains of two genes is equivalent with the presence of a transcription factor communication between corresponding genes at the level of nucleus. Hormonal communication between cells involves the formation of hormone-receptor complex acting as a transcription factor.

The length of human genes ranges to thousands of nucleotides. This would mean that the longest p-adic length scales of human gene would correspond to $L(173) \sim 16$ micro-meters. The total length of a human chromosome is about 75×10^6 DNA triplets. The corresponding p-adic length scale is $L(193) \sim 2$ cm. The next length scales correspond to the pair $(197, 199)$ and correspond roughly to the size of brain hemisphere and brain. The total length of DNA in chromosomes is $48 \times L(193) \sim 1$ meter, the size scale of human body.

Many-sheeted space-time concept suggests that genes actually correspond to DNA sequences glued to a larger space-time sheet defining the gene. Hox clusters could be one example of this.

The geometry of the organism might be coded to these secondary, tertiary, etc. space-time sheet structures of the DNA sequence guaranteeing the coding the topology of the body plan to the topology of the multi-sheeted DNA. These structures are be labelled by p-adic primes and their number would be quite limited.

The linearity of DNA suggests that also the plan of the expression domain should be essentially linear such that each cross section of each module of the expression domain is essentially homogenous phase and its structure is determined by a self organization process constrained by the p-adic length scale hypothesis rather than purely genetically. According to Mae-Wan [I40, I41] living systems are liquid crystals and the basic characteristic of the liquid crystals is that they have crystal like structure in one dimension and are liquids in transversal dimensions [D1] forming. thus layer-like structures. This suggests that p-adic self-organization determines the size of the transversal layer and that DNA only codes some general properties of the liquid phase for a given layer.

The sizes for the expression domains of the genes should form a hierarchy. Effective expression domain can be much larger than the p-adic length scale characterizing it since join along boundaries/flux tube condensates are possible. For instance, the modularization of the genetic programs of plants is perhaps stopped at the level $k = 167$ so that expression domains for plant cells could be regarded as join along boundaries concept of of $k = 167$ plant cells. At the level of organism this perhaps corresponds to the emergence of cell walls hindering the formation of higher level structures formed from cells: plant could perhaps be regarded as a large join along boundaries/flux tube condensate of $k = 167$ plant cells surrounded by a wall. Besides the length of the genome, the number of the p-adic hierarchy levels in the space-time sheet hierarchy of DNA is a natural candidate for a measure of the complexity of the organism.

How the information about morphology is expressed?

One of the fundamental questions of the developmental biology is how the information of genes stored into DNA is translated to the geometry and topology of the organism. The idea of many-sheeted DNA suggests an immediate answer to this question. Expression is "nothing but" the reversal of the coding. The expression domain of the gene contracted effectively to one-dimensional DNA-thread grows back to the expression domain with non-uniqueness and flexibility brought in by self-organization depending on external parameters. This means that various space-time sheets associated with DNA grow during grow to space-time sheets representing actual organs. This process involves the formation of flux tubes between growing space-time sheets associated with various DNA molecules so that coherent macroscopic quantum phases become possible.

One can ask how the growth plan is coded into DNA. Or how much of it is coded into the chemistry of DNA? The idea that DNA is essentially body contracted to a thin thread suggests that the chemical control of DNA is restricted to the local properties of tissues. The space-time sheets of replicating DNA at various body parts simply grow and fuse to form join along boundaries/flux tube condensates growing and giving rise to various organs. The replication of DNA would in turn be quantum self-organization process involving essentially self-hierarchy starting from atomic level and ending up the level of entire organism.

What makes cell differentiation possible?

Cell differentiation is one of the great mysteries of biology. It is known that only part of DNA is active in a cell located in a given part of body and that selective activation of the genome gives rise to differentiation. The problem is to understand the mechanism of activation. Especially difficult challenge for the view about life as mere chemistry is the interaction between large length scales with gene level making possible precise timing of genetic activity.

In TGD framework cell differentiation should correspond to a selection of branch in the flow diagram describing genetic program. This occurs during the growth since the concentrations of the proteins representing the inputs of the gene programs evolve during the growth and generate also spatial gradients. Therefore different branches of the genetic program are activated in different parts of the developing organism. Also the genes associated with space-time sheet of increasing size are activated during growth and this brings in new and higher control levels.

Very probably the mechanism involves interaction between microscopic degrees of freedom for DNA and between macroscopic degrees of freedom representing body part where DNA resides. The control and coordination based on Josephson currents between gene space-time sheets and larger space-time sheets is very probably involved as is suggested by the general time scales of genetic activity. Also the interaction with the classical fields of the space-time sheet of the body part to which DNA has wormhole contacts provides an obvious mechanism of activation. The frequencies of the coherent oscillations of em fields involved could be important in both interaction mechanisms. This kind of interactions with larger space-time sheets makes possible to understand induction phenomenon, which corresponds signalling between cells and entire cells groups. This kind of signalling could be crucially important for morphogenesis. Many-sheeted space-time thus provides explanation for the ability of cells to form organs. The notion of cell cohesion is introduced to explain this: the cohesion would correspond to the formation of join along boundaries/flux tube condensate of extended gene space-time sheets.

3.3.3 What Is The Number Of The Levels In Program Hierarchy?

The obvious idea is that the size of the organism determines the largest p-adic prime contributing to the program hierarchy. It is however not obvious whether to define the size of organism as the "physical", visible size or as electromagnetic size, which is well defined notion in TGD framework.

Does the visible size of the organism determine the number of hierarchy levels?

The simplest working hypothesis is that the number of the levels in the program hierarchy is the number of p-adic length scales between atomic length scale and body size. The larger the visible size of the organism, the larger the number of the levels in the genetic program hierarchy, if this hypothesis is correct. This number is testable characteristic of species and could be valuable guide in attempts to understand how genetic code functions. One can identify the hierarchical level of the gene by looking how many genes it activates before building block protein is coded. It must be however emphasized that visible size need not be a correct criterion: the point is that join along boundaries condensates are possible and give rise to a much larger body size than one might conclude from the value of largest p-adic prime involved.

It is instructive to look the numbers of hierarchy levels in some specific examples assuming that the visible size of the organism determines the number of hierarchy levels. It is assumed that $k = 139$ is the first level which counts as a hierarchy level.

1. Viruses could have 4 hierarchy levels if $k = 139, 149, 151, 157$. Proteins, lipid layers of cell membrane and cell membrane and genes coding building block proteins. It could be that only k=149 is present for the simplest viruses since the formation of the envelope is self-organization process.

2. Bacteria should have 5 levels. $k = 139, 149, 151, 157, 163$.

3. Home fly should have 12 levels since its size is below $L(197) \simeq 1.6$ cm.

4. Animals with size between $L(199) \simeq 16$ cm and $L(211) \simeq 10$ m have 15 hierarchy levels. Note the large gap between $L(199)$ and $L(211) = 64L(199)$.

5. The next level corresponds to the level of dinosauri and whales having sixteen levels unless they correspond to join along boundaries condensates formed from smaller structures which is quite possible. The next level is $L(223)$ and corresponds to size of 640 m!

Does the electromagnetic size of of organism determine the number of hierarchy levels?

There is a large gap between $L(199)$ and $L(211)$ and the next twin length scale corresponds to a length scale of one kilometer. This suggests that new levels of hierarchy possibly emerged after $L(199)$ cannot correspond to the physical growth of body. Mere large size does not guarantee intelligence. Furthermore, if the visible size of the organism determines the number of the hierarchy levels, then dinosauri would have been in a well defined sense more intelligent animals than we! These arguments suggest that the visible size of the organism need not determine the number of genetic program levels.

k	227	229	233	239	241
L_p/m	$2.5E+3$	$5E+3$	$2E+4$	$1.6E+5$	$3.2E+5$
k	251	257	263	269	271
L_p/m	$E+7$	$8E+7$	$6.4E+8$	$5E+9$	$E+10$

Table 3.2: Table of p-adic length scales above $L(211) \simeq 10$ meters. $L(151) = 10^{-8}$ meters is assumed.

1. It could be that DNA codes and even controls also the electromagnetic structure of the organism realized as topologically quantized electromagnetic field, "aura", characterizing the organism.

2. An alternative option inspired by the notion of memetic code, which is next level in the hierarchy of genetic codes predicted by the TGD inspired simple model of abstraction process, is that there are higher hierarchy levels present but they are not controlled by the genetic program but call it as a subprogram.

A natural working hypothesis is that EEG correlates with the electromagnetic size of the organism. EEG has emerged rather lately in the evolution and is possessed only by vertebrates. In case of humans it becomes fully developed only at the age of 18. Meditation in general tends to increase the amplitudes of low frequency waves with 8 Hz (alpha wave s) and also waves with lower frequencies (theta waves). This suggests that growth in electromagnetic degrees of freedom can continue all the lifetime and could be identified as what is called "spiritual growth". It could continue also after the physical death so that the protein based state of life would be only a part of much longer lasting process of self-organization analogous to the development of butterfly. Indeed, in TGD based picture about geometric time the death of the physical body does not mean the end of life.

Schumann resonances are resonances of em fields in the wave cavity defined by the 80 km thick layer between Earth's surface and ionosphere. The frequency range in question correspond to the frequency range of EEG. A hypothesis worth of considering is that human body generates via Schumann resonances topological field quanta, which define electromagnetic sub-selves having the size of Earth. One could even consider the possibility that the highest value of k_G depends on individual and people having tendency to have religious and mystical experiences have exceptionally large value of k_G.

The length scale corresponding to alpha waves is 3.8×10^7 meters and corresponds is roughly 3.75 times the length scale $L(251)$. If levels up to $L(257)$ are present in the human genome then the number of hierarchy levels is 22, not too large number. $L(251) \sim 10^7$ m corresponds to a frequency of 37.5 Hz and is quite near to the 40 Hz frequency claimed by Koch and Crick to be crucial for the visual consciousness! The frequency associated with $k = 257$ corresponds to the frequency of 5 Hz, which also belongs to EEG.

The electromagnetic size of the organ increases rapidly with the number of levels present in the hierarchy as **Table 3.2** demonstrates.

There are even more explicit observations about the importance of ELF em fields for the functioning of living matter and these observations finally led to a breakthrough in TGD based model of conscious brain. The observations about the special effects of ELF em fields on brain at cyclotron frequencies of ions Na^+, Cl^-, K^+ and Ca^{++} in endogenous magnetic fields $B_{end} = 2B_E/5 = .2$ Gauss were made already at 1983 [J9]. These experiments suggest that these ions/their Cooper pairs form are confined in the magnetic field of Earth and form bound states with macroscopic size of order cell size and with extremely small binding energy corresponding to frequency of order 10 Hz. This is impossible in the standard physics framework but can be understood as resulting from the dropping of ions and electrons from the atomic space-time sheet to the space-time sheet of the cell where the density of the matter is very low.

In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero

point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant h_{eff} so that cyclotron energy would be liberated.

Also electron Cooper pairs of high T_c electronic super conductor as well as Cooper pairs of neutrino super conductor are important. Besides magnetic cyclotron frequencies Z^0 magnetic cyclotron frequencies and wormhole cyclotron frequencies make sense: Z^0 currents for ions indeed induce automatically also ionic currents.

One can argue that there is very cold, dry and silent at the cellular space-time sheets and this makes possible macroscopic quantum phases formed by Cooper pairs of ions Na^+, Cl^-, K^+ and electron as well as well as Ca^{++} ions. Later the argument was modified the large values of Planck constant [K26, K24] imply that cyclotron energy scale is above thermal energy at room temperature even if thermal equilibrium of dark space-time sheets with ordinary ones is allowed. Also other ions are possible but these ions are especially important for nerve pulse generation. These super conductors must be effectively one-dimensional (otherwise gap energy is extremely small) and the needed confinement in the transversal degrees of freedom is caused by the presence of B_{end} which could be in TGD framework interpreted as the dark companion of the Earth's magnetic field responsible for controlling biomatter possibly also associated with the personal magnetic body. One could regard these super conductors as associated with the flux quanta of B_{end} having radius 25 μm (the size of a large neuron) by flux quantization and serving as templates for the formation of biostructures.

When the Josephson frequency (potential difference) associated with the weakly coupled super conductors of this kind corresponds to a magnetic transition frequency, quantum jumps between states of either super conductor occur and change the charge distributions and hence potential differences associated with other Josephson junctions associated with either super conductor. Quantum jumps can lead to "wake-up" of either or both super-conductor sub-self giving rise to a mental image. Also emission of ELF photons with resonance frequency is involved. The topological field quanta associated with these photons have typically size of order Earth's circumference. The fact that multiples of the cyclotron frequencies correspond directly to the most important frequencies of EEG and also to some important Schumann frequencies suggests very strongly that the "ELF selves" associated with these topological field quanta represent also selves in our self hierarchy. This leads to a general model for quantum control and for how the space-time sheets representing the self-hierarchy are coupled by join along boundaries bonds serving as Josephson junctions, to a detailed model for the quantum correlates of the sensory qualia and to a model of Boolean mind. ELF selves are a crucial factor of all these models [K28, K30].

The work of Michael Persinger shows that ELF em fields and ELF modulated em fields, affect also gene expression [J13]. Thus it seems that ELF levels, rather than being controlled by gene level, actually control and coordinate gene level rather via the formation of flux tubes between gene space-time sheets and ELF space-time sheet. Whether gene level actually *codes* also ELF levels of the organism is an interesting question. The idea about genome as the entire many -sheeted organism contracted to a thin thread would support this view. On the other hand, the notion of the memetic code identified as the next level of abstraction hierarchy suggests that ELF level corresponds to something genuinely new not reducible to gene level. ELF level could be even seen as a different life form next to the biological life living in symbiosis with biological life. One must also remember that higher levels could couple with gene level only via join along boundaries bonds/flux tubes and that the development of organism could be seen as a "social" process in the sense that growing organism gradually builds flux tubes to the space-time sheets representing higher level selves.

Whether the number of the hierarchy levels in the genetic program hierarchy is larger than the visible size of organism, might be perhaps tested sooner or later by deciphering the number of hierarchy levels in the genetic program. To check the hypothesis about EEG, it is enough to study simplest verterbrates possessing EEG. The identification the levels of various genes in program hierarchy would mean a tremendous boost in the understanding of genetic code and dramatic change in world view.

3.3.4 Band Structure Of Chromosomes As An Evidence ForMany-Sheeted DNA?

In prokaryotes DNA is arranged in single chromosome forming closed circular double strand whereas in eukaryotes DNA genome is organized into chromosome pairs. Chromosome is believed to correspond to single DNA thread which has beads in thread structure. Beads are spherical nucleosomes of diameter 10^{-8} meters ($L(151)$!) consisting of histones of 4 different types forming histone octamer. DNA is wound very tightly around nucleosomes, there is about 70 nanometers (slightly less than $L(157)$ of DNA per nucleosome. chromosome forms a helical coil with diameter found to be 30 nm. In interphase chromosomes are coiled once more to a hollow tube of diameter 200 nm (slightly less than $L(167)$) a helix of thickness about 10^{-7} meters. The transition from interphase chromosome to metaphase chromatid is accompanied by a winding to a helical coil of diameter about 600 nm (slightly more than $L(169)$). A possible interpretation of these transformations is as generation of new space-time sheets.

Chromosome banding was discovered already in eighteenth century by Metzner. Chromosome banding characterizes both the chromosome and the method used to produced the banding structure and there are many methods for revealing the band structure. Increasing resolution implies the division of band structures to smaller structures in fractal like manner. The band structures can be divided into two classes.

1. The highly localized heterochromatic bands, nucleolar organizers and kinetochores appear in all organisms. The latter two structures seem to reflect the purely geometrical organization, "packing", of genome rather than the internal organization of genome. The main features of heterochromatic banding are its universality, diversity and variability. Heterochromatic banding is present in all eukaryotes and can differ widely for closely related species and be very similar to widely different species. Heterochromatin seems to correspond to highly repetitive short DNA sequences of 10 nucleotide pairs (10^6 copies) located near the centromere of the chromosome. This DNA is not transcribed to DNA. Pairs are often duplicated and duplication leads to various physiological defects. Soma cells of some organisms appear to have ability to get rid of of heterochromatin whereas it is present in germ cells. These facts suggest that the regions of chromosome near its center regulate gene expression and that highly repetitive DNA sequences represent sites for genes at which repressor proteins bind. Abnormally large duplication of repressor sites would lead to stronger repression is more effective and could lead to abnormal development.

2. The chromosomes of the eukaryotes contain also non-localized bands called euchromatic bands. Patterns of euchromatic bands resemble closely to the patterns of DNA replication and patterns correlate very strongly with species. Thus euchromatic bands correspond to active RNA. The moderately repetitive DNA which is transcribed corresponds corresponds to euchromatin. It is known that there are several types of euchromatic banding. Band patterns can be used as diagnostic tools to identify various chromosome fusions and splittings. Various bands are of enormous value in providing manner to locate genes in genome.

In TGD framework a natural interpretation of various types euchromatic banding provide evidence for the many-sheeted DNA. Thus euchromatic banding should reflect the modular structure of the genetic program as well as the interspersing of control regions and transcribed regions of genes corresponding to the basic structure "If A then B" of the gene.

3.4 About The Notion Of Genetic Program

This section is devoted to a general discussion of several key ideas which were not available when I formulated the first TGD inspired vision about genetic programs and morphogenesis. The recent view about TGD inspired theory of consciousness and quantum biology allows much deeper formulation for the notion of genetic program. In particular, the vision about DNA as topological quantum computer allows to identify a possible role for the intronic portions of DNA.

3.4.1 What The Notion Of Genetic Program Could Mean?

How to define the notion of genetic program? As TGD inspired view about consciousness and living systems has evolved several several alternative definitions have emerged.

1. The first attempt to answer the question was inspired by the observation that so called Combinatorial Hierarchy might define a hierarchy of codes containing at least genetic code and what I christened as memetic code. The definition is based on the interpretation of DNA sequences - at least genes - as Boolean statements, which define axioms of a formal system which are identically true. The system in question corresponds to Mersenne prime M_7 containing 127 statements about which 64 is identically true and define the axions in question. Memetic code would correspond o M_{126} with 2^{126} axioms and could be realized as sequences of 21 DNA codons.

   The first proposed realization of the memetic code was in terms of temporal sequences of what I called cognitive neutrino pairs. It looks too nonsensical in the framework of standard physics and also in TGD framework it looks questionable.

2. With the advent of zero energy ontology (ZEO) came the observation that one could code "laws of physics" by zero energy states for which positive and negative energy parts of the state correspond to initial and final states for time evolution which conserves total fermion number and other charges. This would give rise to pairs of statements which are consistent with each other identifiable as rules expressed as superpositions of instances which are consistent with the rule.

3. DNA as topological quantum computer vision [K3] led to a considerable progress in the understanding of what genetic programs might mean. The basic idea is that the braiding of flux tubes connecting DNA nucleotides/codons to lipids of nuclear/cell membrane define natural topological quantum computation programs. It is natural to assign them with the intronic portion of the genome. These programs would define the software of the living matter whereas genes would define the hardware. The approach suggests a mapping of the letters A, T, C, G of the genetic code to u and quarks and their antiquarks. The discovery of what I call dark DNA realized as states of dark protons led to alternative realization of the sequences of DNA codons.

4. A deeper understanding of the anatomy of quantum jump in zero energy ontology led to a further insights [K13, K6]. In this framework the state function reductions to the opposite boundaries of causal diamond (CD) produce zero energy states with opposite inherent arrows of embedding space geometric time. These two reductions occur alternately and have interpretation in terms of sensory perception followed by motor action. This process occurs in all length and time scales and is not a property of only biosystems. Memories are represented as negentropically entangled states assignable to CDs and by Negentropy Maximization Principle [K42] they are approximate invariants and defined what might be called self representations or representation for the world. The braiding of the magnetic flux tubes is space-time correlate for the negentropic entanglement.

   The important outcome is that time reversal of memory representation can be interpreted as a plan or prediction realized in terms of braidings of the flux tubes. The interpretation of genetic program would be naturally in terms of the time reversed memories determining how, say, the seed of plant evolves to a plant. Dark photons are key element in the reading process and they can decay to ordinary photons with same energy identifiable as bio-photons. Biophotons give hopes of proving experimentally the existence of the template of the full-grown organism defined by its magnetic body and there is evidence that this kind of template indeed exists.

In the following the earliest proposals for what genetic programs might be, are discussed. These proposals can quite well be consistent with more recent views but are more formal and lack direct connection with the recent view about TGD inspired theory of consciousness and of living matter.

3.4.2 Genes And Genetic Programs

A possible model for the genetic program is based on the interpretation of DNA sequences as statements of a formal system. 64 basic statements represented by DNA triplets correspond to axioms which are identically true. Gene G is interpreted as a theorem of type "If I_1&....&I_n true then O_1&O_2...&O_n true" or generalizations thereof obtained by adding several input statements and allowing also negations of the input statements. It could be that complementary DNA strand represents statements of type "If I_1&....&I_n true then O_1&O_2...&O_n not true". If given DNA sequence has been translated to give rise to some minimum concentration of protein coded by it, the truthness of this statement is emotionally experienced by the genetic computer. Otherwise the truth value of the statement is ill defined.

The information about truth value of I_k is represented by the catalytic action of the enzyme coded by I_k on those parts of gene which are not transcribed, in particular on the promotor sequence of the gene. They give rise to experiences about the truth values of the statements $I_1...I_n$. The conclusion "O_1&, .., &O_n is true" represents the output of the gene. These statements appear as the premises for the statements represented by some other genes. Thus the running of genetic program represents a sequence of becoming conscious about various kinds of truths of the formal systems represented by genome.

Genes as statements of conscious formal system

The assumptions for the model of genes as statements of a conscious formal system are following.

1. DNA sequences are assumed to represent axioms of some formal system. There are 64 basic triplets of DNA, which correspond to basic independent statements, axioms, from which higher level statements are built using many-sheeted DNA making possible the construction of statements about statements about....

2. Genes are assumed to represent statements of type "If I_1&...&I_m then O_1&...&O_n true." or "If I_1&...&I_m then O_1&...&O_n not true." depending on which strand of DNA double helix is transcribed.

3. The output of gene is either true or ill defined gene can only be conscious about truthness of a statement or be unconscious. The logic of our conscious experience (which need not have anything to do with the possible gene level mind) is consistent with this. We can have conscious experience about truth values of a very limited set of statements and have no experience about the infinitely of all possible logical statements. Note that the experience with standard logic would suggest that the value of the statement is either true or false. The experience with ordinary computers would in turn suggest that the value of outputs could be true, false or ill defined.

4. Gene expression is the counterpart for the emotional experience about truthness of the statement represented by the gene. One can say that the output of the gene is true or ill-defined. The output of the gene G generated by gene expression appears as an input for those genes G_i, which represent statements whose premises depend on the statements appearing in the output of G. This implies that the evolution of the genome involves a sequence of conscious emotional experiences about truthness of some statements, which in turn make possible to become conscious about truthness of some other statements.

5. The formal system represented by DNA and many-sheeted DNA sequences has certain Gödelian flavor in it. The truthness of the stopping sign DNA triplets UAA, UAG and UGA cannot be expressed in terms of proteins coded by exons. They are like undecidable statements in an axiomatic systems whose truth value cannot be deduced from the axions. Introns however can contain stopping sign and if mRNA-protein complexes represent truthness of intronic statements, then it is possible to experience the truthness of also the statements containing stopping sign DNA. The analogy with "holy trinity" of mystic and religious thinking is obvious: whether "holy trinity" exists is not decidable by human means! Proteins clearly have finite expressive power. Given amino-acid coded by DNA triplets X_i tells only that the statement $\vee_i X_i$ is true so that the number of emotionally experiencable basic truths reduces to 20.

A more precise but less general model for genome as a conscious formal system is based on the following assumptions.

1. Exon part G of gene and its intron parts I_i are interpreted as logical statements G and I_i. Together they represent the conclusion of a theorem. Hence the running of genetic program means generation of a sequence of conscious experiences of type "*...then* $G_1\&...\&G_n$ is true" or "*...then* $G_1\&\cdots\&G_n$" is false depending on which DNA strand is involved in transcription.

2. The statement represented by a gene G is experienced to be true if G has generated some minimum concentration of the corresponding protein $P(G)$. Under what conditions the intronic statements $I_1,\cdots I_n$ are experienced as being true, is not clear. The basic dogma of genetics suggests that also now overcritical values for the proteins $P(I_i)$ translated from intronic mRNA inside nucleus make possible conscious experience about the truthness of these statements.

3. mRNA-protein complexes are not able to regulate directly the activity of genes having intron statements as premises. The regulation mechanism, if present, must be indirect. Simplest regulation mechanism is based on the observation that gene can be in states in which the roles of some introns and exons are changed. In particular, each gene has complementary gene for which exons and introns (with stopping sign excluded) have changed their roles. If the protein coded by complementary gene has the role of a silencer for the expression of gene protein, the production of mRNA-protein complexes means that the translation of the silencer molecules does not occur anymore. Since the existing silencer molecules gradually decay, these genes are activated. Thus the activation of a gene by intron-exon transformation activates automatically also the genes whose input depends on the output of the gene. Note that exons would code what is very much analogous to "printed output".

It is important to notice that cognition represented basically by a genetic program is not restricted to brain. All cells of body have DNA and elementary cognitive abilities. Perhaps the special role of the frontal lobes in cognition is due to the fact that DNA in cortex has wormhole contacts with topological field quanta representing electromagnetic part of our body not visible to bare eyes. The electromagnetic size of our body could be given the size of entire Earth as suggested by the fact that EEG frequencies correspond to Schumann frequencies associated with the resonances of the wave cavity between Earth's surface and ionosphere.

Genes as modules of a genetic program

Genes can be also regarded as modules of genetic program. The input of module consists of the premises of the statements $I_1\cdots I_n$ and conclusions represent the statements "$O_1\cdots ...O_n$ true" or "$O_1\cdots ...O_n$ not true". $O_1\cdots O_n$ serves as input for other genes and running of genetic program continues as long as premises of some genes are true.

Ordinary programs "If A then B" and "While A do B" as basic control structures. Also genetic program should have some control structures and it seems that both these structures appear in genetic programs.

1. Assuming that genes represent theorems, the general form of statements appearing in genetic program is indeed "If A then B". A is represented in terms of enzyme concentrations and possibly intron mRNA-protein complexes activating or repressing some genes. B is represented by the protein and intronic mRNA-protein complexes transcribed from gene.

   "While $N>0$ do $\cdots$ and $N\to N-1$" is the basic structure of loop in computer program. The simplest function of this loop is to circumvent infinite loops, which are nightmare of programmer. The counterpart of an infinite loop is member of species, which never dies. The presence of too many sufficiently intelligent (and, as one could bet, selfish) individuals of this kind would be a catastrophe from the point of view of species. It seems that this kind of condition is represented. Certain genes crucial for the survival of higher organisms contain certain amount of telomere which is reduced every time when the gene is active. This means that the gene modules effectively contain additional condition "While the amount of telomere $>0\cdots$ and reduce the amount of telomere by one unit".

One can understand basic rules of Mendel easily if the conditions guaranteeing the activity of gene depend on both members of chromosome. For instance, in the case that two traits are such that second on dominates, the output of gene realizing the property is logical AND function having as its arguments the truth values of the statements represented by related genes in the chromosomes. If G_1 in chromosome 1 and G_2 in its partner chromosome have coded sufficient amounts of their specific enzymes then some third G codes the enzyme giving rise to the non-dominant trait, otherwise the dominate trait appears. Second situation is the one in which traits are not yes/no properties but have discrete spectrum like red, white and pink. In this case there are two genes G_1 and G_2 coding red and white directly. Various combinations of color would correspond to three combinations G_1G_1 (red), G_2G_2 (white) and G_1G_2, G_2G_1 (pink).

The notion of many-sheeted DNA implies that gene submodules should correspond to body parts. This raises several interesting questions about what the bodily correlates of the "body part =subprogram calls second body part=subprogram". Is there some kind of communication occurring between body parts also? Perhaps chemical communication based on the same enzymes that regulate gene transcription? Gene modules call gene modules corresponding to smaller sized body parts: is this true also for the communication between body parts? Or does signal transfer occur in dual manner from small body parts to larger ones?

If this kind of correspondence exists, say, at hormonal level, one could directly deduce information about the structure of genetic program from the topology of the hormonal communications. For instance, genome should have central unit analogous to brain receiving information from controlling the activities of the rest of the genome. An obvious candidate for the brain of chromosome is centromere. Centromere seems to be analogous to brain in the sense that lot of repetitive DNA presumably controlling gene expression is situated near the centromere.

What about cognitive fermion pairs as representation of memetic codons?

According to the original speculations, memetic code could be represented as temporal sequences of what I called cognitive neutrino pairs with neutrino and antineutrino assigned with the opposite throats of a wormhole contact carrying Z^0 magnetic flux and assumed to be associated with cell membrane. The possibility of these sequences was argued to be allowed by the failure of the strict determinism for Kähler action. This idea might indeed make sense if cell membrane is near vacuum extremal and corresponds to a scaled variant of weak interaction physics with the weak length scale being of order cell size scale so that classical Z^0 and W fields become important (both non-standard value of $\hbar_{eff}$ and different p-adic length scale for weak bosons could give rise to scaled variants of weak interaction physics). From the point of view of standard model the idea is of course complete non-sense. The basic support for the idea about scaled variants of weak interaction physics is that it could understand the mysterious large parity breaking in living matter in this manner.

The weak point of the original idea was the assumption that the negative sign for neutrino energy is due to its interaction with classical Z^0 electric field. The idea however generalizes considerably in the framework of zero energy ontology (ZEO) inspired much later by the non-determinism of Kähler action. Causal diamond (CD) becomes the basic geometric objects and is identified as correlate for a spotlight of consciousness. The simplest zero energy states assignable to CD would correspond to fermions with opposite quantum numbers localized at the two light-like boundaries of CD (this only approximately since second boundary correspond to a superposition of states appearing as final states for the possible decays of the fermion).

The positive energy fermion has fermion number, weak isospin, and spin and allows representations of binary digit. In particular, nucleotides A, T, C, G could be represented in terms of these quantum numbers. The representation of in terms of u, d and their antiquarks is only one representations. The idea is that one can construct negentropically entangled temporal sequences of this kind of CDs having interpretation as bit sequences. This could give rise to a representation of also memetic codons as sequences of 126 binary digits represented in terms of fermions or as sequences of 21 triplets of binary 2-digits representable as zero energy states representing dark DNA codons.

Could DNA level contribute to our consciousness

The fermionic Boolean algebra defined by fermionic Fock state basis is a natural candidate for a quantum physical correlate for Boolean thoughts [K30]. In zero energy ontology (ZEO) the pairs of positive and negative energy fermion states with opposite net fermion numbers are in turn natural candidates for pairs of Boolean statements consistent with each other: basically they could code for the "laws of physics".

This suggest that some part of neuronal genome, whose dynamics is slow as compared to neural dynamics but consistent with the slow dynamics of the belief system as required, stores information, not only about the physical structure of organism, but also about our belief structures, intentions and long term goals. These beliefs become conscious when gene is activated, perhaps by neural activity: neural transmission is indeed known to induce effects at gene level. The statements represented by genes would correspond directly to our conscious beliefs at various levels of the space-time sheet hierarchy! Perhaps the memetic codewords consisting of 21 DNA codons (also dark DNA codons) could have interpretation as bit sequences representing integers in the range $(1, 2^{126})$ and genuine Boolean thought resides basically at the genome level.

This mechanism becomes possible only at p-adic length scales longer than neuron size scale. Therefore the emergence of genes with a total length larger than the p-adic length scale $L(169) \simeq 5$ μm should correspond to the emergence of the eukaryotes, introns and Boolean consciousness. Thus only some large enough bacteria (at least Fischerella) can have cognitive abilities. The absence of mitochondrial introns is probably due to the short length of the mitochondrial genes. The mitochondrial DNA of fungi is known to contain introns and the reason is perhaps that the length of DNA is longer than the critical length. Obviously, the proposed scenario implies a relationship between DNA level and logical thinking and partial reduction of language structures to DNA level.

In this picture genome is a collection of genes which can be regarded as Boolean algebras $B(N)$ defined by N independent binary digits. Prokaryotes would represent only $B(1)$ algebra and only single statement would be associated with gene: the only possible conscious experience associated with gene statement would be experience about the truthness of the corresponding statements. Higher level Boolean mind realized as Boolean algebras $B(N)$, $N > 1$ are present only in eukaryotes since only their DNA can have Z^0 wormhole contacts to space-times sheets $k \geq 169$. Also the genes associated with cell organelles corresponds almost as a rule to the smallest possible Boolean algebra.

3.4.3 DNA As A Topological Quantum Computer

For years ago I developed a model of topological quantum computation (TQC) combining TGD based view about space-time with basic ideas about topological quantum computation and ended up with the proposal that DNA might act as a topological quantum computer. One can imagine several ways in which DNA or RNA could act as a topological quantum computer and it good to try to state clearly what one wants.

1. Natural requirements are that the topological quantum computer programs can be naturally combined to larger programs and evolution means this kind of process; that the programs have a natural modular structure inherited from the previous stages of evolution; and that the computation is not restricted inside single nucleus.

2. DNA and/or RNA defines the hardware of topological computation and at least for more advanced topological quantum computers this hardware should be static so that only programs would be dynamical. This leaves only DNA in consideration and the entangled initial and quantum states at the ends of braids quantum states would be assignable to static DNA structures.

3. The program would be determined by different braidings connecting the states of DNA in time direction or in spatial direction. Since the genomes are identical in different nuclei, the strands could connect different nuclei or conjugate strands of double DNA strand. Reconnection process would allow to modify the hardware for TQC.

The recent progress in quantum TGD and TGD inspired quantum biology

After the advent of the first model for topological quantum computation in TGD Universe [K4], the mathematical and physical understanding of TGD has developed dramatically and the earlier quite speculative picture can be replaced with a framework which leads to a rather unique view about topological quantum computations by DNA.

1. Universe as a topological quantum computer

One can say that the recent formulation of quantum TGD states that the entire Universe behaves like a topological quantum computer. This notion of topological quantum computer differs however from the standard one in many respects.

1. The emergence of hierarchy of Planck constants realized as a generalization of the notion of embedding space is now a basic piece of TGD allowing an elegant formulation of quantum TGD [K79, K26]. The phases of matter with large Planck constant are interpreted as dark matter. Large values of Planck constant make possible topological quantum computations in arbitrary long time scales so that the most fundamental objection against quantum computation can be circumvented.

2. Zero energy ontology forces to unify S-matrix and density matrix to M-matrix - the product of the square root of density matrix and S-matrix- defined as time-like (or rather light-like) entanglement coefficients between positive and negative energy parts of zero energy state [K16, K15]. Connes tensor product emerging naturally from the notion of finite measurement resolution described in terms of inclusions of hyperfinite factors of type II_1 defines highly uniquely the M-matrix. M-matrix would be natural candidate for defining topological quantum computation in light-like direction. Connes tensor product makes sense also in space-like direction and would define quantum storage of functions represented as entanglement coefficients.

3. The notion of number theoretic braid [K80, K16] has become a basic element of the formulation of quantum TGD based on the requirement of number theoretical universality. As a matter fact, the notion of braid is generalized in the sense that braid strands can fuse and decay. One can make guesses about the details of the braid motion, which do not however matter since only topology is what matters. One could argue that the braid orbits must be light-like curves: the generic curve is locally space-like. The motion of braids corresponds to boundaries of string world sheets and the vanishing of induced weak fields at them gives a strong constraint on them. Note that one expects Kac-Moody type invariance deforming the light-like 3-surfaces and respecting their light-likeness but without changing the Kähler action and conserved quantities associated with preferred extrema.

   For generalized Feynman diagrams partonic light-like 3-surfaces meet at 2-dimensional vertices defined by partonic 2-surfaces [K15]. This implies that braids replicate at vertices: the interpretation is as a copying of classical information. Quantum information is not copied faithfully. The exchange of partonic 2-surfaces in turn corresponds to quantum communications. Hence quantum communication and quantum copying emerge naturally as additional elements. Space-like Connes tensor product in turn defines quantum memory storage.

4. Computation time is a fundamental restriction in both ordinary and quantum computation. Zero energy ontology makes possible communications in both directions of geometric time, which suggests the possibility of geometric time loops in topological quantum computations. Could this mean that computation time ceases to be a restriction and ordinary computations lasting for infinite amount of geometric time could be performed in a finite time interval of observer's time? This is perhaps too much to hope. The subjective time taken by the computation would be infinite if each step in the iteration corresponds to single quantum jump. If this is the case and if each quantum jump of observer corresponds to a finite increment of geometric time perceived by the observer, time loops would not allow miracles.

2. The notion of magnetic body and the generalization of the notion of genome

The evolution of ideas related to quantum biology provides also new valuable insights. In particular, the notion of magnetic body leads to a model of living system in which dark matter at magnetic flux quanta of the field body of biological system uses biological body as a motor instrument and sensory receptor [K24]. Quantum control would be naturally via the genome and sensory input would be from cell membrane containing all kinds of receptors. This would suggest that magnetic flux sheets traverse through DNA strands and cell membranes.

The quantization of magnetic flux with unit defined by Planck constant having arbitrarily large values leads naturally to the notions of super-genome and hyper-genome [K38]. Super-genome would consists of DNA strands of separate nuclei belonging to single magnetic flux sheet and these sequences of genomes would be like lines of text at the page of book. Super-genomes in turn can combine to form text lines at the pages of a bigger book, I have used the term hyper-genome. This hierarchy of genomes would give rise to a collective gene expression at the level of organs, individuals of a species, and at the collective level consisting of populations containing several species. Even biosphere could express itself coherently via all the genomes of the bio-sphere. The model of topological quantum computation performed by DNA should be consistent with this general picture.

Model for DNA based topological quantum computation

The most promising model of DNA as topological quantum computer relies on the hierarchy of genomes. The flux sheets or collections of parallel flux tubes assignable to a magnetic body would traverse the DNA strands of several nuclei so that strands would be analogous to lines of text on the page of a book.

DNA strands would define the intersections of magnetic or number theoretic braids with plane and braiding would be associated with with the magnetic field lines or flux tubes transversal to DNA. The M-matrix defining topological quantum computation would act on quantum states assignable to nucleotides.

1. The interpretation of nucleotides

The interpretation of the A, T, C, G degree of freedom is not obvious and one can consider several options.

1. The quantum numbers entangled by braids having nothing to do with (A, T, C, G) assignable to nucleotides and the braiding does not affect nucleotides.

2. The nucleotides (A, T, C, G) correspond to four different colors (a, t, c, g) for braid strands with conjugate nucleotides defining conjugate colors. The subgroup of allowed braidings would preserve the color patterns. The minimal assumption consistent with the mapping of nucleotides to quarks and antiquarks [K3] is that braid strands connect only nucleotides and conjugate nucleotides.

3. The model requires that the genomes in different nuclei are identical: otherwise it is not possible to realize braidings as symmetry transformations mapping portions of DNA to their conjugates (as noticed, this map would not occur at the chemical level). An interesting question is whether also the permutations of nucleotides of different codons are allowed or whether only codons are permuted so that they would define fundamental sub-programs.

4. One can understand why the minimum number of nucleotides in a codon is three. The point is that braid group is non-commutative only when the number of strands is larger than 2. The braidings acting as symmetries would correspond to a subgroup of ordinary braidings leaving the color pattern of braid invariant. Obviously the group is generated by some minimal number of combinations of ordinary braid generators. For instance, for two braid strands with different colors the generator is e_1^2 rather than e_1 (two exchange operations/full 2π twist). For codons one would have four different subgroups of full braid group corresponding to codons of type XXX, XYY, XXY, and XYZ. Each gene would be characterized by its own subgroup of braid group and thus by an M-matrix defining topological quantum computation.

5. It might be possible to understand the "junk DNA" character of introns. Introns are the most natural candidates for the portions of genome participating topological quantum computations. The transcription process would disturb topological quantum computation so that

introns should be chemically passive. Since the portion of "junk DNA" increases with the evolutionary level of the species evolution would indeed correspond to an increase the amount of topological quantum computations performed.

2. Two realizations of topological quantum computation and their combination

One can imagine two basic realizations of topological quantum computation like processes- or to be more precise - entanglement by braiding. In TGD framework this entanglement could be interpreted in terms of Connes tensor product.

2.1 Space-like entanglement

The first realization would rely space-like braids. Braid strands would connect identical lines of text at the page of book defined by sequences of genomes of different nuclei. Inside nucleus the strands would connect DNA and its conjugate. The braiding operation would take place between lines.

In this case it would be perhaps more appropriate to speak about quantum memory storage of a function realized as entanglement. These functions could represent various rules about the behavior of and survival in the physical world. For this option A, T, C, G cannot correspond to entangled quantum numbers and the interpretation as braid colors is natural. Braiding cannot correspond to a physical braiding of nucleotides so that (A, T, C, G) could correspond to braid color (strands would connect only identical nucleotides).

Strands would not connect strand and its conjugate like hydrogen bonds do but would be like long flux lines of dipole field starting from nucleotide and ending to its conjugate so that braiding would emerge naturally. Color magnetic flux tube structures of almost atom size appear in the TGD based model of nucleus and have light quarks and anti-quarks at their ends [L2] , [L2]. This could be the case also now since quarks and anti-quarks appear also in the model of high T_c superconductivity which should be present also in living matter [K24].

2.2. Light-like entanglement

Second realization would rely on light-like braids at the boundaries of light-like 3-surfaces connecting 2-surfaces assignable to single genome at different moments of time. Braiding would be dynamical and dance metaphor would apply. The light-like surface could intersect genomes only at initial and final moments and strands would connect only identical nucleotides. Light-likeness in the induced metric of course allows the partonic 3-surface to look static at the level of embedding space.

What number theoretic braid is, is far from clear. I have proposed the identification of fundamental number theoretic braids in terms of the minima of the Higgs like field associated with the Kähler-Dirac operator would be very natural in this case. An alternative definition of braids would as boundaries of string world sheets at which spinor modes are located. This definition is not however completely unique.

Genes would define only the hardware unless they code for the magnetic body of DNA too, which looks implausible. The presence of quantum memory and quantum programs would mean a breakdown of genetic determinism since the braidings representing memories and programs would develop quantum jump by quantum jump and distinguish between individuals with the same genome. Also the personal development of individual would take place at this level. It would be these programs (that is magnetic bodies) which would differentiate between us and our cousins with almost identical genome.

2.3 Combination of the two realizations

These two variants of TQC accompany each other automatically if DNA nucleotides are connected to the lipids by magnetic flux tubes [K3]. In this case the 2-D flow of lipids induced by the self organization pattern of the metabolically induced flow of cellular water would induce the TQC as dance and this in turn would would generate braiding of flux tubes connecting lipids to the nucleotides. Presumably a gel-sol transition of cytoplasm accompanies TQC in this kind of situation.

Biological evolution as an evolution of topological quantum computation

This framework allows to understand biological evolution as an evolution of topological quantum computation like processes in which already existing programs become building blocks of more complex programs.

1. The transition from RNA era to DNA era involving also the emergence of cell membrane bounded structures would mean the emergence of the topological quantum computation using a static hardware.

2. For mono-cellulars double DNA strands define space-like topological quantum computations involving only single step if the braids connect the nucleotides of the two DNA strands: obviously a reason why for double DNA strands.

3. For multicellular organisms more complex space-like topological quantum computations would emerge and could code rules about environment and multicellular survival in it. At this step also introns specialized to topological quantum computation would emerge.

4. A further evolution as a generation of super-genomes in turn forming hyper-genomes and even higher structures would have a concrete counterpart as the organization of braids of lower level to form braids at higher level so that topological quantum computations would become increasingly complex and program module structure would emerge very naturally.

3.5 Ideas About Concrete Realization Of Genetic Programs

In this section some ideas about concrete realization of genetic programs are discussed. The ideas derive from the first years of TGD inspired quantum biology and it would be interesting to see how the systematic application of recent understanding of TGD could enrichen the picture.

3.5.1 How Gene Expression Is Regulated?

In case of prokaryotes the regulation of transcription is quite satisfactorily understood. The problem is to understand how transcription is regulated in case of the eukaryotes and here the notion of many-sheeted DNA could be crucial.

Operon theory for the regulation of gene expression in prokaryotes

Jacob, Monod and Pardee [I14] suggested operon theory for the regulation of the transcription of genes responsible for lactose production in E. coli. The presence of lactose induces E. coli to produce 3 enzymes needed in the production of lactose. The enzymes correspond to three structure genes x, y, z of lactose. The mechanism is following.

1. So called i gene regulates the production of the building block proteins of the repressor protein which self-assembles as tetramer of the repressor protein.

2. Repressor protein binds to a specific site next to the promotor and hinders the binding of the RNA polymerase so that transcription becomes impossible.

3. Inductor, in the present case lactose, binds to the repressor protein and hence hinders the formation of the repressor tetrameres so that transcription becomes possible.

4. The transcript contains not only the gene but also the entire operon so that several genes are translated simultaneously.

How eukaryotes differ from prokaryotes?

Operon theory does not generalize as such to eukaryotes. Although the notion of the promoter generalizes, there is no clear-cut evidence for operons [I14]. Rather, silencers and enhancers could take the role of the inducers and repressors in the eukaryotic gene expression. The action of a silencer/enhancer is not sensitive to its precise location or orientation and the distance from

promoter can be more than thousand nucleotide pairs. TGD based explanation is based on the notions of many-sheeted DNA and protein. Silencers and enhancers mediate the interaction of the atomic space-time sheet of DNA with the classical fields of some larger space-time sheet. This interaction makes possible top-bottom type control analogous to the control of slave by master in Haken's theory of self-organization. Both classical em and Z^0 fields can control the gene expression in this manner. In eukaryotes classical Z^0 fields could have especially important role. Classical Z^0 fields are believed to be crucial for the model of cognition and this suggests that "mind-matter" interaction could at least partially relay on classical Z^0 fields and enhancers/silencers. Silencers and enhancers could make also possible Josephson junctions between gene space-time sheet and some larger space-time sheet and thus realize "biofeedback".

Second difference is related to introns. It is known that introns and exons can change their roles and it is known that there are several pathways for splicing leading to different proteins, isoforms. The replacement of single-valued gene→ polypeptide map with many-valued map obviously increases the information content of gene. The interpretation of introns and exons as two interspersed computer codes with intron lines of code separated from exons by "comment signs" marking each nucleotide of intron is attractive model for the situation. Dropping of some comment signs changes the result of the splicing process. Comment sign distribution could be dynamical and tissue specific so that one could say that genome is not invariant of species but only of a particular tissue type. This obviously reduces the genetic determinism and gives organism better abilities to survive. In human genome 1 percent of gene corresponds to exons in the "normal" state (in whatever manner that state is defined). The number of various combinations of exon and intron combinations is 2^N where N denotes the numbers of basic components of gene (perhaps coding proteins having no decomposition to modular proteins). The number of combinations increases exponentially with N and provides huge flexibility.

The interpretation of various exon-intron decompositions as statements of Boolean algebra of statements about N basic statements suggests strongly itself. In particular, exonic and intronic proteins for same intron-exon decomposition would naturally correspond to a statement and its negation. Thus one could regard eukaryotes as representing higher levels in the hierarchy of abstractions in which prokaryotes represent the lowest level. Eukaryotic genome would be a collection of genes identifiable as Boolean algebras and the running of the genetic program would mean that at given moment some statement in some of these Boolean algebras is experienced to be true. This kind of identification would mean effectively understanding of the logical meaning of the genetic code. The dominance of particular exon-intron decomposition over its complement would simply mean that this Boolean statement is true while its complement is not true. This suggests the possibility that only those 2^{N-1} exon-intron configuration which represent statements consistent with a given atomic statement are usually realized (atomic statement corresponds to a one-element subset in the set theoretic representation of Boolean algebra).

The fact that introns and exons are set theoretical complements of each other raises the possibility that the proteins coded by introns and exons have opposite effects as transcription factors. For instance, exons could code enhancer and introns could code silencer. This implies that same gene can act as both enhancer and silencer. The only thing needed is that the roles of introns and exons are changed. When this occurs, the production of intron-RNA complexes begins and the production of the composite protein coded by introns acting as exons stops. When the production of silencer protein coded by introns ceases, the silencer proteins associated with the operator sites gradually decay and gene expression also enhanced by enhancer proteins can start. Thus the activation of the gene module activates automatically the gene modules which it calls and genetic program runs.

This would suggests rather general mechanism of gene expression.

1. There exists 2^{N-1} exon-intron decomposition plus their complements. Depending on the state of gene with given exon-intron decomposition, exons or introns are translated to protein. Both introns and exons represent statements. The modular decomposition of protein to subproteins often represented by the decomposition to exons corresponds to the decomposition of the statement E to $E = E_1 \& E_2 ... \& E_n$. Same holds true for I: $I = I_1 \& I_2 ... \& I_n$.

2. The proteins coded usually by exons activate some genes and these proteins appear as prerequisites of type

$$IF\ [E_1\ OR\ E_2 \cdots\ OR\ E_n]\ THEN \cdots\ .$$

The presence of all activators is not necessary.

3. Introns correspond to repressors quite generally. The proteins coded by introns in the "abnormal" state of the gene correspond to prerequisites of type

$$\cdots IF\,[NOT(I_1)\&NOT(I_2)...\&NOT(I_n)]\ THEN \cdots\ .$$

This means that the absence of all repressors from operator site is necessary. The general form of gene statement is

$$IF\ [E_1\ OR\ E_2 \cdots\ OR\ E_n]\,\&IF\,[NOT(I_1)\&NOT(I_2)...\&NOT(I_n)]\ THEN \cdots\ .$$

Various E_k: s and I_k: s represent proteins in turn having modular decomposition to a product of more primitive statements.

The role of the hierarchy of Josephson currents

The control– and coordination hierarchy formed by super conductors represented by space-time sheets coupled to each other by join along boundaries bonds suggests new quantum level control mechanisms for genetic expression. Josephson currents at resonant frequencies corresponding to some magnetic transition of gene or its substructure could "wake-up" the gene self and initiate the self-organization process leading to the gene activity. Silencers and enhancers could correspond to proteins which have join along boundaries bonds/flux tube contacts to larger space-time sheets serving as masters. This would explain why neither the exact position nor orientation of the silencer or enhancer is not important for their functioning.

Various genesandassociated control structures have mutual Josephson junctions controlling gene expression. This would mean the presence of extremely weak longitudinal electromagnetic fields (the potential differences over Josephson junctions would be in 10^{-14} eV range). The control mechanisms behind morphogenesis are poorly understood and phase gradients along chromosomes and along the growing organism could be involved with the control of morphogenesis. The fact that the rate of the translation process is about 20 amino-acids per seconds is in accordance with the idea that this process is controlled by a Josephson current associated with some ion having this frequency.

3.5.2 Model For The Physical Distinction Between Exons And Introns

Introns seem to begin with nucleotide pair CT and end with pair TC: the assumption that this is the sole signature of the beginning of intron is however not consistent with the observation about the change of the roles of intron and exons. Furthermore, this criterion is obviously not sufficient for telling where intron begins and ends since also ordinary genes can contain similar section.

There are several constraints on the marking telling whether a given nucleotide is exon or intron.

1. The splicing mechanism or DNA telling which portions of it are transcribed to mRNA should rely on the marking mechanism. This requires that the enzymes responsible for the splicing are able to distinguish between introns and exons.

2. Introns can start and end in the middle of DNA triplet. This suggests that the marking is assigned with each nucleotide separately rather than each codon.

3. Both intronic and exon portions of DNA are transcribed to mRNA and splicing of the intronic portions of mRNA occurs only after that. Therefore the total length of the exon portions of DNA corresponding to a given gene must correspond to integer multiple of codons and there must exist some mechanism forcing this. The length of the intronic portions seems to be free.

4. The transformations of exons and introns to each other are known to occur. Tere must exist a physical mechanism changing the marking.

Could magnetic flux tubes serving as braid strands distinguish between introns and exons?

A priori one can imagine an endless number of possibilities for the physical realization of the binary digit distinguishing between exon and intron nucleotide. The vision about DNA as topological quantum computer with flux tubes connecting introns to the lipids of nuclear and cell membranes (not necessarily those of same nucleus or cell) acting as braid strands would realize this distinction naturally: the introduction of the connecting flux tube would transform exon an intron. Reconnection of pairs of flux tubes between DNA nucleotides or codons and lipids would allow to effectively eliminate the braid strands and transform pair of introns to exons. The first guess would be that the presence of braid strand could make it impossible to perform transcription. This is not the case: both intronic and exon portions are transcribed to mRNA and slicing process cuts off the intronic portions of mRNA after that.

1. The original model of DNA as topological quantum computer [K3] assigns to the nucleotides A, T, C, G quarks u and d and antiquarks $\overline{u}$ and $\overline{d}$. This model has intriguing properties: for instance, matter-antimatter asymmetry would have representation at the level of genetic code. This representation is consistent with the fact that the intron-exon boundary can occur in the middle of the codon.

2. An alternative highly attractive option is inspired by the notion of dark DNA [L2, K31]. The model for dark proton predicts under rather general assumptions that the states of dark proton correspond to those of DNA, RNA, tRNA, amino-acids. The model also predicts vertebrate genetic code correctly. This leads to quite far reaching vision about the role of dark nuclear physics in biology and evolution. Dark proton consists of three quarks (uud) but since the quarks are entangled one cannot assign a decomposition to counterparts of nucleotides to the dark proton.

   The observation of Hu and Wu [J12] related to the magnetic properties of cell membrane inspire the proposal that the dark proton sequences representing DNA sequences are associated with the lipid layers of the cell membrane as analog of double DNA strand [K12]. Unfortunately this identification is not consistent with the finding that exon-intron distinction is defined at the level of nucleotides rather than codons.

Can one save the latter option, and could both options be mutually consistent? In many-sheeted space-time nucleotides and codons naturally correspond to different space-time sheets being analogous to quark and hadron space-time sheets. Hence the two models could be consistent.

What distinguishes between the lipids to which nucleotides and codons connect? Do codons connect to sequences of three lipids such that each of them connects to nucleotide of the codon? Or do nucleotides connect to the lipids of the nuclear membrane and codons to the lipids of the cell membrane. The latter option looks rather elegant and would also provide an answer to the question "Nuclear or cell membranes or both?". Note that one can also consider memetic codons realised as sequences of 21 DNA codons connected by flux tubes to sequences of 21 dark protons as even higher level structures. This kind of flux tubes could connect DNAs of nuclei of different cells.

What forces exons and introns to contain integer multiple of 3 nucleotides?

What could be the physical mechanism forcing the total length of the exonic and intronic sections to be integer multiples of codons?

1. A possible mechanism is based on the existence of a phase gradient along the DNA sequence such that the increments of the phase Φ for exons of a given gene would sum up to an integer multiple of $\Delta\Phi_{tot} = n2\pi$. For intronic portions the phase gradient could vanish- The phase gradient could correspond to the phase difference associated with the weakly coupled super

conductors formed by the two DNA strands or the phases of the supra currents flowing in DNA strands.

Phase gradient is naturally accompanied by an electric field and electric fields parallel to linear molecules appear frequently in biology: DC currents of Beck indeed require the existence of electric voltage along linear structure in question [L15]. Thus flux tubes would carry both electric and magnetic fields for exon portions and could be purely magnetic for intron portions.

This mechanism allows a variant for which only exon portions are accompanied by magnetic flux tubes carrying also electric field.

2. The phase gradient must be transferred also to mRNA and splicing mechanism must detect its presence in order to cut away the portions of mRNA for which the phase gradient vanishes. This would mean that also flux tubes marking gene portions must be transcribed.

3. An attractive possibility is that the phase gradient is related with the helical structure of DNA double helix: the minimum number of DNA triplets giving rise to a multiple of 2π rotation of the helix is 10 and corresponds to the p-adic length scale $L(151)$ defining the thickness of the cell membrane. The helix can be characterized by the tangent vector of helix having axial and azimutal components:

$$K = (1, \frac{d\phi}{dz}) = (1, 10 \times 2\pi) \times \frac{1}{L(151)} \quad .$$

The phase gradient would be naturally a multiple of this vector

$$\frac{d\Phi}{dz} = nK \quad .$$

For $n = 10$ the increase of Φ would be 2π per single DNA triplet. For $n = 1$, $n = 2$, $n = 5$ and $n = 10$ the allowed lengths would come in multiples of periods 10, 5 and 2 and 1 DNA triplets respectively. Note that 5 triplets corresponds to the p-adic length scale $L(149)$ associated with the lipid layer of the cell membrane. The presence of this gradient would naturally define the splitting of the nucleotide sequence to DNA triplets and might be important in the dynamics of DNA translation and transcription.

Are the properties of the introns consistent with the proposed model?

The proposed interpretation of introns is consistent with the basic facts about them.

1. It has been found that the precise positions of introns in gene do not seem to affect the gene expression. Introns can start in the middle of protein building block or even in the middle of codeword.

The content of intron DNA does not correlate with the content of protein DNA. This is just what the model predicts. Introns are known to wander around genome and between cells. One could interpret their presence as some kind of experimentation with small modifications of the quantum software. The addition of intronic section to the gene does not in general have any dramatic consequences as far as gene expression is considered. If DNA acts as topological quantum computer, the addition of intronic portion would be like addition of software to a computer: a topological quantum computer program defined by the braiding assignable to the intronic section of DNA.

An interesting question is how much intron distribution affects genetic during the evolution of individual and how large the differences between members of species are.

2. In the proposed picture the evolutionary step leading from prokaryotes to eukaryotes was the emergence of the introns and gene programs having also intronic mRNA as output. This was perhaps necessitated by the emergence of the cell nucleus since introns were needed as input by the genetic program transferring mRNA out of nucleus. The emergence of the cell nucleus as $L(163)$ structure could in principle have occurred already for a cell of size $L(k) = 167$.

It seems that in cells of animals the size of the nucleus corresponds to $L(163)$ or perhaps even $L(167)$. Cell nucleus is however not all that is needed for the emergence of introns: the model requires the presence of $k = 169$ level in the hierarchy.

3. What is beautiful is that homing [I30] and retrohoming [I17] phenomena can be regarded as modification of the genetic program in a way which is automatically internally consistent! The addition of intron does not spoil the running of the genetic program. One can quite well consider the possibility that organisms are continually experimenting with various modifications of genetic program. It might even be that homing and retrohoming phenomena make possible the evolution of the genetic program during the lifetime of individual.

If the entire mRNA corresponds to intronic portion of DNA, it remains inside nucleus. These DNA sequences might appear in cells and the mRNA in question could be seen as a remnant of RNA era. Part of silent DNA could correspond to purely intronic genes.

1. Histones form the basic protein building block of chromosomes. Histone genes are known to contain no introns. The interpretation is that the gene coding histone is in exon state permanently. If histone genes contained intron parts, histones could act as repressor genes and regulate gene activity. Since histones appear as building block proteins of nucleosomes of chromosomes, this would mean that the programs of operating system would depend on the quantum software defined by introns: obviously a highly undesired situation. Also interferons are known to have no introns. The explanation might be similar. This could explain also why the DNA of mitochondria contains no introns.

2. It is known that the pseudogenes obtained by splitting the introns are not active. For instance, the noncoding RNA and mRNA coded by gene is not translated and is left inside the nucleus. The simplest interpretation is that intronic portions define topological quantum computer programs need to carry out mRNA and transfer it from the nucleus. This interpretation would suggest that the TQC: s defined by the flux tubes connecting nucleotides to nuclear membrane are responsible for this. The TQC: s responsible for transferring molecules through the cell membrane would involves braids connecting DNA and cell membrane. The hierarchy could continue to multicellular level. In this picture the braid strands would also serve as molecular highways along which the transfer would take place.

3.5.3 The Phenomenon Of Superimposed Genes

Before the discovery of the structure of the genome of $\phi X174$, it was thought that the Central Dogma is absolute truth. It has however turned out that genes within genes and even overlapping genes are possible [I14]. Bacteriophage $\phi X174$, which is virus with single stranded circular DNA, contains two genes, denoted by A and D, containing genes B and E within them. A gene contains also gene A^* which starts in the middle of A and ends in the same codeword. Also the translation of a gene overlapping with A and gene C next to it have been observed in G4 bacteriophage having genome very similar to that of $\phi X174$.

To understand how the translation of mRNA can give rise to genes inside genes, one is forced to introduce the notion of reading frame shift. This concept is somewhat ad hoc since it requires that the translation of a gene within gene does not obey the usual rules since reading is stopped without stopping sign.

The geometric realization of the subprogram structure might make possible to understand gene superimposition.

1. Geometrically gene would be a linear model for its expression domain obtained by thinning it to DNA thread. Two subsequent genes G_1 and G_2 are like two subsequent body parts. If gene superposition occurs, there is third body part having overlap with both and "glued" to both: kind of joint connecting two body parts.

2. In computer analogy these "body parts" correspond would represent subprograms. Transcription generates protein which refers to some other program module realized as "body part". If the requirement that each "body part" generates program call to existing "body part", is satisfied, then gene superimposition is possible. This requirement is actually very

natural consistency condition. That our body is full of this kind of joints would suggest that gene superposition is a general phenomenon.

A concrete model is obtained in terms of many-sheeted DNA and many-sheeted versions of various RNAs. As a matter of fact, the notion of many-sheeted DNA conforms with what the picture based on the notion of magnetic body having hierarchical structure with flux quanta inside flux quanta and flux sheets traversing through sub-units of DNA sequence, suggests.

3.5.4 Possible Explanations Of The Silent DNA

Genome contains large amounts of silent DNA which is not transcribed. One can consider several explanations of silent DNA in TGD framework.

1. Each gene consists of a transcribed part and control part contained in region between gene and its precedessor. It might be that highly repetitive DNA located near the centromere corresponds actually to a control part of DNA and is therefore not transcribed. Enhancers and silencers could be in question and they could have contacts to larger space-time sheets and take care of the control in long length scale enhancing or silencing a large number of genes simultaneously.

2. Genome can be regarded as a large collection of program modules calling each other. Large programs typically contain a great number of modules not used by the average user. There is also a larger number of program modules whose output is not visible to the user. Silent DNA could correspond to program modules of this kind. The counterpart of unused program modules are genes which are permanently repressed. This kind of permanent repression certainly occurs during differentiation and most of DNA in given part of organism is this kind of DNA.

3. Silent DNA could also correspond to purely intronic genes which correspond to dead ends of the genetic program and are decoupled from genetic program by selection.

4. The most radical possibility is that silent DNA corresponds to genes which are expressed non-chemically and corresponding control regions affected by non-chemical transcription factors. A possible test for the existence of non-chemical gene expression is to modify the silent part of, say, neural genome and find whether and how this affects the behavior of the organism.

5. The vision about DNA as topological quantum computer [K3] had not emerged as I wrote the above list for the first time. This vision would identify silent DNA as part of software whereas genes in this framework could be seen as hardware. What makes this option especially attractive is that the detailed nucleotide composition of the DNA strand is not crucial for the functioning of the TQC program: what matters mostly is the braiding of the flux tubes connecting nucleotides/codons to lipids. The nucleotide decomposition brings only effective coloring of the braid strands which causes additional delicate effects. Therefore the braidings associated with the repetitive structures suggesting strongly the interpretation as "junk" can quite well serve as TQC programs.

3.5.5 About Genetic Evolution

The proposed general model of genetic program provides nontrivial insights to evolution of genome.

ORP and the structure of the genetic program

An interesting question is whether "ontogeny recapitulates phylogeny" principle in its original form (to be distinguished by its TGD based analog applying much more generally) could give nontrivial constraints on the structure of the genetic program.

1. One could argue that the structure of the genetic program must reflect its evolution. In the beginning of development only the lowest level genes are activated and in turn activate more evolved genes which in turn $\cdots$. The gradual emergence of new hierarchy levels would

have interpretation as emergence of new abstraction levels: statements about statements about... are formed. These levels correspond to emergence of higher level selves having more abstracted experiences about the state of organism or its organs. Geometrically the new levels would correspond to the appearance of new space-time sheets in the hierarchy of space-time sheets assignable to the magnetic body of the genome.

2. One can also defend quite different point of view. The evolution starts from simple main program corresponding to, say the length scale of a fertilized egg. Gradually subprograms corresponding to the emergence of smaller length scale structures are activated. In growth stage simple replication of the basic structure together with the activation of the lower level programs giving rise to differentiation occurs. This leads to join along boundaries/flux tube condensates of the fundamental expression domains having some finite size determined by the metabolic resources available and by self-organization. In fact, the general structure of embryogenesis supports this view whereas evolution of more complex organisms supports the first option.

3. Option 2) suggests that genetic program modules call only modules associated with shorter length scales so that higher levels cannot be activated by program call. If this is the case new levels should emerge when some space-time sheet associated with DNA expands in phase transition like manner and fuses with corresponding space-time sheets associated with neighboring cells. These phase transitions would represent the self-organization aspect of development.

4. Cell differentiation could be understood as resulting from the branching of genetic program in position dependent manner caused by diffusion gradients of transcription factors. For instance, these transcription factors would correspond to hormones which bind to receptors to form a complex binding to gene.

Homeostasis, loops, tautologies

If P then P is the simplest loop one can imagine and corresponds to a gene coding protein activating the gene itself. Biologically this represents endless cancer like growth limited only by lifetime of protein and resources and hence possible breakdown of the system! More complicated statement structures of this type represent n-fold tautologies: *If* P_1 *then* P_2 , *If* P_2 *then* P_3 , ..., *If* P_n *then* P_1 . These systems are also self-amplifying and correspond to a cyclic reaction in which genes code enzymes activating other genes in the cycle.

This kind of cycles might be involved with the very early evolution of life. For instance, DNA-RNA-protein trinity might have developed from a situation in which RNA coded protein which catalyzed both the reverse transcription of RNA to DNA and transcription of DNA to RNA. Thus simplest life form would have represented tautology *If P then P* ! Reverse transcription such that the reverse transcriptase also catalyzes transcription is indeed known to occur. Certain plant viruses contain inverse transcriptase synthetizing in infected cell DNA from its RNA and then DNA complementary to this. This double strand joins to the genome of the host cell and duplicates itself.

More complicated cycles involving several equivalent statements would have evolved gradually (note the parallel with the generation of mathematical theorems stating equivalence of statements!). Bacteria replicate endlessly and might perhaps be regarded as example of life form which corresponds to n-fold tautology.

The role of chromosomes

An interesting question is whether the organization of the genome to chromosomes could have some deeper organizational meaning. The fact that chromosome fusions and splittings are possible, suggests that chromosomes as a whole cannot have direct identification in terms of any body structure. Indeed, the realization of genetic program in terms of protein concentrations representing inputs and outputs of genes interpreted as subprograms is very flexible as far as the location of gene subprograms is considered. Only genes which form larger program structures should form geometrically connected units and the relative locations of these units could be rather free. As already found, genes seem indeed form clear geometrical subunits.

Animal	Man	Chimpanzee	Cow	Dog	Cat
N_c	23	24	30	39	19
Animal	Horse	Rat	Rabbit	Alligator	Frog
N_c	32	21	22	16	13
Animal	House fly	Fruit fly	Honeybee	Flatworm	Harpalinae
N_c	6	4	16	8	$18+x$

Table 3.3: Chromosome numbers for some species.

Chromosomes could be identified as a set of mutually interacting parallelly running genetic programs. One can of course consider the possibility that chromosomes mean the composition of body part to N_c linear structures, N_c being the number of chromosome pairs. Parallel interacting processing would bind these structures to single coherent hole. This division to N_c parts should be detectable at all levels of body organization. One can also consider the possibility is that the structure of chromosome parallels the structure of body and that centrosome corresponds in some sense to the brains of chromosome and the branches of chromosome correspond to right and left halves of the body. Genetic programs associated with different chromosomes are known to run in very precise synchrony. Many -sheeted DNA could explain this synchrony naturally as resulting from the interaction of genes with with classical em fields with space-time sheet containing the chromosomes.

Table 3.4 gives chromosome numbers for some animals. For the home fly the number of chromosome pairs is 6 whereas the number of the p-adic hierarchy levels determined by the size of the home fly is 12. For fruit fly the number of chromosome pairs is 4. Horse has 32 pairs of chromosomes and dog has 39 pairs of chromosomes whereas Homo sapiens has 23 chromosomes. The large number of chromosomes can be understand as a way to produce large number of outcomes in breeding. The number of possible combinations of chromosomes in sexual breeding is 2^{N_c}, 2^{16} more than in case of Homo Sapiens. There are indeed very many different looking dogs barking around! The number of chromosomes varies wildly. For instance, the number of chromosomes in Harpalinae is $18+x$ [I4]! The size of this insect is about one centimeter.

The natural expectation is that the size of chromosomes has gradually grown during evolution when new p-adic space-time sheets have emerged. This process could correspond to insertion of introns to the basic DNA. The possibility coming first in mind is that the value of k_G in genes of given chromosome tends to increase as a function of the distance from the second end of gene. Genetic program realized in terms of many-sheeted space-time concept does not however require this. The genes involved in the coding the structure of given body part are known to be linearly arranged according to the structure of body part itself. This is certainly consistent with TGD picture in which body parts grow from space-time sheets associated with DNA. It seems that the highest activated space-time sheets in genes must correspond to brain, in particular frontal lobes, in case of human. This would suggest that also in chromosome the largest active length scales correspond to the region around centrosome.

p-Adic evolution of DNA

p-Adic evolution should involve two aspects.

1. The increase of the p-adic length scale characterizing the basic DNA modules. This suggest the classification of the basic building blocks of the genome by the p-adic length scale associated with the corresponding DNA sequences.

2. The fractal evolution involving emergence of longer p-adic length scales characterizing the size of the space-time sheets to which basic DNA sequences had # contacts. Thus the lengths of introns and exons are not expected to correlate with the p-adic scale of the space-time sheet to which they possibly have # contacts. Rather, same gene can have # contacts to arbitrarily large space-time sheets.

Consider first the critical lengths of the basic program modules. The lengths $L(149), L(151), L(157), ...$ of gene or DNA sequence might mean the emergence of something genuinely new in the evolution. This length scale hierarchy expressed in terms of $L(137)$ comes in powers of 2 as $N_{137} = 1, 2, 64, 128, 2^{10}, 2^{13}, 2^{15}, ...$

Single nucleotide pair corresponds to in double helix to distance of .34 nanometers which is larger than the length scale of $L(139)$. The structure of the double helix is such that there is a periodicity of 3.4 nanometers: this means that basic period corresponds to 10 nucleotides. This implies that 5 DNA triplets correspond to a length of 5.05 nanometers, which equals to p-adic length scale $L(149)$ if $L(151)$ is defined to be $L(151) = 10.2$ nm. $L(149)$ corresponds to the thickness of the lipid layer of cell membrane and $L(151)$ corresponds to 10 DNA triplets, to the thickness of the cell membrane and the basic period of DNA sequence when DNA triplet is regarded as a basic unit. Perhaps this periodicity is not accident but has deeper meaning possibly related to the periodicity of phase variable associated with DNA. The lengths of DNA sequences corresponding to p-adic length scale $L(k)$, $p \simeq k$, k power of prime are $N(DNA) = 2^{k-149} \times 5$ DNA triplets.

This means that the critical numbers of DNA triplets possible leading to the emergence of qualitatively new properties of organism are given by

$$\begin{aligned} N(DNA) &= 2^{(k-149)/2} \times 5 \ , \\ k &\in \{149, 151, 157, 163, 167, 169, 174, 179, 181, 191, 193, ..\} \end{aligned} \tag{3.5.1}$$

The few lowest critical values of DNA triplets in gene are

$$N(DNA) = n \times 5 \ ,$$
$$n = 1, 2, 2^4 = 16, 2^7 = 128, 2^9 = 512, 2^{10} = 1024, 2^{12}, 2^{15}, 2^{16}, \cdots$$

The steps of this hierarchy resembles bring in mind the evolution for the length of the basic memory unit of computer memory! One must however notice that 5 DNA triplets seems to serve as a basic unit.

The emergence of new p-adic length scales could have meant emergence of new levels of modularization in the genetic program and it is interesting to look these numbers from this point of view.

1. One could think that short sequences of precursors of DNA, mRNA and tRNA molecules were generated spontaneously by self-assemly. This implied automatically the generation of amino-acids by the more primitive counterparts of transcription and translation processes. The lengths of DNA molecules began gradually grow and at the critical lengths of DNA corresponding to p-adic length scales dramatic new effects emerged. Also new space-time sheets emerged in the genome and the first guess is that this occurred for the critical sizes of the organism given by p-adic length scales.

2. Formation of lipid layers might have been the revolution occurring at this stage and since lipids should have had size of order $L(149)$. This revolution should have occurred when the length of the genome became longer than 5 DNA triplets and meant formation of lipid layers by self organization process known to occur in all liquid crystals: these layers were perhaps formed in the surface of water such that hydrophobic ends of proteins would have pointed out of water. Self organization presumably led simultaneously to the formation of double membranes having thickness $L(151)$ such that the hydrophobic ends of proteins pointed in the interior of the double membrane. Second revolution became possible when the number of DNA triplets became larger than 10 triplets so that proteins connecting cell interior of the double membrane to its exterior became possible and the control of ion concentrations became in principle possible. Transfer RNA (tRNA) has length of at most 27 triplets. Third revolution should have occurred $L(157)$, which corresponds to 80 triplets.

3. Smallest viruses possessing single strand of DNA have lengths between 15-100 nanometers and this suggest that genome correspond to p-adic length scales $L(149)$, $L(151)$ and $L(157)$. These length scales could characterize largest space-time sheets also present in genome. The

building blocks of the envelope of viruses are genetically coded separately and self-assemble spontaneously so that only building blocks need to be coded. Therefore p-adic prime associated with the genome of virus could be smaller than that determined by the size of the virus. Viruses with two DNA strands have sizes between $250 - 1000$ nanometers. This suggest that the emergence of $k = 163$ length scale in the genome of virus was accompanied by the emergence of double stranded DNA. $k = 163$ is perhaps the largest p-adic length scale associated with virus genome.

4. Bacteria have typically sizes of $1 - 10$ micro-meters. This suggests that $k = 163, 167, 169$ are the possible space-time sheets associated with the bacterial genome. The emergence of $k = 169$ could have meant the emergence of multicellulars and generation of epithelial sheet like structure consisting of two cell layers as well as emergence of introns and DNA cognition.

Consider now the typical lengths for the structures of the eukaryotic genome.

1. The presence of introns means that the length of a gene coding given protein plus introns is much longer than the DNA coding only the protein. The higher the evolutionary level of species, the larger the fraction of introns. For human genome the fraction of exons is roughly 1 per cent. The typical length of hnRNA in nucleus is 6.000-8.000 np (nucleotide pairs) which corresponds to 18 micro-meters and length scale $L(163)$ and $L(167)$. Even genes with length 20.000 np are possible and correspond to $L(169)$. The lengths of mRNA vary between 500-3.000 nucleotides corresponding to interval 1.7×10^{-7}-10^{-6} meters and length scales $L(157)$ and $L(163)$. RNA sequences coding typical protein consisting of roughly 300 amino acids are about 3×10^{-7} meters and correspond to $L(159)$.

2. Most of the highly repetitive DNA has rather short length between $5 - 300$ nucleotides. Introns having typically lengths between $10 - 1000$ nucleotide pairs. The length of ribosomal DNA is not longer than 10^3 nucleotides. These examples suggests that the basic program modules correspond to p-adic length scales between $L(139)$ and $L(157)$ and that introns and genes are built as fractal versions of the basic program modules possibly present in all plants and animals. The basic programs are chemically identical. They could however have wormhole contacts to increasingly larger space-time sheets so that organism possesses fractal like structural hierarchy. Alternatively, the contacts are on space-time sheets with same p in all animals but the sizes of the join along boundaries/flux tube condensates formed by fundamental expression domains depend on organism. The frequent occurrence of Hox genes in the genetic code of body parts of various sizes in the entire animal kingdom is consistent with both options.

3.6 Ideas About Concrete Realization Of Genetic Programs

In this section some ideas about concrete realization of genetic programs are discussed. The ideas derive from the first years of TGD inspired quantum biology and it would be interesting to see how the systematic application of recent understanding of TGD could enrichen the picture.

3.6.1 How Gene Expression Is Regulated?

In case of prokaryotes the regulation of transcription is quite satisfactorily understood. The problem is to understand how transcription is regulated in case of the eukaryotes and here the notion of many-sheeted DNA could be crucial.

Operon theory for the regulation of gene expression in prokaryotes

Jacob, Monod and Pardee [I14] suggested operon theory for the regulation of the transcription of genes responsible for lactose production in E. coli. The presence of lactose induces E. coli to produce 3 enzymes needed in the production of lactose. The enzymes correspond to three structure genes x, y, z of lactose. The mechanism is following.

1. So called i gene regulates the production of the building block proteins of the repressor protein which self-assembles as tetramer of the repressor protein.

2. Repressor protein binds to a specific site next to the promotor and hinders the binding of the RNA polymerase so that transcription becomes impossible.

3. Inductor, in the present case lactose, binds to the repressor protein and hence hinders the formation of the repressor tetrameres so that transcription becomes possible.

4. The transcript contains not only the gene but also the entire operon so that several genes are translated simultaneously.

How eukaryotes differ from prokaryotes?

Operon theory does not generalize as such to eukaryotes. Although the notion of the promoter generalizes, there is no clear-cut evidence for operons [I14]. Rather, silencers and enhancers could take the role of the inducers and repressors in the eukaryotic gene expression. The action of a silencer/enhancer is not sensitive to its precise location or orientation and the distance from promoter can be more than thousand nucleotide pairs. TGD based explanation is based on the notions of many-sheeted DNA and protein. Silencers and enhancers mediate the interaction of the atomic space-time sheet of DNA with the classical fields of some larger space-time sheet. This interaction makes possible top-bottom type control analogous to the control of slave by master in Haken's theory of self-organization. Both classical em and Z^0 fields can control the gene expression in this manner. In eukaryotes classical Z^0 fields could have especially important role. Classical Z^0 fields are believed to be crucial for the model of cognition and this suggests that "mind-matter" interaction could at least partially relay on classical Z^0 fields and enhancers/silencers. Silencers and enhancers could make also possible Josephson junctions between gene space-time sheet and some larger space-time sheet and thus realize "biofeedback".

Second difference is related to introns. It is known that introns and exons can change their roles and it is known that there are several pathways for splicing leading to different proteins, isoforms. The replacement of single-valued gene→ polypeptide map with many-valued map obviously increases the information content of gene. The interpretation of introns and exons as two interspersed computer codes with intron lines of code separated from exons by "comment signs" marking each nucleotide of intron is attractive model for the situation. Dropping of some comment signs changes the result of the splicing process. Comment sign distribution could be dynamical and tissue specific so that one could say that genome is not invariant of species but only of a particular tissue type. This obviously reduces the genetic determinism and gives organism better abilities to survive. In human genome 1 percent of gene corresponds to exons in the "normal" state (in whatever manner that state is defined). The number of various combinations of exon and intron combinations is 2^N where N denotes the numbers of basic components of gene (perhaps coding proteins having no decomposition to modular proteins). The number of combinations increases exponentially with N and provides huge flexibility.

The interpretation of various exon-intron decompositions as statements of Boolean algebra of statements about N basic statements suggests strongly itself. In particular, exonic and intronic proteins for same intron-exon decomposition would naturally correspond to a statement and its negation. Thus one could regard eukaryotes as representing higher levels in the hierarchy of abstractions in which prokaryotes represent the lowest level. Eukaryotic genome would be a collection of genes identifiable as Boolean algebras and the running of the genetic program would mean that at given moment some statement in some of these Boolean algebras is experienced to be true. This kind of identification would mean effectively understanding of the logical meaning of the genetic code. The dominance of particular exon-intron decomposition over its complement would simply mean that this Boolean statement is true while its complement is not true. This suggests the possibility that only those 2^{N-1} exon-intron configuration which represent statements consistent with a given atomic statement are usually realized (atomic statement corresponds to a one-element subset in the set theoretic representation of Boolean algebra).

The fact that introns and exons are set theoretical complements of each other raises the possibility that the proteins coded by introns and exons have opposite effects as transcription factors. For instance, exons could code enhancer and introns could code silencer. This implies that same gene can act as both enhancer and silencer. The only thing needed is that the roles of introns and exons are changed. When this occurs, the production of intron-RNA complexes begins and the production of the composite protein coded by introns acting as exons stops. When the

production of silencer protein coded by introns ceases, the silencer proteins associated with the operator sites gradually decay and gene expression also enhanced by enhancer proteins can start. Thus the activation of the gene module activates automatically the gene modules which it calls and genetic program runs.

This would suggests rather general mechanism of gene expression.

1. There exists 2^{N-1} exon-intron decomposition plus their complements. Depending on the state of gene with given exon-intron decomposition, exons or introns are translated to protein. Both introns and exons represent statements. The modular decomposition of protein to subproteins often represented by the decomposition to exons corresponds to the decomposition of the statement E to $E = E_1\&E_2...\&E_n$. Same holds true for I: $I = I_1\&I_2...\&I_n$.

2. The proteins coded usually by exons activate some genes and these proteins appear as prerequisites of type

$$IF\ [E_1\ OR\ E_2 \cdots\ OR\ E_n]\ THEN \cdots\ .$$

   The presence of all activators is not necessary.

3. Introns correspond to repressors quite generally. The proteins coded by introns in the "abnormal" state of the gene correspond to prerequisites of type

$$\cdots IF\,[NOT(I_1)\&NOT(I_2)...\&NOT(I_n)]\ THEN \cdots\ .$$

   This means that the absence of all repressors from operator site is necessary. The general form of gene statement is

$$IF\ [E_1\ OR\ E_2 \cdots\ OR\ E_n]\,\&IF\,[NOT(I_1)\&NOT(I_2)...\&NOT(I_n)]\ THEN \cdots\ .$$

   Various E_k: s and I_k: s represent proteins in turn having modular decomposition to a product of more primitive statements.

The role of the hierarchy of Josephson currents

The control– and coordination hierarchy formed by super conductors represented by space-time sheets coupled to each other by join along boundaries bonds suggests new quantum level control mechanisms for genetic expression. Josephson currents at resonant frequencies corresponding to some magnetic transition of gene or its substructure could "wake-up" the gene self and initiate the self-organization process leading to the gene activity. Silencers and enhancers could correspond to proteins which have join along boundaries bonds/flux tube contacts to larger space-time sheets serving as masters. This would explain why neither the exact position nor orientation of the silencer or enhancer is not important for their functioning.

Various genesandassociated control structures have mutual Josephson junctions controlling gene expression. This would mean the presence of extremely weak longitudinal electromagnetic fields (the potential differences over Josephson junctions would be in 10^{-14} eV range). The control mechanisms behind morphogenesis are poorly understood and phase gradients along chromosomes and along the growing organism could be involved with the control of morphogenesis. The fact that the rate of the translation process is about 20 amino-acids per seconds is in accordance with the idea that this process is controlled by a Josephson current associated with some ion having this frequency.

3.6.2 Model For The Physical Distinction Between Exons And Introns

Introns seem to begin with nucleotide pair CT and end with pair TC: the assumption that this is the sole signature of the beginning of intron is however not consistent with the observation about the change of the roles of intron and exons. Furthermore, this criterion is obviously not sufficient for telling where intron begins and ends since also ordinary genes can contain similar section.

There are several constraints on the marking telling whether a given nucleotide is exon or intron.

1. The splicing mechanism or DNA telling which portions of it are transcribed to mRNA should rely on the marking mechanism. This requires that the enzymes responsible for the splicing are able to distinguish between introns and exons.

2. Introns can start and end in the middle of DNA triplet. This suggests that the marking is assigned with each nucleotide separately rather than each codon.

3. Both intronic and exon portions of DNA are transcribed to mRNA and splicing of the intronic portions of mRNA occurs only after that. Therefore the total length of the exon portions of DNA corresponding to a given gene must correspond to integer multiple of codons and there must exist some mechanism forcing this. The length of the intronic portions seems to be free.

4. The transformations of exons and introns to each other are known to occur. Tere must exist a physical mechanism changing the marking.

Could magnetic flux tubes serving as braid strands distinguish between introns and exons?

A priori one can imagine an endless number of possibilities for the physical realization of the binary digit distinguishing between exon and intron nucleotide. The vision about DNA as topological quantum computer with flux tubes connecting introns to the lipids of nuclear and cell membranes (not necessarily those of same nucleus or cell) acting as braid strands would realize this distinction naturally: the introduction of the connecting flux tube would transform exon an intron. Reconnection of pairs of flux tubes between DNA nucleotides or codons and lipids would allow to effectively eliminate the braid strands and transform pair of introns to exons. The first guess would be that the presence of braid strand could make it impossible to perform transcription. This is not the case: both intronic and exon portions are transcribed to mRNA and slicing process cuts off the intronic portions of mRNA after that.

1. The original model of DNA as topological quantum computer [K3] assigns to the nucleotides A, T, C, G quarks u and d and antiquarks $\overline{u}$ and $\overline{d}$. This model has intriguing properties: for instance, matter-antimatter asymmetry would have representation at the level of genetic code. This representation is consistent with the fact that the intron-exon boundary can occur in the middle of the codon.

2. An alternative highly attractive option is inspired by the notion of dark DNA [L2, K31]. The model for dark proton predicts under rather general assumptions that the states of dark proton correspond to those of DNA, RNA, tRNA, amino-acids. The model also predicts vertebrate genetic code correctly. This leads to quite far reaching vision about the role of dark nuclear physics in biology and evolution. Dark proton consists of three quarks (uud) but since the quarks are entangled one cannot assign a decomposition to counterparts of nucleotides to the dark proton.

   The observation of Hu and Wu [J12] related to the magnetic properties of cell membrane inspire the proposal that the dark proton sequences representing DNA sequences are associated with the lipid layers of the cell membrane as analog of double DNA strand [K12]. Unfortunately this identification is not consistent with the finding that exon-intron distinction is defined at the level of nucleotides rather than codons.

Can one save the latter option, and could both options be mutually consistent? In many-sheeted space-time nucleotides and codons naturally correspond to different space-time sheets being analogous to quark and hadron space-time sheets. Hence the two models could be consistent.

What distinguishes between the lipids to which nucleotides and codons connect? Do codons connect to sequences of three lipids such that each of them connects to nucleotide of the codon? Or do nucleotides connect to the lipids of the nuclear membrane and codons to the lipids of the cell membrane. The latter option looks rather elegant and would also provide an answer to the

question "Nuclear or cell membranes or both?". Note that one can also consider memetic codons realised as sequences of 21 DNA codons connected by flux tubes to sequences of 21 dark protons as even higher level structures. This kind of flux tubes could connect DNAs of nuclei of different cells.

What forces exons and introns to contain integer multiple of 3 nucleotides?

What could be the physical mechanism forcing the total length of the exonic and intronic sections to be integer multiples of codons?

1. A possible mechanism is based on the existence of a phase gradient along the DNA sequence such that the increments of the phase Φ for exons of a given gene would sum up to an integer multiple of $\Delta\Phi_{tot} = n2\pi$. For intronic portions the phase gradient could vanish- The phase gradient could correspond to the phase difference associated with the weakly coupled super conductors formed by the two DNA strands or the phases of the supra currents flowing in DNA strands.

   Phase gradient is naturally accompanied by an electric field and electric fields parallel to linear molecules appear frequently in biology: DC currents of Beck indeed require the existence of electric voltage along linear structure in question [L15]. Thus flux tubes would carry both electric and magnetic fields for exon portions and could be purely magnetic for intron portions.

   This mechanism allows a variant for which only exon portions are accompanied by magnetic flux tubes carrying also electric field.

2. The phase gradient must be transferred also to mRNA and splicing mechanism must detect its presence in order to cut away the portions of mRNA for which the phase gradient vanishes. This would mean that also flux tubes marking gene portions must be transcribed.

3. An attractive possibility is that the phase gradient is related with the helical structure of DNA double helix: the minimum number of DNA triplets giving rise to a multiple of 2π rotation of the helix is 10 and corresponds to the p-adic length scale $L(151)$ defining the thickness of the cell membrane. The helix can be characterized by the tangent vector of helix having axial and azimutal components:

$$K = (1, \frac{d\phi}{dz}) = (1, 10 \times 2\pi) \times \frac{1}{L(151)} \quad .$$

   The phase gradient would be naturally a multiple of this vector

$$\frac{d\Phi}{dz} = nK \quad .$$

   For $n = 10$ the increase of Φ would be 2π per single DNA triplet. For $n = 1$, $n = 2$, $n = 5$ and $n = 10$ the allowed lengths would come in multiples of periods 10, 5 and 2 and 1 DNA triplets respectively. Note that 5 triplets corresponds to the p-adic length scale $L(149)$ associated with the lipid layer of the cell membrane. The presence of this gradient would naturally define the splitting of the nucleotide sequence to DNA triplets and might be important in the dynamics of DNA translation and transcription.

Are the properties of the introns consistent with the proposed model?

The proposed interpretation of introns is consistent with the basic facts about them.

1. It has been found that the precise positions of introns in gene do not seem to affect the gene expression. Introns can start in the middle of protein building block or even in the middle of codeword.

   The content of intron DNA does not correlate with the content of protein DNA. This is just what the model predicts. Introns are known to wander around genome and between cells. One could interpret their presence as some kind of experimentation with small modifications

of the quantum software. The addition of intronic section to the gene does not in general have any dramatic consequences as far as gene expression is considered. If DNA acts as topological quantum computer, the addition of intronic portion would be like addition of software to a computer: a topological quantum computer program defined by the braiding assignable to the intronic section of DNA.

An interesting question is how much intron distribution affects genetic during the evolution of individual and how large the differences between members of species are.

2. In the proposed picture the evolutionary step leading from prokaryotes to eukaryotes was the emergence of the introns and gene programs having also intronic mRNA as output. This was perhaps necessitated by the emergence of the cell nucleus since introns were needed as input by the genetic program transferring mRNA out of nucleus. The emergence of the cell nucleus as $L(163)$ structure could in principle have occurred already for a cell of size $L(k) = 167$. It seems that in cells of animals the size of the nucleus corresponds to $L(163)$ or perhaps even $L(167)$. Cell nucleus is however not all that is needed for the emergence of introns: the model requires the presence of $k = 169$ level in the hierarchy.

3. What is beautiful is that homing [I30] and retrohoming [I17] phenomena can be regarded as modification of the genetic program in a way which is automatically internally consistent! The addition of intron does not spoil the running of the genetic program. One can quite well consider the possibility that organisms are continually experimenting with various modifications of genetic program. It might even be that homing and retrohoming phenomena make possible the evolution of the genetic program during the lifetime of individual.

If the entire mRNA corresponds to intronic portion of DNA, it remains inside nucleus. These DNA sequences might appear in cells and the mRNA in question could be seen as a remnant of RNA era. Part of silent DNA could correspond to purely intronic genes.

1. Histones form the basic protein building block of chromosomes. Histone genes are known to contain no introns. The interpretation is that the gene coding histone is in exon state permanently. If histone genes contained intron parts, histones could act as repressor genes and regulate gene activity. Since histones appear as building block proteins of nucleosomes of chromosomes, this would mean that the programs of operating system would depend on the quantum software defined by introns: obviously a highly undesired situation. Also interferons are known to have no introns. The explanation might be similar. This could explain also why the DNA of mitochondria contains no introns.

2. It is known that the pseudogenes obtained by splitting the introns are not active. For instance, the noncoding RNA and mRNA coded by gene is not translated and is left inside the nucleus. The simplest interpretation is that intronic portions define topological quantum computer programs need to carry out mRNA and transfer it from the nucleus. This interpretation would suggest that the TQC: s defined by the flux tubes connecting nucleotides to nuclear membrane are responsible for this. The TQC: s responsible for transferring molecules through the cell membrane would involves braids connecting DNA and cell membrane. The hierarchy could continue to multicellular level. In this picture the braid strands would also serve as molecular highways along which the transfer would take place.

3.6.3 The Phenomenon Of Superimposed Genes

Before the discovery of the structure of the genome of $\phi X174$, it was thought that the Central Dogma is absolute truth. It has however turned out that genes within genes and even overlapping genes are possible [I14]. Bacteriophage $\phi X174$, which is virus with single stranded circular DNA, contains two genes, denoted by A and D, containing genes B and E within them. A gene contains also gene A^* which starts in the middle of A and ends in the same codeword. Also the translation of a gene overlapping with A and gene C next to it have been observed in G4 bacteriophage having genome very similar to that of $\phi X174$.

To understand how the translation of mRNA can give rise to genes inside genes, one is forced to introduce the notion of reading frame shift. This concept is somewhat ad hoc since it requires

that the translation of a gene within gene does not obey the usual rules since reading is stopped without stopping sign.

The geometric realization of the subprogram structure might make possible to understand gene superimposition.

1. Geometrically gene would be a linear model for its expression domain obtained by thinning it to DNA thread. Two subsequent genes G_1 and G_2 are like two subsequent body parts. If gene superposition occurs, there is third body part having overlap with both and "glued" to both: kind of joint connecting two body parts.

2. In computer analogy these "body parts" correspond would represent subprograms. Transcription generates protein which refers to some other program module realized as "body part". If the requirement that each "body part" generates program call to existing "body part", is satisfied, then gene superimposition is possible. This requirement is actually very natural consistency condition. That our body is full of this kind of joints would suggest that gene superposition is a general phenomenon.

A concrete model is obtained in terms of many-sheeted DNA and many-sheeted versions of various RNAs. As a matter of fact, the notion of many-sheeted DNA conforms with what the picture based on the notion of magnetic body having hierarchical structure with flux quanta inside flux quanta and flux sheets traversing through sub-units of DNA sequence, suggests.

3.6.4 Possible Explanations Of The Silent DNA

Genome contains large amounts of silent DNA which is not transcribed. One can consider several explanations of silent DNA in TGD framework.

1. Each gene consists of a transcribed part and control part contained in region between gene and its precedessor. It might be that highly repetitive DNA located near the centromere corresponds actually to a control part of DNA and is therefore not transcribed. Enhancers and silencers could be in question and they could have contacts to larger space-time sheets and take care of the control in long length scale enhancing or silencing a large number of genes simultaneously.

2. Genome can be regarded as a large collection of program modules calling each other. Large programs typically contain a great number of modules not used by the average user. There is also a larger number of program modules whose output is not visible to the user. Silent DNA could correspond to program modules of this kind. The counterpart of unused program modules are genes which are permanently repressed. This kind of permanent repression certainly occurs during differentiation and most of DNA in given part of organism is this kind of DNA.

3. Silent DNA could also correspond to purely intronic genes which correspond to dead ends of the genetic program and are decoupled from genetic program by selection.

4. The most radical possibility is that silent DNA corresponds to genes which are expressed non-chemically and corresponding control regions affected by non-chemical transcription factors. A possible test for the existence of non-chemical gene expression is to modify the silent part of, say, neural genome and find whether and how this affects the behavior of the organism.

5. The vision about DNA as topological quantum computer [K3] had not emerged as I wrote the above list for the first time. This vision would identify silent DNA as part of software whereas genes in this framework could be seen as hardware. What makes this option especially attractive is that the detailed nucleotide composition of the DNA strand is not crucial for the functioning of the TQC program: what matters mostly is the braiding of the flux tubes connecting nucleotides/codons to lipids. The nucleotide decomposition brings only effective coloring of the braid strands which causes additional delicate effects. Therefore the braidings associated with the repetitive structures suggesting strongly the interpretation as "junk" can quite well serve as TQC programs.

3.6.5 About Genetic Evolution

The proposed general model of genetic program provides nontrivial insights to evolution of genome.

ORP and the structure of the genetic program

An interesting question is whether "ontogeny recapitulates phylogeny" principle in its original form (to be distinguished by its TGD based analog applying much more generally) could give nontrivial constraints on the structure of the genetic program.

1. One could argue that the structure of the genetic program must reflect its evolution. In the beginning of development only the lowest level genes are activated and in turn activate more evolved genes which in turn $\cdots$. The gradual emergence of new hierarchy levels would have interpretation as emergence of new abstraction levels: statements about statements about... are formed. These levels correspond to emergence of higher level selves having more abstracted experiences about the state of organism or its organs. Geometrically the new levels would correspond to the appearance of new space-time sheets in the hierarchy of space-time sheets assignable to the magnetic body of the genome.

2. One can also defend quite different point of view. The evolution starts from simple main program corresponding to, say the length scale of a fertilized egg. Gradually subprograms corresponding to the emergence of smaller length scale structures are activated. In growth stage simple replication of the basic structure together with the activation of the lower level programs giving rise to differentiation occurs. This leads to join along boundaries/flux tube condensates of the fundamental expression domains having some finite size determined by the metabolic resources available and by self-organization. In fact, the general structure of embryogenesis supports this view whereas evolution of more complex organisms supports the first option.

3. Option 2) suggests that genetic program modules call only modules associated with shorter length scales so that higher levels cannot be activated by program call. If this is the case new levels should emerge when some space-time sheet associated with DNA expands in phase transition like manner and fuses with corresponding space-time sheets associated with neighboring cells. These phase transitions would represent the self-organization aspect of development.

4. Cell differentiation could be understood as resulting from the branching of genetic program in position dependent manner caused by diffusion gradients of transcription factors. For instance, these transcription factors would correspond to hormones which bind to receptors to form a complex binding to gene.

Homeostasis, loops, tautologies

If P then P is the simplest loop one can imagine and corresponds to a gene coding protein activating the gene itself. Biologically this represents endless cancer like growth limited only by lifetime of protein and resources and hence possible breakdown of the system! More complicated statement structures of this type represent n-fold tautologies: *If* P_1 *then* P_2 , *If* P_2 *then* P_3 , ..., *If* P_n *then* P_1 . These systems are also self-amplifying and correspond to a cyclic reaction in which genes code enzymes activating other genes in the cycle.

This kind of cycles might be involved with the very early evolution of life. For instance, DNA-RNA-protein trinity might have developed from a situation in which RNA coded protein which catalyzed both the reverse transcription of RNA to DNA and transcription of DNA to RNA. Thus simplest life form would have represented tautology *If P then P* ! Reverse transcription such that the reverse transcriptase also catalyzes transcription is indeed known to occur. Certain plant viruses contain inverse transcriptase synthetizing in infected cell DNA from its RNA and then DNA complementary to this. This double strand joins to the genome of the host cell and duplicates itself.

Animal	Man	Chimpanzee	Cow	Dog	Cat
N_c	23	24	30	39	19
Animal	Horse	Rat	Rabbit	Alligator	Frog
N_c	32	21	22	16	13
Animal	House fly	Fruit fly	Honeybee	Flatworm	Harpalinae
N_c	6	4	16	8	$18+x$

Table 3.4: Chromosome numbers for some species.

More complicated cycles involving several equivalent statements would have evolved gradually (note the parallel with the generation of mathematical theorems stating equivalence of statements!). Bacteria replicate endlessly and might perhaps be regarded as example of life form which corresponds to n-fold tautology.

The role of chromosomes

An interesting question is whether the organization of the genome to chromosomes could have some deeper organizational meaning. The fact that chromosome fusions and splittings are possible, suggests that chromosomes as a whole cannot have direct identification in terms of any body structure. Indeed, the realization of genetic program in terms of protein concentrations representing inputs and outputs of genes interpreted as subprograms is very flexible as far as the location of gene subprograms is considered. Only genes which form larger program structures should form geometrically connected units and the relative locations of these units could be rather free. As already found, genes seem indeed form clear geometrical subunits.

Chromosomes could be identified as a set of mutually interacting parallelly running genetic programs. One can of course consider the possibility that chromosomes mean the composition of body part to N_c linear structures, N_c being the number of chromosome pairs. Parallel interacting processing would bind these structures to single coherent hole. This division to N_c parts should be detectable at all levels of body organization. One can also consider the possibility is that the structure of chromosome parallels the structure of body and that centrosome corresponds in some sense to the brains of chromosome and the branches of chromosome correspond to right and left halves of the body. Genetic programs associated with different chromosomes are known to run in very precise synchrony. Many -sheeted DNA could explain this synchrony naturally as resulting from the interaction of genes with with classical em fields with space-time sheet containing the chromosomes.

Table 3.4 gives chromosome numbers for some animals. For the home fly the number of chromosome pairs is 6 whereas the number of the p-adic hierarchy levels determined by the size of the home fly is 12. For fruit fly the number of chromosome pairs is 4. Horse has 32 pairs of chromosomes and dog has 39 pairs of chromosomes whereas Homo sapiens has 23 chromosomes. The large number of chromosomes can be understand as a way to produce large number of outcomes in breeding. The number of possible combinations of chromosomes in sexual breeding is 2^{N_c}, 2^{16} more than in case of Homo Sapiens. There are indeed very many different looking dogs barking around! The number of chromosomes varies wildly. For instance, the number of chromosomes in Harpalinae is $18+x$ [I4]! The size of this insect is about one centimeter.

The natural expectation is that the size of chromosomes has gradually grown during evolution when new p-adic space-time sheets have emerged. This process could correspond to insertion of introns to the basic DNA. The possibility coming first in mind is that the value of k_G in genes of given chromosome tends to increase as a function of the distance from the second end of gene. Genetic program realized in terms of many-sheeted space-time concept does not however require this. The genes involved in the coding the structure of given body part are known to be linearly arranged according to the structure of body part itself. This is certainly consistent with TGD picture in which body parts grow from space-time sheets associated with DNA. It seems that the highest activated space-time sheets in genes must correspond to brain, in particular frontal lobes,

in case of human. This would suggest that also in chromosome the largest active length scales correspond to the region around centrosome.

p-Adic evolution of DNA

p-Adic evolution should involve two aspects.

1. The increase of the p-adic length scale characterizing the basic DNA modules. This suggest the classification of the basic building blocks of the genome by the p-adic length scale associated with the corresponding DNA sequences.

2. The fractal evolution involving emergence of longer p-adic length scales characterizing the size of the space-time sheets to which basic DNA sequences had # contacts. Thus the lengths of introns and exons are not expected to correlate with the p-adic scale of the space-time sheet to which they possibly have # contacts. Rather, same gene can have # contacts to arbitrarily large space-time sheets.

Consider first the critical lengths of the basic program modules. The lengths $L(149), L(151), L(157), ...$ of gene or DNA sequence might mean the emergence of something genuinely new in the evolution. This length scale hierarchy expressed in terms of $L(137)$ comes in powers of 2 as $N_{137} = 1, 2, 64, 128, 2^{10}, 2^{13}, 2^{15}, ...$

Single nucleotide pair corresponds to in double helix to distance of .34 nanometers which is larger than the length scale of $L(139)$. The structure of the double helix is such that there is a periodicity of 3.4 nanometers: this means that basic period corresponds to 10 nucleotides. This implies that 5 DNA triplets correspond to a length of 5.05 nanometers, which equals to p-adic length scale $L(149)$ if $L(151)$ is defined to be $L(151) = 10.2$ nm. $L(149)$ corresponds to the thickness of the lipid layer of cell membrane and $L(151)$ corresponds to 10 DNA triplets, to the thickness of the cell membrane and the basic period of DNA sequence when DNA triplet is regarded as a basic unit. Perhaps this periodicity is not accident but has deeper meaning possibly related to the periodicity of phase variable associated with DNA. The lengths of DNA sequences corresponding to p-adic length scale $L(k)$, $p \simeq k$, k power of prime are $N(DNA) = 2^{k-149} \times 5$ DNA triplets.

This means that the critical numbers of DNA triplets possible leading to the emergence of qualitatively new properties of organism are given by

$$\begin{aligned} N(DNA) &= 2^{(k-149)/2} \times 5 \ , \\ k &\in \{149, 151, 157, 163, 167, 169, 174, 179, 181, 191, 193, ..\} \end{aligned} \tag{3.6.1}$$

The few lowest critical values of DNA triplets in gene are

$$N(DNA) = n \times 5 \ ,$$
$$n = 1, 2, 2^4 = 16, 2^7 = 128, 2^9 = 512, 2^{10} = 1024, 2^{12}, 2^{15}, 2^{16}, \cdots$$

The steps of this hierarchy resembles bring in mind the evolution for the length of the basic memory unit of computer memory! One must however notice that 5 DNA triplets seems to serve as a basic unit.

The emergence of new p-adic length scales could have meant emergence of new levels of modularization in the genetic program and it is interesting to look these numbers from this point of view.

1. One could think that short sequences of precursors of DNA, mRNA and tRNA molecules were generated spontaneously by self-assemly. This implied automatically the generation of amino-acids by the more primitive counterparts of transcription and translation processes. The lengths of DNA molecules began gradually grow and at the critical lengths of DNA corresponding to p-adic length scales dramatic new effects emerged. Also new space-time sheets emerged in the genome and the first guess is that this occurred for the critical sizes of the organism given by p-adic length scales.

2. Formation of lipid layers might have been the revolution occurring at this stage and since lipids should have had size of order $L(149)$. This revolution should have occurred when the length of the genome became longer than 5 DNA triplets and meant formation of lipid layers by self organization process known to occur in all liquid crystals: these layers were perhaps formed in the surface of water such that hydrophobic ends of proteins would have pointed out of water. Self organization presumably led simultaneously to the formation of double membranes having thickness $L(151)$ such that the hydrophobic ends of proteins pointed in the interior of the double membrane. Second revolution became possible when the number of DNA triplets became larger than 10 triplets so that proteins connecting cell interior of the double membrane to its exterior became possible and the control of ion concentrations became in principle possible. Transfer RNA (tRNA) has length of at most 27 triplets. Third revolution should have occurred $L(157)$, which corresponds to 80 triplets.

3. Smallest viruses possessing single strand of DNA have lengths between 15-100 nanometers and this suggest that genome correspond to p-adic length scales $L(149)$, $L(151)$ and $L(157)$. These length scales could characterize largest space-time sheets also present in genome. The building blocks of the envelope of viruses are genetically coded separately and self-assemble spontaneously so that only building blocks need to be coded. Therefore p-adic prime associated with the genome of virus could be smaller than that determined by the size of the virus. Viruses with two DNA strands have sizes between $250 - 1000$ nanometers. This suggest that the emergence of $k = 163$ length scale in the genome of virus was accompanied by the emergence of double stranded DNA. $k = 163$ is perhaps the largest p-adic length scale associated with virus genome.

4. Bacteria have typically sizes of $1 - 10$ micro-meters. This suggests that $k = 163, 167, 169$ are the possible space-time sheets associated with the bacterial genome. The emergence of $k = 169$ could have meant the emergence of multicellulars and generation of epithelial sheet like structure consisting of two cell layers as well as emergence of introns and DNA cognition.

Consider now the typical lengths for the structures of the eukaryotic genome.

1. The presence of introns means that the length of a gene coding given protein plus introns is much longer than the DNA coding only the protein. The higher the evolutionary level of species, the larger the fraction of introns. For human genome the fraction of exons is roughly 1 per cent. The typical length of hnRNA in nucleus is 6.000-8.000 np (nucleotide pairs) which corresponds to 18 micro-meters and length scale $L(163)$ and $L(167)$. Even genes with length 20.000 np are possible and correspond to $L(169)$. The lengths of mRNA vary between 500-3.000 nucleotides corresponding to interval 1.7×10^{-7}-10^{-6} meters and length scales $L(157)$ and $L(163)$. RNA sequences coding typical protein consisting of roughly 300 amino acids are about 3×10^{-7} meters and correspond to $L(159)$.

2. Most of the highly repetitive DNA has rather short length between $5 - 300$ nucleotides. Introns having typically lengths between $10 - 1000$ nucleotide pairs. The length of ribosomal DNA is not longer than 10^3 nucleotides. These examples suggests that the basic program modules correspond to p-adic length scales between $L(139)$ and $L(157)$ and that introns and genes are built as fractal versions of the basic program modules possibly present in all plants and animals. The basic programs are chemically identical. They could however have wormhole contacts to increasingly larger space-time sheets so that organism possesses fractal like structural hierarchy. Alternatively, the contacts are on space-time sheets with same p in all animals but the sizes of the join along boundaries/flux tube condensates formed by fundamental expression domains depend on organism. The frequent occurrence of Hox genes in the genetic code of body parts of various sizes in the entire animal kingdom is consistent with both options.

3.7 TGD Inspired Ideas About The Regulation Of Morphogenesis

The understanding of morphogenesis provides a challenge for the TGD inspired notion of the many-sheeted DNA. The difficult task is to separate chemistry from geometry and identify those features of morphogenesis necessitating the concept of the many-sheeted DNA. Also the role of quantum control mechanisms must be understood. In the sequel general ideas about the quantum control of morphogenesis are discussed and a very brief review about the morphogenesis in Drosophila is given to provide bird's eye of view about genetic control. Also Hox genes and TGD based model for Hox genes is discussed.

3.7.1 Biological Alarm Clocks And Morphogenesis

Gene expression is known to involve non-chemical transcription factors (enhancers silencers), whose underlying interaction mechanism is not not known. TGD suggest an extremely general mechanism of quantum control and coordination based on Josephson currents flowing between space-time sheets representing various levels of the biological self-hierarchy [K52, K51]. Josephson currents themselves act as clocks. In case that the potential difference over Josephson junction corresponds to the difference of the energies for the states of charge carriers localized inside either super conductor, Josephson current "wakes-up" "clock self" and initiates self-organization process. Therefore alarm clock is in question. Besides clocks and alarm clocks one can build pattern recognizers and novelty detectors and these circuits could serve as building bricks of complicated Boolean circuits controlling the functioning of living systems and also morphogenesis. Potential differences between gene space-time sheets and some larger space-time sheets, such as growing organs serving as the controllers of the gene expresion, would act as transcription factors in the sense that suitable input supra-current would "wake-up" gene self and activate self-organization process leading to gene expression.

Some examples are in order to show that this idea might have relevance.

1. The replication of the cell is an extremely complicated process but could be understood as quantum self-organization process leading to final state patter which only very mildly depends on the initial state. This process must be initiated by a "wake-up" self representing perhaps the cell. The alarm clocks must now be contained to the membrane surrounding the cell nucleus and probably also to the cell membrane since the cell membrane is known to be coupled to the division process of the cell nucleus, too [I43]. The reference currents are generated, when the new cell is born. The process leading to the replication of the cell involves a reduction in the density of super conducting charge carriers in the critical region and this could initiate the replication of the cell. This is achieved if Josephson currents run away from certain region of the membrane of the cell nucleus implying depletion of charge carriers.

2. The generation of completely new spatial structures during the morphogenesis is second extremely complicated process which should be understandable in terms of quantum self-organization. An example is afforded by the generation of somites [A7], which later give rise to brain and spinal cord. The homogenous longitudinal cell mass divides in a phase transition like manner into somites with clock wise regularity and the number of the somites is a constant characteristic for the species in question [A7]. The catastrophe theoretic models proposed in [A7] are based on the assumption that the pulse triggering the formation of somites is coupled to a biological clock, so that the motion of the boundary between differentiated and undifferentiated cell mass alternately slows down or fastens up and implies the generation of discrete regions, where the formation of the somites takes place.

A qualitative TGD based description is provided by the alarm clock model:

1. There is certain biorhythm realized using Josephson junctions (rhythms (minute scale) of this kind have indeed been identified [A7]) at cell level.

2. Josephson currents flow between the cells belonging to the longitudinal cell mass and neighboring cells in transversal direction. Due to the presence of the cell level reference currents,

Josephson currents interfere destructively and variations in density of charge carriers are small.

3. There is slow dependence of the phase of the order parameter ψ along the linear cell mass implying a phase lag between the clocks.

4. Reference current dissipates gradually through phase slippages and when the time is ripe the amplitude of the Josephson current becomes large and makes the density of charge carriers small inside the longitudinal region. The formation of the somites begins since the stability criterion implies that the stable size of topological field quantum decreases.

5. Time regulation is achieved through the presence of the biological clock: nothing happens unless the phase of the clock is correct since Josephson current runs to a "wrong" direction.

6. The process begins from the cells, which were born first since the clocks associated with them were created first and propagates in the order, in which the cells were born. In fact, the spatial dependence of the phase of the order parameter might code this order. The spatial dependence of the phase means that the rate for the propagation of the somite formation varies with position and guarantees in this manner the formation of spatially separated structures (compare with clock wave front model of [A7]). The number of the somites is just the multiple of 2π: s that the phase of the order parameter increases along the longitudinal cell mass.

3.7.2 Could Vacuum Quantum Numbers Control Gene Expression Via Josephson Currents

Controlled and synchronized gene expression is the most fundamental aspect of morphogenesis and implies surprising determinism of the development. When developing organism achieves certain level of development, certain gene activates. This requires feedback mechanism from long length scales of size of order organ to the gene level. In standard physics, the most plausible mechanisms are chemical. Whether this is the case is an unanswered question yet. In any case, it is very difficult to imagine how chemical concentrations which carry purely local information, could code information about the size of the organ and how the evolution could have led to a chemical kinetics initiating gene expression for critical values of the various chemical concentrations. The notions of many-sheeted space-time and general hypothesis about bio-control and coordination based on a hierarchy of weakly coupled super conductors provides a fresh and more promising approach to this process. This hypothesis is discussed in detail in [K52, K51].

Many-sheeted space-time concept suggests hierarchies of biological alarm clocks whose ringing induces ringing of some clocks at a lower level of hierarchy so that finally the alarm clock waking-up and activating definite gene, rings. One mechanism causing the ringing would be a situation in which the potential difference associated with the Josephson junction becomes equal to the energy difference for states associated with either super conductor: cyclotron resonance, which seems to be crucial for brain functioning and EEG, is basic example of this. This could at DNA level lead to the activation of gene and start up of a self-organization process. One could imagine complicated circuits in which ringing would occur only provided all the required conditions are achieved.

The correlation of gene expression with the size of the growing organ could be achieved as follows. Topological field quanta are characterized by a handful of vacuum quantum numbers associated with the dependence of the phases of the two CP_2 complex coordinates ξ^i on space-time coordinates (Appendix). In particular, two frequency type quantum numbers emerges. If the potential difference corresponds to the difference of the vacuum frequencies ω_1 associated with the coupled super conductors and if ω_1 correlates with the size of the corresponding structures, the ringing of the clock occurs when the size difference is critical. If the first super conductor corresponds to some structure with a fixed size (say gene) and second super conductor corresponds to the growing organ, this mechanism could indeed initiate new kind of gene expression when the growing organ reaches critical size.

3.7.3 Early Morphogenesis Of Drosophila

During the last years the understanding about the regulation of morphogenesis has grown dramatically [I47, I50]. For instance, in case of Drosophila (fruit fly) surprisingly detailed knowledge about the regulatory cascade occurring during embryogenesis exists. It is known that genetic program with 6 hierarchy levels is in action.

1. The so called maternal factors act before the onset of cellularization and lead to the segmentation of embryo. This cascade begins with the diffusion of transcription products of maternal-effect (coordinate-) genes from the anterior and posterior poles of the embryo during oögenesis. These genes define anterior-posterior polarization.

2. Maternal factors control the spatial pattern for the transcription of gap genes which are expressed in domains along the anterior to posterior axis of the embryo. Gap genes divide embryo to anterior, middle and posterior parts.

3. Gap genes regulate each other and the next set of genes in the hierarchy, pair-rule genes. These are expressed in 7 stripes of cells corresponding to every other segment.

4. At the next level of hierarchy are segment polarity genes, many of which are expressed in 14 segmentally repeated stripes. Segment polarity genes include also proteins other than transcription factors (i.e. secreted signalling molecules, receptors, kinases, etc.) and they mediate interactions between cells.

5. During cellular phase (blastula) Hox genes controlling the formation of various body parts are expressed. The lowest level of the hierarchy is represented by tissue specific genes.

The expression domains of these genes are indeed two-dimensional slices in accordance with the idea that genes can be regarded as obtained by compressing the expression domain of gene to DNA thread. This principle might be realized quite generally in the sense that the expression domains of all genes expressed inside particular body part are also slices formed as join along boundaries/flux tube condensates of fundamental expression domains whose size corresponds to some p-adic length scale.

3.7.4 Hox Genes

The discovery of the universality of so called hox (homeo box) genes has been one of the great discoveries in genetics during last few years years [I47, I50]. Surprisingly, animal species with widely different morphologies (hydra, flies, leeches, mouses and humans) seem to obey very similar body plan coded by Hox genes. Hox genes contain highly conserved nucleotide sequence called homeobox coding protein consisting of 61 amino-acids (which corresponds to DNA length of about 61 nanometers which is slightly below $L(157)$). Hox genes are also known as "selector" genes because their expression within a region of the embryo causes its cells to select a particular route of morphogenetic development determined by detailed nucleotide content of Hox gene. Hox genes function by coding what are called transcription factor proteins: these proteins bind to and activate all downstream genes necessary for the production of, say leg. Hence Hox gene for leg functions like a main program for the development of leg. Obviously, Hox genes provide a possibility to test and develop TGD based ideas about the coding and decoding of the morphology in terms of the many-sheeted DNA.

3.7.5 Evolution Of Hox Genes

The conserved nature of the homeobox sequence indicates that all Hox genes are homologous, having arisen by divergence from a common ancestral gene. Note however that the control parts of genetic program (promoter and operator regions at which various activating and repressing proteins bind) involved with Hox genes seem to vary widely. Second basic feature of Hox genes is their clustering. The development of this clustering has been studied and it has been found that all animals species must have inherited their Hox genes from a common ancestor.

1. Already plants possess single homeobox unit in their Hox gene. Doubling of the hox gene meant the emergence of a primitive head-body structure and thus of primitive animals (hydra, which are freshwater polypes, represent one studied example). Next step was doubling of this gene pair, which lead to the formation of nematode worms. The further doublings lead gradually to more complicated animals. For instance, beetle possesses 8 Hox genes, amphioxus, which is almost vertebrate, has 12 Hox genes.

2. The next step in the evolution was the doubling of the entire chromosome containing Hox cluster. The next doubling led to vertebrates with four Hox clusters located in four chromosomes. Each cluster contains a subset of 13 nonhomologous Hox genes. These clusters are labelled as Hox-A, Hox-B, Hox-C, Hox-D. n: th gene in, say cluster A, is denoted by Hox-A-n, $n = 1, .., 13$. The homologous Hox genes in various chromosomes, Hox-A-n, ..., Hox-D-n, whose number is never larger than four, form 13 groups called prologues. The maximum number of Hox genes is 52 but some of genes are missing. Each vertebrate has its own Hox-bode telling which Hox genes are absent and which are not. For instance, human 39 Hox genes.

Doubling of Hox clusters led to a more flexible gene expression since the conditions associated with gene statements involve protein outputs from all four Hox clusters. For instance, the condition in genetic program could have the form *IF [Hox-A-n or Hox-B-n] then...* This implies that the mutation of Hox gene in single cluster, which otherwise might be lethal, need not have any dramatic consequences. Doubling of the Hox cluster leads also to a multiplication of possible Hox patterns in breeding by a factor of 4 and hence to the large variation of the progeny, which is selective advantage. It is known that doublings of Hox clusters where followed by an emergence of large number of Hox-codes and only some of these codes have survived.

The presence of 4 Hox clusters in vertebrates could relate to four different tissue types corresponding to epithelial, connective, muscular and nervous tissues. Certainly this correspondence is not simply tissue-type $\leftrightarrow$ Hox cluster although there is some evidence that given Hox cluster dominates the expression of given tissue type under normal circumstances. For animals with 2 or 1 Hox clusters this kind of correspondence cannot hold true.

3.7.6 Characteristic Features Of Hox Genes

The characteristic features related to the expression of Hox genes give clues as how many-sheeted DNA is expressed.

Posterior Hox genes dominate over anterior Hox genes

Posterior Hox genes dominate over more anterior genes. For instance, if posterior Hox gene is removed to more anterior position the phenotype is more posterior. A simple illustrative example is based on a toy model of insect based on 3 Hox genes. The protein product of the Hox 1 gene instructs the formation of the head. The cells in the middle of body respond to both Hox1 and Hox2 genes. The protein product of Hox gene 2 is however believed to instruct the cells in this region not to not respond to Hox gene 1 so that Hox 2 genes determine the resulting structure. In the similar manner Hox 3 gene dominates over Hox 1 and Hox 2 genes in the tail part of the fictitious insect. Actually this picture is oversimplified but gives a good grasp of the idea.

This corresponds to a simple recursive control structure in genetic program.
P(n-1): IF protein coded by n: th Hox gene is the highest Hox protein present then DO B(n) ELSE DO P(n+1).
B(n): Form the n: th body part.

The problem is to understand how this control structure is realized. If Hox gene corresponds to program B(n) and does not serve as repressor of lower level Hox gene expression then it would seem that control structure must involve some "new genetics".

1. Hox genes select genetic programs. The mechanism of selection is based on attachment of the protein products to the control regions of corresponding genes could be such that gene program n is activated only if Hox proteins Hox-m $m \leq n$ are attached to the gene program.

2. One possibility involving introns in essential manner is that the activation of n: th Hox gene deactivates lower level Hox genes automatically. One possibility is that activation corresponds to the change of roles of introns and exons in Hox gene. Before activation Hox-n gene would be in "abnormal" state so that its intron parts would code protein. This protein could enhance the expression of the lower level Hox genes. After the activation this protein product would be absent and lower level Hox expression would not be enhanced anymore.

Hox expression domains are co-linear with the gene ordering inside Hox cluster

The development of embryo occurs in anterior to posterior (head to tail) direction. In all species hitherto examined, there is a strict correspondence between the ordering of the Hox genes inside clusters and the anterior boundaries of the expression domains along the head-tail axis of the developing embryo. Presence of the anterior boundary means that gene is not expressed above this boundary. The anterior boundaries of homologous genes in different clusters are same.

Establishment of Hox gene expression patterns in vertebrates

It is known that in vertebrates Hox gene expression patterns in developing embryo are established by waves propagating in posterior-anterior direction (tail to head). This means that there is also temporal co-linearity. Wave proceeds and ultimately stops at the anterior boundary of the expression domain. These anterior boundaries are characteristics of Hox genes and their ordering is the same as the ordering of Hox genes.

It is known that this pattern is not due to a forward spreading of cells. The presence of chemical signalling during the wave propagation is also excluded by the result of an experiment in which embryo was transversally sectioned [I47]. What happened that the wave propagated through the sectioning. Of course, it could be that chemical concentration gradient has been formed in earlier stage of development.

3.7.7 TGD Based Model For Hox Genes

The attempt to understand the known facts about Hox genes and their expression provides strong constraints on the general TGD based model of many-sheeted DNA and the results might be generalized to build more general models of gene expression during morphogenesis.

Hox cluster as a set of many-sheeted Hox genes?

Hox genes define division of developing embryo to slices of roughly same size. This suggests strongly that the largest space-time sheets associated with Hox genes correspond to the same p-adic prime $p \simeq 2^k$, k prime or power of prime. It could be that Hox genes are glued on same space-time sheet to form Hox cluster. Dominance of the posterior genes over anterior genes and spatial and temporal co-linearity reflect some kind of hierarchical ordering of Hox genes. This hierarchical ordering does not however seem to reflect the hierarchy of space-time sheets but gene program hierarchy.

Does activation of Hox gene involve a phase transition?

In vertebrates the activation of Hox genes occurs as a wave propagating from tail to head. A possible TGD based identification for the wave is as a phase transition leading to an expansion of a new space-time sheet associated with the many-sheeted Hox gene propagating in head to tail direction. This phase transition is determined solely by the internal state of the genome in given embryonic cell. In this phase transition the DNA space-time sheets would expand and join to form larger space-time sheet determining the size of the "imaginary disk" associated with the organ in question.

In Drosophila the length of DNA per single Hox gene plus its control region is about 10^{-5} meters. This suggests that the maximal space-time sheets of Hox genes correspond to $k = 173$, and that in activation this space-time sheet grows to its actual size. Of course, this growth could have occurred already in the segmentation stage. This would imply that the cells containing Hox genes

are glued together by flux tubes to form larger space-time sheets which later grow to space-time sheets corresponding to various organs.

How to understand basic facts about Hox gene expression?

There are several aspects involved with Hox gene expression which one should understand.

1. Co-linearity.
   Somehow the activation of n: th Hox gene leads to the activation of n+1: th Hox gene independently of what the n+1: th gene is. One possibility is that there is transcription factor gradient along the Hox gene which grows with time and gradually activates Hox genes in linear order. Perhaps enhancer is in question. Second possibility is that many-sheeted nature of Hox genes is crucially involved. Suppose that activation of Hox gene involves expansion of the largest space-time sheet associated with Hox gene. If the expansion of the space-time sheet of n: th Hox gene is necessary condition for the expansion of n+1: th space-time sheet, co-linearity follows automatically. This looks natural if the expansion of the Hox gene space-time sheet proceeds slowly along the Hox cluster so that expanding space-time sheet of n: th Hox gene is glued with that of n+1: th Hox gene

   This picture explains automatically also why the relocation of the Hox gene to a more anterior position makes Hox expression more posterior. The anterior boundaries in Hox clusters located in different chromosomes are the same. This suggest that the control for the beginning of the Hox expression program is associated with the space-time sheet representing entire embryo. Control could involve classical field affecting acting via enhancer or silencer type transcription factors whose effect is known to be not purely chemical.

2. Temporal co-linearity.
   This is present in vertebrates but not in Drosophila. Chemical signalling between cells cannot explain temporal co-linearity and it must be due to the independent development of the cell genomes. The simplest explanation is that there is lag in the activation time for the genetic program activating Hox genes increasing monotonically as a function of the distance along the anterior-posterior axis. This dependence could be generated by a gradient of corresponding transcription factor concentration, perhaps created already in maternal period. This gradient should be generated by a DNA sequence located at the $5'$ end of the Hox cluster so that transcription factor in question must be repressor: activation takes place when the concentration is subcritical.

3. The presence of the anterior boundaries.
   The presence of the anterior boundaries is most naturally due to determination of cells occurred before the activation of Hox genes. Segmentation genes indeed force various segments to different branches of genetic program and it is quite plausible that the activation of the Hox genes depends on segment. What is needed that the Hox genes above anterior boundary are too far from criticality for the activation to occur. It is also possible that cells in anterior end of the embryo generate repressor concentration which gradually grows and shifts anterior boundary in posterior direction during morphogenesis. If the expansion of space-time sheets associated with Hox genes is responsible for activation, this expansion should stop at n: th gene in n: th expression domain. It is not clear why this should occur without the proposed mechanism.

4. Posterior prevalence.
   An explanation in terms of the control mechanisms of gene programs activated by Hox genes has been already considered. Second explanation for posterior prevalence is that the expansion of the space-time sheet associated with Hox genes to a single space-time sheet common to first n Hox genes somehow represses the expression of all Hox genes expect n: th one. Perhaps only the gene on the boundary of this space-time can be active.

Quantum model for the expression of Hox genes

There are too much unknown factors to allow a construction of a detailed quantum model for the situation. What however seems clear that the differences of the vacuum frequencies representing

potential differences over Josephson junctions should effectively appear as transcription factors and control parameters. A quantum model possibly catching some aspects of Hox gene expression might involve at least the following assumptions.

1. Assume that genes along chromosome are characterized by vacuum frequencies ω_i. This frequency does not depend on gene but only on its position in the chromosome. This assumption guarantees spatial co-linearity. The dependence of the gene's vacuum frequency on the position of gene along the chromosome could be understood if chromosome forms linear join along boundaries/flux tube condensate with Josephson junctions connecting subsequent gene space-time sheets. This would mean that there is electric field along the chromosome. These Josephson junctions could be involved with the activation of the gene by the control DNA section preceding it. Also the effect of the enhancers and silencers might involve resonant Josephson current between control section of DNA and gene leading to the wake-up of the gene.

2. The vacuum frequency Ω characterizing the size of the growing organism increases with time and Ω changes in a phase transition like manner step by step. Temporal co-linearity can be understood if there is some (possibly phase) gradient along the growing organism implying that the phase transition leading to the increase of Ω proceeds from tail to head. The gradient could act like a concentration of a chemical suppressor decreasing in head-to tail direction and established already before the Hox gene expression started.

3. The space-time sheet of the organism and gene space-time sheets form weakly coupled super conductors and potential differences over the Josephson junctions serve as transcription factors. When the frequency $\Omega - \omega_i$, which corresponds to potential difference eV, equals to critical frequency, resonant currents are generated waking-up i: th gene and activating it. Given gene is active only during the time interval when $\Omega - \omega_i$ is critical. With the assumed dependence of ω_i on the position of gene, this implies spatial co-linearity and posterior prevalence.

Chapter 4

Model for the Findings about Hologram Generating Properties of DNA

4.1 Introduction

The findings of Gariaev's group include the rotation of polarization plane of laser light by DNA [I20], phantom DNA effect [I21], the transformation of laser light to radio wave photons having biological effects [I23], the coding of DNA sequences to the modulated polarization plane of laser light and the ability of this kind of light to induce gene expression in another organisms provided the modulated polarization pattern corresponds to an "address" characterizing the organism [I20]. and the formation of images of what is believed to be DNA sample itself and of the objects of environment by DNA sample in a cell irradiated by ordinary light in UV-IR range [I33]. This chapter represents an article which is an outcome of a collaboration with Peter Gariaev and I want to thank Peter for an enjoyable and instructive co-operation. The article will be published in DNADJ (DNA Decipher Journal) in January 2011 and can be found as preprint in Scireprints archive (see `http://scireprints.lu.lv/160/`) [K1].

4.1.1 The Notion Of Wave Genome

Peter Gariaev and collaborators have introduced the notion of wave genome [I20] requiring the coding of DNA sequences to temporal patterns of coherent em fields forming a bio-hologram representing geometric information about the organism. Code could mean that nucleotide is represented by a characteristic rotation angle for the polarization plane of linearly polarized laser radiation scattering from it. The experiments of Peter Gariaev's team [I23] suggest that this kind rotation is induced by chromosomes by a mechanism which to my best knowledge is poorly understood. Other open questions concern the precise identification of the substrate of the bio-hologram, of the reference wave and of information carrying wave, and of the mechanism making possible (quantum) coherence in macroscopic length scales.

The reading of the DNA sequence to a radiation pattern is assumed to rely on the propagation of an acoustic soliton along DNA [I20]. Whatever this process is, one should also identify the reverse process inducing the activation of the genome as the target organism receives the radiation coding for the DNA provided the genetic "address" is correct. One should also identify the mechanism transforming laser radiation to radio-waves at various frequencies as well as the mechanism creating what is believed to be the image of DNA sample and replicated images of some instruments used in experiment.

4.1.2 Hologram Like Radiation Patterns Generated By DNA

In this article one particular experiment, namely the already mentioned experiment involving the formation of two kinds of strange replica structures resulting when DNA sample is radiated by

red, IR, and UV light using two methods by Gariaev's group [I33] will be discussed. The original interpretation of the image produce by first method is as a replica image of DNA sample. This interpretation can be challenged. The second image is interpreted as a hologram image of the environment. In the following the interpretation of these images in TGD framework is discussed.

The first method produces what was originally interpreted as replica images of either DNA sample or of five red lamps used to irradiate the sample. Second method produce replica image of environment with replication in horizontal direction but only at the right hand side of the apparatus. Also a white phantom variant of the replica trajectory observed in the first experiment is observed and has in vertical dir

4.1.3 Basic TGD Based Notions Involved With The Model

In this article a model explaining the characteristic features of the replica patterns is developed. The model is inspired by Topological Geometrodynamics (TGD), the recent state of which is discussed in Prespace-time Journal [L7, L8, L11, L12, L9, L6, L10, L1]. TGD is a proposal for a unified theory of the fundamental interactions based on a generalization of the notion of space-time having perhaps its most important consequences at the level of living systems. TGD inspired theory of consciousness and of quantum biology is discussed in the articles [L5, L4, L3] of Journal of Consciousness Research & Exploration. The model differs in many respects from the general model of proposed by Peter Gariaev and collaborators [I20] but shares with it the vision about holograms as a basic element of information processing in living systems at DNA level.

The basic notions are magnetic body, massless extremal (topological light ray), the existence of Bose-Einstein condensates of Cooper pairs at magnetic flux tubes, and dark photons with large value of Planck constant for which macroscopic quantum coherence is possible. Also the hypothesis that the differences of zero point kinetic energies for space-time sheets with different p-adic length scales define universal metabolic energy quanta is used in the model for pumping of radiation energy to the system. The hypothesis is that the first method makes part of the magnetic body of DNA sample visible whereas method II would produce replica hologram of environment using dark photons and also the phantom image of the flux tubes becoming visible by method I.

Replicas would result by mirror hall effect in the sense that the dark photons would move back and forth between the part of magnetic body becoming visible by method I and serving as a mirror and the objects of environment serving also as mirrors. What is however required is that not only the outer boundaries of objects visible via ordinary reflection act as mirrors but also the parts of the outer boundary not usually visible perform mirror function so that an essentially 3-D vision providing information about the geometry of the entire object would be in question. Many-sheeted space-time allows this.

The presence of the hologram image for method II requires the self-sustainment of the reference beam only whereas the presence of phantom DNA image for method I requires the self-sustainment of both beams. Non-linear dynamics for the energy feed from DNA to the magnetic body could make possible self-sustainment for both beams simultaneously. Non-linear dynamics for beams themselves could allow for the self-sustainment of reference beam and/or reflected beam. The latter option is favored by data.

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` [L16].

4.2 Observations

Two methods are involved to produce images with replica structure in the experiments of Gariaev's team. The detailed experimental arrangement and results of these experiments are described in [I33]. Reader can get a concrete idea about the experiments from the figures at the end of this article.

For both methods one uses sources of red and IR photons emitted by diodes as well as sources of UV-B and UV-C photons (for a schematic representation of the experimental apparatus **Fig. 4.13**). The wave lengths and energies for red and IR photons are given by the following equations.

$$\begin{array}{ll} \lambda/nm & 650 \quad 920 \\ E/eV & 1.91 \quad 1.35 \end{array} \tag{4.2.1}$$

The wave-length and energy intervals for UV-B and UB-C radiation are given by the following equations.

$$\begin{array}{lll} Energy\ range & [\lambda_1, \lambda_2]/nm & [E_1, E_2]/eV \\ UV-B & [315, 280] & [3.94, 4.43] \\ UV-C & [280, 100]] & [4.43, 12.40] \end{array} \tag{4.2.2}$$

1. In method I red, IR, and UV-B and UV-C beams are present all the time. During irradiation is one detects what are called DNA replica trajectories (**Figs. 4.3** and **4.4**) These roughly vertical tubular structures (or less probably, planar structures orthogonal to the preferred horizontal direction) have grainy structure (**Fig. 4.3**). Replica trajectories decompose to five sub-trajectories which probably correspond to the five red diodes irradiating DNA directly (**Fig. 4.4**). One could interpret the replica trajectories as images of DNA sample or of red diodes created by the DNA sample.

   Long-lived red DNA replica trajectories called phantom DNA trajectories are present also when the irradiation has ceased (**Fig. 4.5**). The distributions of brightness for these images in RGB model are represented in **Fig. 4.6** representing especially clearly the structure of the trajectories.

2. In method II same beams are present but only periodically. The replicas appear when the beams are not on and are in horizontal direction representing environment (**Fig. 4.2**). The basic feature is that the objects of environment are replicated in horizontal direction with distance defined by the horizontal size of the object so that fractal structure results. There are also phantom DNA replicas which are white and to the left of DNA sample and could correspond to the red replicas seen by method I (**Fig. 4.2**). These structures are thicker than than the red replica trajectories of method I.

   What is remarkable that the replicas representing environment carry information about the geometry of the *entire* objects rather than that for the outer surface of these objects seen in reflection: a kind of 3-dimensional vision seems to be in question which cannot be explained in terms of ordinary holograms alone. The vertical region in which replicas are obtained corresponds to the height of the roughly vertical replica structures produced by method I.

   What is equally remarkable is that the replicas appear only at the right hand side of the system but not at the left hand side. Strangely, the touching of the DNA sample however shifts replicas to the left after which they disappear in about 5 to 8 seconds (**Fig.** s **4.7** and **??**). The color of the replicas can be white, reddish, red and even blue. It is not quite clear whether the left replicas are mirror images of right replicas or images of the left hand side of the environment.

In both cases the key question is whether the replica trajectories represent real physical objects or whether they are analogous to a sequence of mirror images resulting when one has object between two mirrors and repeated reflections create a sequence of images replicas (mirror hall effect).

4.3 Model For The Findings

The model for the findings is based on TGD inspired model of quantum biology. The key physical input of the TGD based model are the notions of magnetic body [K36] and of massless extremal (ME) or topological light ray [K50], and the identification of dark matter in terms of a hierarchy of Planck constants [K26] assumed to play a key role in living matter. These notions are described briefly in [L3]. A more detailed descriptions can be found in online books about TGD: for magnetic body in [K36], for MEs in [K50] and for the hierarchy of Planck constants in [K26].

4.3.1 Basic Notions And Ideas

The key notions and ideas of the TGD inspired model are the same as of the model discussed in [K75] as a possible framework for understanding the findings of Gariaev's team. Only the treatment is considerably more detailed.

1. In TGD inspired theory of quantum biology one assigns to all biological structures magnetic bodies which use biological bodies as sensory receptors and motor instruments. This is assumed to hold true for DNA nucleotides, DNA strands, and even DNA sample itself so that an onion like hierarchy of magnetic bodies results. The basic vision is that magnetic flux sheets traversing through DNA integrate the DNAs of various nuclei to super DNA and that this occurs at level of organs, organisms and even populations and makes possible coherent gene expression responsible for the ability of living organisms to behave as single unit and also co-operate [K3, K24]. The magnetic flux quanta and flux sheets can also end to the objects of the environment and this is essential for the model to be proposed.

   The matter at flux quanta is identified as dark matter and has Planck constant which is integer multiple of the ordinary one, and can be quite large so that macroscopic quantum coherence becomes possible. This makes possible the formation of holograms and mirror hall effect since the dark counterparts of the ordinary photons can have wave length much longer than the size scale of the experimental apparatus.

   Although the DNA preparation in the experiments of Gariaev's team is formed from a cellular structure by a violent chemical process removing proteins and cellular and nuclear membranes, the magnetic body of DNA sample could remain intact so that a natural hypothesis is that magnetic body are involved with the formation of both DNA replica trajectories and hologram like replica trajectories.

2. Topological light rays (MEs) are tubular structures very much analogous to laser beams. They carry radiation moving with light velocity and without dispersion and dissipation in *single* space-time direction that they are ideal for communication and control purposes. This linear superposition of only modes with parallel 4-D wave vectors is a key distinction from Maxwell's electrodynamics and due to non-linearity of the fundamental variational principle. More precisely, if one changes the direction of the 4-D wave vector opposite, both 3-D wave vector and frequency change sign so that the counterpart of phase conjugate laser light is in question. Hence one would have superpositions of beams and their phase conjugates having interpretation as positive and negative energy signals traversing in opposite spatial and temporal directions. At quantum level one might perhaps speak positive and negative energy photons.

   MEs could topologically condense at magnetic flux quanta and would be accompanied by the TGD counterparts of Alfven waves [F1] representing transverse geometric oscillations of the magnetic flux quanta (sheets and tubes) regarded as space-time surfaces. It would be very natural to assume that topological light rays serve as correlates for the photons reflected from DNA sample to its magnetic body. In rather precise sense these photons would represent the scaled variant of EEG used by magnetic body to control brain and receive information from brain in TGD based model of brain.

4.3.2 Method I

The details of method I and the absence of the image of the environment (**Fig. 4.3**) in this case do not encourage hologram interpretation. The interpretation coming first in mind is that the DNA replica trajectory is realized at magnetic flux tubes serving as a screen. Flux sheets orthogonal to the plane of the images cannot be excluded but are less not plausible. The simplest assumption is that the photons of red light travel scattered from DNA sample to the magnetic flux tube like structures defining the screen along MEs topologically condensed at magnetic flux sheets traversing through DNA strands which are partially un-winded and have length of order 1 cm. Red light could transform to dark photons with large Planck constant with wavelength of order 1 cm but at the magnetic body it would transform partially back to visible photons. This is however not necessary. Also UV and IR photons would interact with the DNA sample and could provide the

metabolic energy allowing also to amplify the signal. Also UV and IR photons could transform to dark photons and define part of the "EEG" of the DNA sample.

4.3.3 Method Ii

For method II the interpretation in terms of a hologram like structure resulting when light traveling in horizontal direction is reflected from the objects of the environment is suggestive.

1. For white cable like structures left from DNA sample referred to as phantom DNA replicas the grainy replica structure is actually not present (**Fig. 4.2**) so that phantom DNA replica is perhaps not the proper term. As in the case of method I these structures could be interpreted as images of the magnetic body serving as the hologram substrate. Since red light source is off, only the white light emitted by the DNA substrate is present. These structures are wider than the red DNA replicas and a rough estimate for their thickness is about 1 cm so that the interpretation as a flux tube of magnetic body is suggestive. The interpretation of the signal as counterparts of bio-photons [I28] generated when dark photons transform to ordinary visible photons is suggestive.

2. Hologram interpretation for the replica of environment (**Fig.** 4.2) requires the system generates the reference beam prevailing for some time although the irradiations are turned off. The reflected beams due to the irradiation would disappear as the irradiation is turned off so that the reference beam can generate the hologram image.

3. The simplest assumption is that there are horizontal flux tubes or sheet(s) in the plane defined by the vertical and horizontal directions and that the part of the magnetic body corresponding to DNA replica trajectory serves as source of dark photons with large $\hbar$ [K26], which travel to the right in horizontal direction and along flux tubes connected to the outer surfaces of the objects of environment. If the dark photons emanate from the structures visible as phantom DNA replica, one can understand why the image is from the right hand side.

4. Similar connections to other living organisms would explain the original observations of Gurwitsch about mitogenetic radiation at UV frequencies [I37]: the UV radiation would represent decay products of dark variants of UV photons. One could also interpret bio-photons [I28] at visible wavelengths as decay products of their dark variants with much longer wave lengths. These photons could produce also bunches of EEG photons for large enough value of $\hbar$ [K24]. Also the findings of Gariaev's group about the transformation of laser light irradiating DNA to a radiation in a wide range of frequencies extending at least down to 10^4 Hz (corresponds to a wavelength of about 10 km) and having biological effects [I23] could be interpreted in terms of long wave length dark photons with energies of visible photons. The role of low frequencies down to 10^4 Hz at least in water memory [I18, I19] suggests that the basic mechanism of water memory is based on dark radio wave photons. The recent findings of the group led by HIV nobelist Jean-Luc Montagnier [I26] relating to water memory suggest an interaction between DNA samples based on radiation and also a new non-chemical representation of genetic code in terms of electromagnetic radiation patterns proposed also by Gariaev's team [I20, I23]. TGD approach suggests besides field representation based on MEs [K31], a representation in terms of flux tubes connecting DNA and lipids of cell membrane [K3], and a representation of genetic code in terms of the states of dark nucleons [K76]. Computer science inspired view indeed suggests DNA provides only one of the many representations of the genetic code.

5. What differentiates the hologram from the ordinary one is that reflections occur from the entire outer surfaces- not only from the outer surface visible in ordinary sense but also from the "inner side" of the part not usually visible so that information about entire 3-D geometry is obtained (**Fig. 4.2**). Without this assumption it is difficult to understand the replication in the scale of the replicated object. The repeated travel back and forth along these flux tubes or sheets would produce mirror hall effect and the observed replica structure could be understood.

6. A possible reason for why replicas are horizontal is that the magnetic body of DNA sample receives information from the environment and the objects are of environment tend to be in the horizontal direction. Phantom DNA replicas which might relate to phantom DNA effect [I21] discovered also by Gariaev's group appear only at the left hand side of the DNA sample and if they represent ordinary images of the hologram substrate and serve as mirrors, the appearance of the hologram replicas at the right hand side only can be understood. These images would result as dark photons emitted by the hologram substrate transforms to visible light.

   What happens in phantom DNA effect is that laser light scatters from the chamber weakly even after the DNA sample has been removed. The simplest explanation could be that some fraction of DNA leaves their magnetic bodies to the sample and that the scattering involves these magnetic bodies already in the original situation. Also water memory [I18, I19, I26] could be due to the fact that for some fraction of the biological molecules originally present in the solution before dilution leaves the magnetic bodies in the sample and generate the radiation responsible for the biological effects as cyclotron radiation [K31].

7. The hologram image would result as the photons of the reflected reference beam transform back to photons of visible (and possibly UV and IR) light. The reflection preserves only the vertical momentum of photon parallel to the flux tube so that reflections occur also in the direction of the camera. The photons in question need not correspond to single wave length. The UV radiation necessary for the experiment might serve as a metabolic energy source allowing to generate dark photons but it could also transform to dark photons defining the hologram. The longitudinal coherence length [I38]

$$\xi = \frac{c}{\Delta f} = \frac{\lambda_d^2}{\Delta\lambda_d} = r\frac{\lambda^2}{\Delta\lambda} \quad , \quad r = \frac{\hbar}{\hbar_0}$$

   of dark photons must be larger than the size scale $L \sim 20$ cm of the experimental apparatus in order to produce mirror hall effect. From the assumption that the size scale $l \sim 1$ cm of the grains of the replica trajectory is of order $l \sim r\lambda$, one obtains the estimate $r = 15 \times 2^{10}$. This gives $\lambda/\Delta\lambda \sim 20$, which looks rather reasonable value.

The transformation of the right-handed mirror hall image to left handed as the DNA sample is touched should be also understood.

1. The first question is whether the effect of touch (**Figs. 4.7** and **4.8**) is mechanical or biological. The proposed model encourages to consider the possibility that the magnetic body assignable to the hand or finger touching the sample generates the external irradiation generating dark photons needed to generate a replica hologram from the left hand side of the apparatus. When the finger is removed from the vicinity of the sample, one expects that the hologram disappears as it indeed does within 5-8 seconds. The mechanical instability induced by the direct touch could be the reason for the disappearance of the right sided hologram. Also the intensity of the irradiation from the magnetic body assignable to hand is expected to be stronger than the original reference beam so that the hologram is transformed to left-sided hologram. This explanation could be tested by touching the sample from another side to see whether the hologram remains right sided in this case.

2. One can imagine also alternative but more complex explanation not favored by Occam's razor. What comes in mind that the reference beam needed for the hologram and generated by DNA sample of the magnetic body is transformed to its unstable phase conjugate and thus travels from left to right and produces a left sided replica hologram. An open question is whether this hologram is from left hand side of the system or a mirror image of the hologram from right hand side. Perhaps this could be tested.

   DNA strands and their conjugates should correspond to separate flux sheets and one can wonder whether the double DNA strand maps to a doublet of magnetic bodies (note the analogy with two brain hemispheres and EEG) and whether left-right dichotomy could correspond to DNA-conjugate DNA dichotomy. If so, then touching would lead to the disappearance of DNA reference beam and the generation of its conjugate beam assignable to conjugate strand of DNA and perhaps scattering from the conjugate hologram also formed in the process.

4.4 The Realization Of The Hologram At The Level Of Magnetic Body

How the reference beam is generated and how the hologram substrate is realized? These are the basic questions to be answered. Reference beam should be generated by the magnetic body itself and/or by DNA sample since it exists in absence of irradiation. Magnetic body should define the photosensitive substrate and the thickness of the analog of the photographic plate should be of the order of scaled up wavelength in order to achieve this. Note that in the case of EEG photons similar mechanism would mean that the size for the analog of the photographic plate is of order Earth size scale!

4.4.1 How The Reference Beams And Reflected Beams Are Generated?

The explanation for the replica assumes that the reflected beams are horizontal. Reference beams should be such that there exists a mechanism taking care the that they are preserved after the irradiations cease. The mechanism generating the reference beam would be most naturally the coherent decay of the excited state of a Bose-Einstein condensate. This condensate must be however assigned with some other structure than hologram substrate itself.

One can distinguish two DNA replica trajectories near DNA sample and there are even more of them at higher height (**Fig. 4.3**. The decay of the first replica trajectory could provide reference beam and reflected beam for the second replica trajectory acting as hologram substrate and vice versa. This mechanism works for an arbitrary number of hologram substrates and could be at work at red, IR, and UV wave lengths. The mechanism is actually the same as the one generating ordinary laser beams and skeptic can of course ask whether the large value of Planck constant is absolutely necessary.

The replica hologram obtained by method II involves several colors. The figures about the holograms show the presence of red light, reddish or white light, and also blue light and one must understand also this. Holograms are constructed using monochromatic laser light. The reading of the hologram is however possible using even white light if the reference beam is orthogonal to the hologram substrate since in the idealization that hologram is infinitely thin, the information about the wavelength of reference beam is completely lost in this case. The proposed model for the generation of reference is consistent with the orthogonality.

The picture that emerges would be following.

1. At least the incoming red beam is transformed after the passage through the sample to a beam with large value of Planck constant and wavelength of order say.2-.5 m corresponding to the size of the region appearing in the hologram. It is quite possible that also UV and IR photons transform to dark photons. At the magnetic flux tube this beam of dark photons is split to two pieces defining reference bream and the beam reflected from the objects of the environment. All these beams are nearly horizontal. The reflected beam and reference beam recombine and form a hologram substrate defined by magnetic flux tubes assigned to the DNA replica trajectory.

2. The cyclotron Bose-Einstein condensates at magnetic bodies function as analogs of lasers. Instead of the excitations of atomic states one has excitations of cyclotron states of a Bose-Einstein condensate with a large value of Planck constant. The excitation of these states requires pumping of energy. The simplest possibility is that both UV, IR, red, and IR light pump energy to the respective modes so that one would have multi-laser operation. The magnetic body is predicted to have a hierarchical fractal structure with magnetic fields whose strengths correspond to the p-adic length scale in question with p-adic length scales coming as half octaves of basic scale which conveniently can be taken 10 nm defining the thickness of cell membrane (for p-adic length scale hypothesis, which forms one of the corner stones of TGD based particle physics and of quantum biology see [L7, L8, L11, L12, L9, L6, L10, L13]. These irradiations would excite different parts of the magnetic body giving rise to a fractal hierarchy of holograms. The camera operating at visible wave lengths would not allow to see UV and IR holograms.

3. It is important to notice that the presence of only say red beam of light is not r enough to generate the hologram so that an interaction between these irradiations must be present. Some of the beams could act as control signals activating the DNA or as sources of metabolic energy (say UV beams).

4. The holograms appear periodically for method II [I33]: **Figs. 4.9**, **4.10**, **4.11**, **4.12** at the end of the article illustrate what is involved. The periodic irradiation of the sample certainly induces a periodically appearing hologram image: when all irradiating beams are turned on, the conditions for the appearance of hologram are not satisfied and hologram disappears. The period is however considerably longer than the time interval between irradiation periods. This suggests a threshold for the effect.

   When the amount of pumped energy reaches a threshold, the intensity of the reference beam increases dramatically and the hologram becomes visible. This kind of effect requires a non-linear dynamics. The simplest model would be in terms of a potential containing the net value of the pumped energy as a parameter. As this parameter exceeds a threshold value, a phase transition the equilibrium position of the system would change from that with a vanishing reference beams to that with a large reference beam and the energy stored to the system would be utilized. DNA sample would be the natural storage of the energy.

4.4.2 A Simple Model For The Dynamics Of Pumping And Sustainment Of Dark Photon Beams

The basic question is what the pumping of energy could mean at the level of DNA. It seems clear that at least part of the pumped energy is transformed to metabolic energy in turn transformed to dark photons. It is also possible that the chemical energy of stored in DNA molecules is transformed to metabolic energy. The existence of a hierarchy of universal metabolic energy quanta predicted by TGD provides the physical basis of the model.

One should also have a qualitative model for the transformation of the energy of radiation to metabolic energy and to the self sustainment of the dark photon beams.

1. The basic idea is simple. The irradiation kicks particles in DNA to higher energy state and these states decay to the ground state by emission of dark photons making allowing to realize the reference beam for holograms during reading period and both reflected and references beams during irradiation period.

2. For method I both the reference beam and reflected beam remain when irradiation ceases and give rise to the red phantom DNA replica (**Fig. 4.5**). For method II the presence of hologram image (**Fig. 4.2**) means that only reference beam is sustained. Self-sustainment requires non-linear dynamics. This dynamics could appear either at the level of DNA sample or at the level of the reference beam and reflected beams. For method II the white cable like structures appearing to the left of DNA sample could also correspond phantom DNA replica. They cannot however correspond to hologram like mechanism but ordinary radiation emitted by the hologram substrate.

3. The first possibility (option I) that the non-linear dynamics is realized at the level of DNA. DNA might be able to liberate chemical energy as metabolic energy or store the energy of irradiation and then liberate it. It is however difficult to understand why only the reference beam is sustained in method II. Both beams should be present if they result by a splitting of a beam coming from DNA meaning the absence of replica hologram. Internal consistency would require giving up hologram interpretation.

4. Second possibility (option II) is that non-linear dynamics is realized at the level of reference beam and reflected beams. For method II this dynamics could lead to a self sustainment in the case of reference beam if it is more intense than the reflected beams. For method I the irradiation lasts much longer and both reference beam and reflected beam could be sustained and one would not obtain hologram image but only phantom DNA replica image.

The following qualitative model has same general form for both options.

p-Adic length scale hypothesis and hierarchy of metabolic energy quanta

If one takes seriously the TGD inspired model for metabolic energy quanta, the irradiation would kick charged particles from larger space-time sheets to smaller ones so that the energy would go to the zero point kinetic energy plus surplus. The particles would drop back to the larger space-time sheets emitting the surplus zero point kinetic energy in this process as dark photon going to the magnetic flux tubes to be used to build reference beams and reflected beams for the holograms.

The kicked particles could be electrons or protons but electrons are more plausible candidates.

1. The nominal value of zero point kinetic energy given by

$$E_0 = \frac{3\hbar^2}{2mL^2} , \tag{4.4.1}$$

and corresponds to zero point kinetic energy for a particle in box with side of length L.

2. Possible values of L can be estimated by assuming $L = L(k)$, with $L(k)$ given by the p-adic length scale hypothesis stating

$$L(k) = 2^{(k-151)/2} L(151) , \tag{4.4.2}$$

where electron Comptonlength $L_e(151) = \sqrt{5}L(151) \simeq 10$ nm corresponds to Gaussian Mersenne prime $M_{151,G} = (1+i)^{151} - 1$, which is one of the Gaussian Mersennes $M_{k,G}$, $k = 1151, 157, 163, 167$ between cell membrane thickness 10 nm and length scale 2.5 μm which is roughly one half of the size scale of cell nucleus. For $k = 148$ one obtains $E_0(148) \simeq .5$ eV which is the nominal value of metabolic energy quantum. Other zero point kinetic energies would come as octaves of $E_0(148)$ so that one has has the series (..., .25, .5, 1, 2, 4, ..) eV. Nominal values are in question: the variation can be at least 10 per cent around the nominal value and is due to the fact that in reality space-time sheets do not have the geometry of cube and because the particles inside space-time sheets are not free.

3. Metabolic energy quanta correspond to the zero point kinetic energies liberated as particle drops from space-time sheet characterized by k_1 to $k_1 + \Delta k$ and are given as differences

$$\Delta E_0(k, k+\Delta k) = \frac{3\hbar^2}{2mL^2(151)} 2^{-k+151}(1 - 2^{-\Delta k}) . \tag{4.4.3}$$

This gives a geometric series of metabolic energy quanta for each value of k. Two cases are of special interest: dropping next space-time sheet in the hierarchy ($\Delta k = 1$) and dropping to very large space-time ($\Delta k \to \infty$).

$$\begin{aligned} \Delta E_0(k,1) &= \frac{3\hbar^2}{2mL^2(151)} 2^{-k+151} , \\ \Delta E_0(k,\infty) &= \Delta E_0(k-1,1) = \frac{3\hbar^2}{4mL^2(151)} 2^{-k+151} . \end{aligned} \tag{4.4.4}$$

4. Note that the energy levels form a cascade converging to $\Delta E_0(k,\infty) = \Delta E_0(k-1,1)$. The scaling $\hbar = r\hbar_0$ of Planck constant does not affect the spectrum of metabolic energy quanta if $L(k)$ scales as $L(k) \to rL(k)$.

5. The following equation lists the three p-adic length scales, which are possible for the radiation sources used assuming that $\Delta k = 1$ transitions dominate.

$$\begin{array}{llll} k & 145 & 144 & 143 \\ \Delta E_0(k,1)/eV & 2 & 4 & 8 \\ \lambda/nm & 620 & 310 & 155 \\ L_e(k)/nm & 1.23 & .88 & .625 \end{array} \tag{4.4.5}$$

   The 2 eV metabolic energy is five percent larger than the energy 1.91 eV assignable to 650 nm wavelength of the red light used in irradiation. These wave lengths would be preferred but in principle entire range of metabolic energy quanta is allowed and if one assigns metabolic energy quanta to the transitions $\Delta k \to \infty$ the values of k in the equation are scaled down by one unit: $k \to k-1$. The p-adic length scales correspond to length scales naturally associated with DNA.

   In the case of proton the length scales would be obtained by the replacement $k \to k - 11$ and would be considerably below the atomic length scale $L_e(137)$ for the ordinary value of Planck constant and dark protons would be required.

Comment: It has turned that this view about metabolic quanta can be modified without changing the values of metabolic energy quanta. Instead of dropping of particles to a larger space-time sheet the p-adic prime assignable to the space-time sheet itself could change leading typically to a reduction of single particle energies since the size of the space-time sheet increases. Quantum numbers do not change in this transition if it takes place adiabatically. This applies not only to particles in box but also to cyclotron states: in this case the strength of the magnetic field is reduced to conserve magnetic flux as p-adic prime increases and induces the increase of the flux tube thickness. This yields same predictions as the earlier model explaining the quantal effects of ELF radiation on vertebrate brain. The nice feature of this mechanism and its variants [K35] is that the transition liberates energy of a large number of particles simultaneously. This is not obvious for when particles drop to larger space-time sheets.

Linear model for the pumping of energy

If one assumes that the non-linear behavior responsible for self-sustainment is realize at the level of the reference beams and reflected beams the model for pumping of energy to DNA sample can assumed to be linear. The simplest model for the pumping involves only two space-time sheets. The proper variable would be either the number N of charged particles -presumably electrons- and/or net zero point kinetic energy feed to the smaller space-time sheet. One has just population dynamics for the numbers of electrons at the two space-time sheets involved.

1. The equations for the population dynamics have the general form

$$\begin{aligned} \frac{dN_1}{dt} &= k_0(t)N_2 - k_1(t)N \ , \\ \frac{dN_2}{dt} &= -k_0(t)N_2 + k_1(t)N \ , \end{aligned} \tag{4.4.6}$$

   The first term on the right hand side corresponds to the energy feed from irradiation and second term the energy leakage through the dropping of the particles back to the smaller space-time sheet.

2. If the N_2 is very large it can be taken as constant not affected by the process and with an obvious redefinition of $k_0(t)$ one can write

$$\frac{dN_1}{dt} = k_0(t) - k_1(t)N_1 \ . \tag{4.4.7}$$

The general solution of the equation is

$$N_1(t) = N_0 exp(-\int k_1 dt) + \int_0^t N_1 exp(\int_0^t k_1 dt) k_0(t) dt \ . \tag{4.4.8}$$

As noticed, this model cannot explain self-sustainment in terms of metabolism.

A catastrophe theoretic model for the self-sustainment

The self-sustainment of the beams requires non-linear dynamics. The non-linearity could be assigned with the pumping of energy to DNA by irradiation and would mean the addition of non-linear terms to the population dynamics of electrons (Eq. 4.4.7). This model does not however allow to distinguish between reference beams and reflected beams. The same formal model however applies also to the dark reference beams and reflected beams by re-interpreting number N of electrons as the number of photons in the beam. The following model is only an attempt to characterize the situation qualitatively and does not depend on the interpretation of N. The two alternative interpretations will be referred to as options I and II.

1. The basic equation is

$$\frac{dN}{dt} = P_3(N, k_0) = k_0(t) - k_1(t)N + k_2(t)N^2 - k_3(t)N^3 \ . \tag{4.4.9}$$

The parameters $k_i(t)$ are assumed to be slowly varying in the time scale of the dynamics for N. In catastrophe theoretic setting [A7] k_i *resp.* N would be called control parameters *resp.* behavior variable. Depending on option N denotes either the number of electrons kicked to a smaller space-time sheet of photons in the analog of laser beam.

   (a) For option I $k_0(t)$ characterizes the rate at which the irradiation kicks electrons to the smaller space-time sheet. For option II the interpretation is as a rate with which photons in the dark analog of laser beam are produced by irradiation. One can assume that $k_0(t)$ is constant during periods of irradiation and is small and vanishes when there is no irradiation.

$$\begin{aligned} k_0(t) &= k_0 \text{ during irradiation} \ , \\ k_0(t) &= 0 \text{ in absence of irradiation} \ . \end{aligned} \tag{4.4.10}$$

   (b) For option I the term $-k_1N_1$ corresponds to the dropping of the electrons back to the large space-time sheets. For option II it corresponds to the leakage and absorption of photons from the beam.

   (c) For option I the presence of k_2N^2 can make possible self-sustained metabolism and therefore also that of dark photon beams. DNA itself can somehow kick the electrons to smaller space-time sheets. This could be due to the liberation of metabolic energy from DNA, which cannot continue indefinitely so that $k_2(t)$ must go to zero in some time scale of the order of the time period between successive shots (few seconds). For option II this term correspond to non-linear self-amplifying interaction of laser beams and could be due to a resonant interaction of beams associated with different parts of the magnetic body.

(d) The term $-k_3N^3$ is necessary in order to avoid endlessly increasing N, which is definitely something non-realistic.

2. By construction the system realizes cusp catastrophe [A7] describing the simplest possible situation in which some parameter region of parameter space allow 3 or only 1 root to the stationarity condition $P_3(N,k_0)=0$ so that one has a phase transition like behavior. The following considerations show that if $P_3(N,0)$ allows three non-negative roots and $P_3(N,k_0)$ only one positive root, then sufficiently many and sufficiently long irradiation periods allow to achieve a self-sustaining situation, which lasts as long as $k_2(t)$ characterizing self-sustainment remains large enough. After this a phase transition to a phase characterized by a rapid decrease of N, occurs.

3. One can concretize the situation by imagining that the system climbs to a mountain during the irradiation periods and slides down when the irradiation is off in the case that one has

$$R \equiv \lim_{t\to t_f,+} dN/dt(t) = P_3(N(t_f),0) < 0 \ . \tag{4.4.11}$$

Here t_f denotes the value of time when irradiation ends. For $R>0$ the climbing up continues spontaneously but with a slower rate.

4. Quite generally, $P_3(N,k_0)$ can have $n=0,1$ or $n=3$ zeros in the region $N\geq 0$. $P_3(N,0)$ has always zero at origin and can have two additional zeros of $k_2(t)$ is large enough. Since the polynomials $P_3(N,k_0)$ and $P_3(N,0)$ differ only by a downwards shift by k_0, one finds the following.

(a) If one has

$$P_3(N,k_0) < k_0 \tag{4.4.12}$$

for $N>0$, $P_3(N,0)$ has only one non-negative zero for all positive values of N. The system slides dow towards $N=0$ as the irradiation ceases.

(b) If the condition

$$P_3(N_f,k_0) \geq k_0 \tag{4.4.13}$$

is satisfied, $P_3(N_f,0)$ has two positive roots $(N_{2,0},N_{3,0})$ besides $N_{1,0}=0$. If R is in the region above $N_{2,0}$, the system slides down to or climbs up to $N_{3,0}$ after the irradiation has ceased. This situation is obviously the interesting one in the recent case. Whether the region $N>N_{2,0}$ can be reached during irradiation depends on the properties of $P_3(N,k_0)$.

5. Consider first what happens during irradiation assuming that $P_3(N_f,0)$ has two positive roots $(N_{2,0},N_{3,0})$ besides $N_{1,0}=0$ (the interesting case). $P_3(N,k_0)$ has certainly one root since $P_3(N,f)$ becomes eventually negative due to the term $-k_3N^3$.

(a) If k_0 is large enough there is only one root - call it N_3. One has $N_3>N_{3,0}$ and the energy feed - if allowed to continue long enough or for sufficiently many times- drives the system above $N_{2,0}$ and eventually to N_3, which is stable and is reduced only slowly as $k_2(t)$ decreases. When irradiation ceases, the system goes to $N_{2,0}$, which represents a stable situation and only adiabatically approaches to zero as long as the number of roots remains three. After this N goes rapidly to zero.

(b) If k_0 is small enough one has one or three roots- let the three roots be $N_1 < N_2 < N_3$. N_1 corresponds to a stable situation in which the linear term has driven dN/dt to zero. One ends up to this situation either from $N \leq N_2$ for three roots and always if one has only one root. Only N_1 is achievable by starting from $N(t=0) = 0$ or from $N(t_f)$ achievable during irradiation period. Since the graphs of $P_3(N, k_0)$ and $P_3(N, 0)$ differ only by a shift, it is clear that one has $N_1 < N_{2,0}$ so that the system rapidly slides down to $N = 0$.

6. The conclusion is that the desired situation can be achieved only if $k_2(t)$ is so large that $P_3(N, k_0) > k_0$ holds true at the maximum of $P_3(N, k_0)$ (for $N > 0$) and k_0 is so large that $P_3(N, k_0)$ has only single root. This means that the minimum of $P_3(N, k_0)$ is positive. The extrema $N_\pm$ of $P_3(N, k_0)$ correspond to the vanishing of $dP_3(N, k_0)/dN$ so that one has

$$\begin{aligned} N_\pm &= \frac{k_2}{3k_3} \pm \sqrt{(\frac{k_2}{3k_3})^2 - \frac{k_1}{3k_3}} \ , \\ (\frac{k_2}{3k_3})^2 - \frac{k_1}{3k_3} &\geq 0 \ , \end{aligned} \tag{4.4.14}$$

The conditions for self-sustainment boil down to the equations

$$\begin{aligned} P_3(N_+, 0) &> 0 \ , \\ P_3(N_-, k_0) &> 0 \quad . \end{aligned} \tag{4.4.15}$$

Self-sustaining situation continues as long as $k_2(t)$ is so large that one has 3 roots for $P_3(N, 0)$. For small enough $k_2(t)$ the two roots disappear and the system slides rapidly to $N = 0$. **Fig. ??** illustrates these conditions graphically.

4.4.3 A General Model For The Hologram Substrate

The following model for the hologram substrate is based on the earlier vision about the role of Bose-Einstein condensates of Cooper pairs and bosonic ions in TGD inspired quantum biology.

1. DNA replica trajectory should define the analog of the photosensitive substrate so that the scaled up wave length defining its thickness should be of order 1 cm. The TGD inspired model for the effects of ELF em fields on vertebrate brain [K24] leads to the proposal that Bose-Einstein condensates of various biologically important ions and of Cooper pairs of electrons in the magnetic field associated with the flux quantum define a key element of biological information processing.

   The natural guess is that this process involves in an essential manner the formation of holograms by a radiation generating cyclotron transitions and in this manner affecting the reflective properties of the hologram substrate determined by the rates of elastic scattering. If the flux quanta are flux tubes, one has photo-sensitive tubes instead of photosensitive plates and only the vertical component of the photon momentum is conserved in the scattering and reflected photons can have any direction in the plane orthogonal to the flux tube so that the reflected radiation indeed reaches camera. The properties of the hologram seem to be consistent with the prediction that the information carried by it is only about the vertical and preferred horizontal direction.

2. Cyclotron energies E_c are proportional to $\hbar eB/m$ so that they increase with Planck constant and are inversely proportional the mass of the charged particle. This selects the Cooper pairs of electrons as a unique candidate for the Bose-Einstein condensate. TGD assigns to elementary particles macroscopic time scales as fundamental time scales and in the case of

electron this time scale is.1 seconds which corresponds to 10 Hz fundamental biorhythm. Also for this reason Bose-Einstein condensate of Cooper pairs of electrons defines a natural candidate for the hologram substrate.

3. Cyclotron transitions induced by the incoming dark photons should in the recent case have frequency of order 30 GHz if $\lambda_d \sim 1$ cm is assumed for the dark variant of red light. In the case of electron the magnetic field .2 Gauss (this is the value of endogenous magnetic field deducible from the effects of ELF em fields on vertebrate brain [K24], [L3]) corresponds to frequency of about 6×10^5 Hz so that a magnetic field of order .1 Tesla would give rise to a cyclotron frequency of order 30 GHz. The corresponding magnetic length is $L_B = \sqrt{\hbar/eB}$, which for ordinary value of Planck constant is 4.7×10 nm (note that 10 nm corresponds to cell membrane thickness and thickness of chromosomes). For $r = 15 \times 10^3$ the magnetic length would correspond to 5.8 μm length scale to be compared with the size scale 6 μm of cell nucleus. If one requires the quantization of magnetic flux in multiples of $\hbar$ this field corresponds flux tube with thickness of order 6 μm. Therefore there might be a connection with the size of nucleus and the quantization of magnetic flux meaning that the thickness of the DNA replica trajectory reflects the basic cellular length scales.

4. The cyclotron states of Cooper pairs are harmonic oscillator states in the radial direction of flux tube and eigen states of angular momentum and momentum in the direction of the flux tube labelled by (n, m, k). The integer n is harmonic oscillator quantum number. m and k characterize the projections of angular momentum and momentum in the direction of the flux tube. m is integer and also k is quantized from periodic boundary conditions for the flux tube.

5. The hologram would be generated when the incoming dark photons excite Cooper pairs from the lowest energy eigenstate with oscillator quantum number $n = 0$ to the first eigenstate with $n = 1$ and in this manner affect the reflection properties of the system. The life-time of the hologram is determined by the rate at which the system decays back to the ground state so that one would have dynamical rather than static hologram which is of course what biological system needs.

6. The reflection from the hologram corresponds to an elastic scattering in which the Cooper pair condensate receives momentum but its energy is not affected. Elasticity means that the transition does not affect the energy of the Cooper pair which is the sum

$$E_{n,m,k} = n\hbar\omega + \frac{\hbar^2 k^2}{2m}$$

of the cyclotron energy and kinetic energy of free motion in the direction of the flux tube. If the longitudinal momentum k vanishes as the formation mechanism of the hologram strongly suggests, the value of n remains unchanged but the value of angular momentum projection m in the direction of flux tube can change in elastic scattering. The scattering takes place coherently so that the rate is proportional to N^2, N the number of Cooper pairs. The rate of these transitions is affected when a position dependent portion of the Cooper pairs of the Bose-Einstein condensate is in higher energy state. Therefore the transmittance depends on the point of hologram and the change is in the lowest approximation proportional to the intensity $|A + A_R|^2$ of the incoming dark light as in the case of the ordinary hologram.

4.4.4 Is The Lifetime Of The Hologram Long Enough?

The lower bound for the lifetime of the physical realization of the hologram must be measured in seconds from the results of method II. The lifetime can be also longer since the fading of the physical hologram after the irradiation has ceased can be due do the decay of the reference bream. This means a killer test for the model since the decay rate of the hologram is easy to estimate. The decay rate of hologram can be estimated from the decay rate of excited cyclotron state and the calculation reduces to standard first order perturbation theory for interacting system of charged particles and electromagnetic field which can be found in text books [B9].

1. The lifetime of the hologram can be estimated as the life-time of the excited state. The excited state decays by a spontaneous emission of photons. The lifetime can be estimated by using standard perturbation theory for the interaction of radiation fields and electrons with a scaled up value of Planck constant. Electrons form cyclotron states at flux tubes characterized by three quantum numbers: the harmonic oscillator quantum number $n = 0, 1, 2..$, the angular momentum projection m in the direction of flux tube, and the momentum of electron in the direction of flux tube.

   The interaction Hamiltonian is obtained by the minimal coupling prescription by adding to the vector potential associated with the static magnetic field of the flux tube time dependent radiation part. This means the replacement

$$\mathbf{A} = \mathbf{A}_{flux} \to \mathbf{A}_{flux} + \mathbf{A}_{rad} \tag{4.4.16}$$

   of the vector potential of the static magnetic field determining cyclotron energy spectrum in the magnetic field parallel to the flux tube with a vector potential containing also the vector potential of the second quantized radiation field.

2. This replacement affects the Hamiltonian of the system in the following manner

$$\begin{aligned} H_0 &= \frac{1}{2m}(\mathbf{p} - Ze\mathbf{A}_{flux}) \cdot (\mathbf{p} - Ze(\mathbf{A}_{flux}) \to H \ , \\ H &\equiv H_0 + H_{int} = \frac{1}{2m}(\mathbf{p} - Ze(\mathbf{A}_{flux} + \mathbf{A}_{rad})) \cdot (\mathbf{p} - Ze(\mathbf{A}_{flux} + \mathbf{A}_{rad})) \ , \\ H_{int} &= -\frac{1}{2m}\left[(Ze\mathbf{p} \cdot \mathbf{A}_{rad} + \mathbf{A}_{rad} \cdot \mathbf{p}) + Z^2e^2\mathbf{A}_{flux} \cdot \mathbf{A}_{rad} + Z^2e^2\mathbf{A}_{rad} \cdot \mathbf{A}_{rad}\right] \end{aligned} \tag{4.4.17}$$

   $Z = 2$ is the charge of the electron Cooper pair and $m = 2m_e$ is its mass. In Coulomb gauge one has

$$\nabla \cdot \mathbf{A}_{rad} = 0$$

   and the the interaction Hamiltonian H_{int} determining the transition rate reduces in the lowest order to

$$\begin{aligned} H_{int} &= -\frac{Ze}{m}\mathbf{A}_{rad} \cdot \mathbf{p} \ , \\ \mathbf{p} &\equiv \frac{\hbar}{i}\nabla \ . \end{aligned} \tag{4.4.18}$$

3. If the radiation generating hologram is in horizontal plane, cyclotron states have vanishing momentum quantum number in the vertical direction. Therefore also the emitted radiation has momentum and polarization in this plane. In principle this could be tested by using polarization sensitive camera.

4. The rate for the return to the ground state is calculable by using standard time dependent perturbation theory the result of which can be expressed as a formula for the total transition rate to the ground state

$$\Gamma = \frac{mE}{(2\pi)^2\hbar^4}\int d\Omega |\langle f, \hbar\mathbf{k}|H_{int}|i\rangle|^2 \ . \tag{4.4.19}$$

   Here integration is over the solid angle that is over the momentum directions of the emitted photon. Here m is the mass of Cooper pair (two times electron mass) and E is photon energy (in eV range for visible photons).

5. The matrix element $|\langle f,\hbar\mathbf{k}|H_{int}|i\rangle$ of the interaction Hamiltonian is expressible in the lowest order approximation as

$$\langle f,\hbar\mathbf{k}|H_{int}|i\rangle \;=\; -i\frac{\hbar Ze}{m\sqrt{\omega}}\int \overline{\Psi}_{n_f,m_f,k_f}e^{i\mathbf{k}\cdot\mathbf{r}}\mathbf{e}\cdot\nabla\Psi_{n_i,m_i,k_i}dV \quad . \tag{4.4.20}$$

$\mathbf{e}$ denotes the polarization vector of the photon and $\mathbf{k}$ its wave vector. The integration is over the flux tube volume.

In dipole approximation one can expand the plane wave to the first non-trivial order. If one assumes that the transitions responsible for the decay of the hologram correspond to the transitions $(n_i,m_i,0)=(1,\pm 1,0)\to(n_f,m_f,0)=(0,0,0)$, one has

$$\langle f,\hbar\mathbf{k}|H_{int}|i\rangle \;\simeq\; \frac{\hbar Ze}{m\sqrt{\omega}}\int \overline{\Psi}_{0,0,0}\mathbf{e}\cdot\nabla\Psi_{1,\pm 1,0}dV \quad . \tag{4.4.21}$$

The result does not depend on photon energy at all. Angular momentum conservation requires that the angular momentum projection of the state in the direction of the flux tube changes by one unit corresponding to the spin of the photon. This allows to transform the matrix element to

$$\langle f,\hbar\mathbf{k}|H_{int}|i\rangle \;\simeq\; \pm i\frac{\hbar Ze}{m\sqrt{\omega}}\int \overline{\Psi}_{0,0,0}\mathbf{e}\times\mathbf{e}_\rho\frac{1}{\rho}\Psi_{1,\pm 1,0}dV \quad . \tag{4.4.22}$$

Here $\mathbf{e}_\rho$ denote the unit vector $(x\mathbf{i}+y\mathbf{j})/\rho$ in radial direction. The magnitude of the matrix element is of order

$$\langle H_{int}\rangle \;\sim\; (\hbar Ze/m\sqrt{\omega})\times\langle\frac{1}{\rho}\rangle\sim\frac{\hbar e}{mR\sqrt{\omega}} \quad , \tag{4.4.23}$$

where R is the radius of the flux tube.

6. The overall rate for the decay of the hologram has the order of magnitude

$$\Gamma \;\sim\; \frac{4\pi^2\alpha}{r}\frac{\hbar_0}{R^2m_e}\sim\frac{4\pi^2\alpha}{r^3}\frac{\hbar_0}{\lambda^2m_e} \quad , \quad r=\frac{\hbar}{\hbar_0} \quad . \tag{4.4.24}$$

Here λ denotes the wave length of ordinary visible photon. Formally the rate scales as $1/r$ as the naïve dimensional estimate suggests but $R\simeq r\lambda$ brings in an additional $1/r^2$ reduction factor so that $1/r^3$ over-all dependence results. For $r=\hbar/\hbar_0\sim 10^4$ the order of magnitude for the decay rate is for visible light $\Gamma\sim 10^{-5}$ s^{-1}, which is consistent with the observed slow rate of decay. As noticed, the fading of the hologram in experiment two could be due to the decay of the reference beam rather than the decay of hologram. Maybe also this could be tested. In any case, the model survives the first killer test.

4.4.5 The Amplitude For The Elastic Scattering From Hologram

The rate for the elastic scattering of photons of the reference beam from the hologram substrate defines the intensity of the hologram image and should be high enough.

1. This process involves two photons. The term

$$H_{int}^{2)} = \frac{e^2}{2m}\mathbf{A}_{rad}\cdot\mathbf{A}_{rad} \tag{4.4.25}$$

   in H_{int} makes this transition possible in the first order of perturbation theory.

2. One can worry about second order perturbation theoretic contribution to the rate which is also of order e^2. The generalization of the Golden Rule is obtained by the replacement

$$\langle f|H_{int}|i\rangle \quad \rightarrow \quad \langle f|H_{int}|i\rangle + \sum_m \frac{\langle f|H_{int}|m\rangle\langle m|H_{int}|i\rangle}{E_n - E_0 + i\eta\hbar} \quad , \quad \eta \rightarrow 0_+ \quad . \tag{4.4.26}$$

   The sum over m denotes sum over intermediate states. In the second order of perturbation theory the scattering can be thought of as taking place via intermediate states of Cooper pairs decaying back to the original state via the emission of photon. In the following rough estimate only the lowest ordinary contribution is taken into account.

3. In this approximation the amplitude for elastic scattering responsible for the hologram formation with $(n_i, m_i, k_i) = (n_f, m_f, k_f)$ and $\omega_i = \omega_f = \omega$ with the amplitude is apart from numerical factor of order unity given by

$$\langle f, \hbar\mathbf{k}|H_{int}|i\rangle \quad = \quad \frac{e^2\hbar^{1/2}\mathbf{e}_i\cdot\mathbf{e}_f\omega_i}{m\sqrt{\omega_f}}\int \overline{\Psi}_{n_i,m_i,0}e^{i(\mathbf{k}_i-\mathbf{k}_f)\cdot\mathbf{r}}\Psi_{n_i,m_i,0}dV \quad . \tag{4.4.27}$$

   In the lowest order approximation plane wave factor can be neglected. The order of magnitude for rate differs by a factor $4\pi\alpha(\omega R)^2$ from the matrix element for the decay of the hologram. For $R \sim \lambda_d$ the rates are of the same order. This rate corresponds to single photon case. In the case of many-photon state defined by the reference beam the rate is amplified by a factor N^2, where N is the number of photons in the reference beam.

4.5 Appendix: Details About Methods I And II

Two methods represent the two schemes developed for our experimental purposes. In order to adduce and visualize DNA wave replicas, the following is to be performed: by means of timing relay (**Fig.** 4.13, position #3) in varied combinations the operator switches on the required emitters BS (UV-B, which is incandescent lamp in blue spectrum, glass type- **Fig. 4.13**, position #5), a matrix with red and infrared diodes (**Fig. 4.13**, position #8) and germicidal mercurial lamp/bulb or lamp Compact electronic CEST26E27 Black (UV-C, **Fig. 4.13**, position #6), or BS (UV-B) and MXT-90 (cold catode – **Fig. 4.13**, position #4).

1. Method I.
   Dehydrated/dry DNA sample from bull's spleen - about 100 milligrams in a sealed plastic conical test tube, which is 4 centimeters long and 0.9 cm in its upper end; or 3 milliliters of DNA water solution, 1mg/ml) are placed in the effective zone of the emitters (1mm-50cm from the light emitters) and then the emitters are activated. The progression of the experiment was filmed using Fuji 24-27 DIN film. Oscillograph is in operation during the experiment and is to register and record the electromagnetic fields/frequencies within the

zone of the experiment; averaged normal electromagnetic background noise from within the premises is recorded, defined by the behavior of sinusoid in the oscillograph. Further, by means of the timing relay the emitter UV-C is turned off 10 minutes later. The camera captures an emergence of unique dynamic wave structures – multi-replicated DNA replicas and of the surrounding objects invisible to the naked eye, yet perceivable by the camera and fixed on the film. These are directly related to the photonic influences effected by the emitters on the DNA samples. In other words, multiplication of a number of reflection of DNA samples occurs and is redistributed in space on complex trajectory patterns (the first method) and on horizontal patterns (the second method), including mapping of the objects responsible for exciting the DNA samples.

2. Method II
The second method to obtain and visualize DNA wave replicas involves the following: dehydrated/dry DNA sample, 100 milligrams is placed in an open mode into a holder made of aluminum foil. With intervals of 2-3 seconds the BS (UV-B) lamp, Compact Electronic CEST26E27 Black lamp and apparatus Duna-M are turned on and off. Photographs are taken 5 minutes later. By this method the DNA replicas and of close objects are registered and they are propagating strictly to the right hand side. With external mechanical interference (a touch) with the DNA samples the distribution vector alters to the opposite – that is the DNA replicas begin propagating to the left hand side and than 5-8 seconds after the mechanical interference the replicas disappear or are not perceived by the present equipment4 or the utilized film, regardless of the equipment still being in an activated state.

4.6 Figures

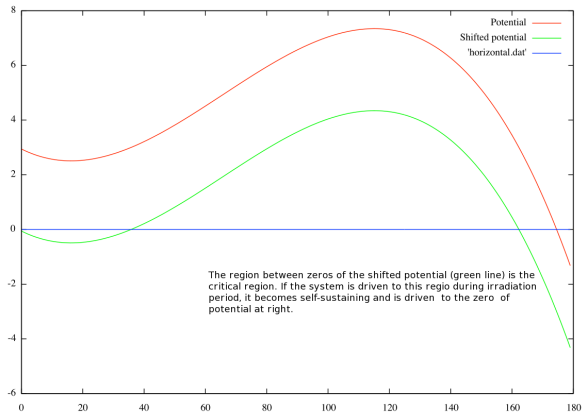


Figure 4.1: Illustrations of a potential $V(x) = P_3(x) = a - bx + cx^2 - dx^3$ and shifted potential $V(x) - a$ allowing self-sustainment. Note that the full potential allows only single zero and shifted potential two zeros. If the system ends up to the region between the two zeros of the shifted potential during irradiation, it ends up to the rightmost zero after the irradiation period. When the value of the parameter c decreases adiabatically below certain critical value, the value of x (having interpretation as photon number) goes rapidly to zero.

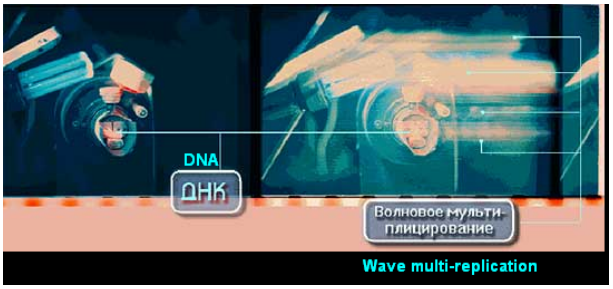


Figure 4.2: The left hand side figure is from [K8] and represents the replica images of the instruments and the image interpreted by experimenters as a replica image of DNA sample (method II). The white cable like structures to the left from DNA sample have interpretation as phantom DNA image.

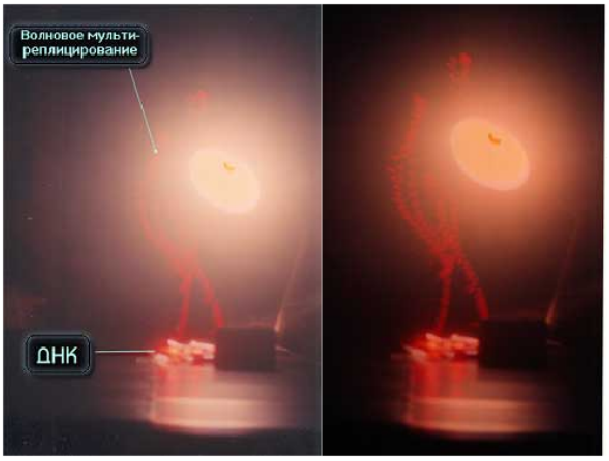


Figure 4.3: The picture shows the discrete replica like structure of the band like image obtained by method I and interpreted by experimenters as replica image of DNA sample.To the left image is the original image and to the right the contrasted one.

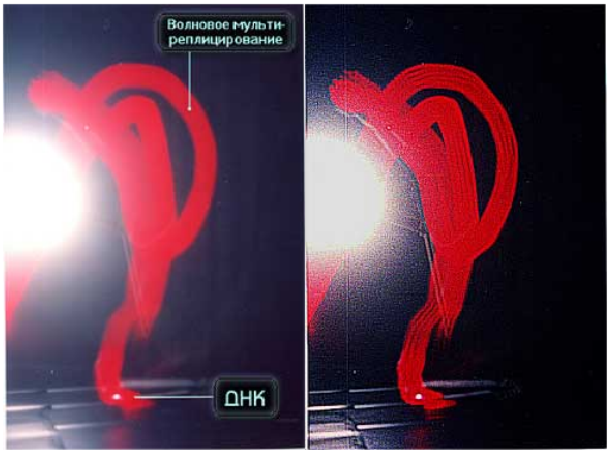


Figure 4.4: Spatial structure of DNA wave replicas obtained by method I. The picture reveals the 5-fold fine structure of the tube like image interpreted by experimenters as replica image of DNA sample. The 5-fold character probably correspond to five red LEDs above the sample. To the left image is the original image and to the right the contrasted one.

Figure 4.5: Long living DNA wave replica from the experiment in **Fig.** 3 (referred to as phantom image as opposed to the image seen during irradiation) subsequent to switching off of the initiating electromagnetic fields/frequencies sources.

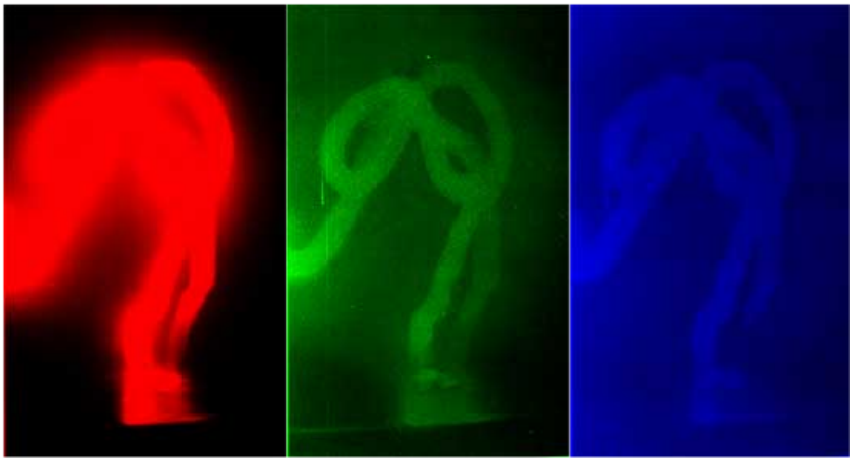


Figure 4.6: Distribution of the brightness values per RGB color model, Red, Green, Blue of the phantom DNA image of previous figure. The green image gives especially clear picture about the structure of phanton DNA image.

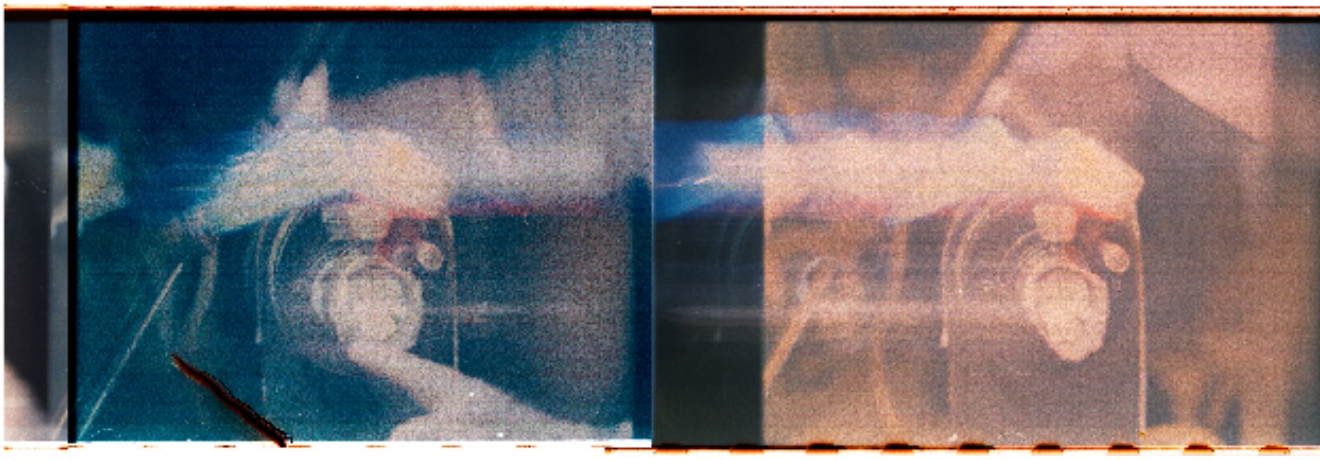


Figure 4.7: a) The moment of mechanical external interference (touch, which could have also biological effect) with DNA sample. The second method of elicitation of DNA wave replicas. b) Shift to the left of the wave replicas immediately after the interference. It is also commonly noticed that there is a sharp distinction of the shot from others by brightness and color scheme, which is unrelated to the working of the camera.

Figure 4.8: Disappearance of DNA wave replica formation effect after 5-8 seconds following the interference with the DNA sample (touch, see previous figure) while the entire equipment initializing the replicas is still on.

Figure 4.9: One of the modified experiments, shown in **Fig.** 5 (old DNA sample replaced by new). Refer to the shots # 3 and #4 above. The shot #4 reveals replicas of the "Duna-M" diodes, shifting to the right side. Note the appearance of replicas of perforation and exposed parts of the film close to diodes.

Figure 4.10: Shots #11 and #12 above. It is to be mentioned that from shot #1 until shot #11 the Duna-M diodes wave replicas are absent, however appearing again in the shot #12.

Figure 4.11: Shots #13 and #14 above. In the #13 we can distinguish wave replicas of the Duna-M diodes with the commonly observed intrusion in into the unexpected space between the shots. The shot #14 does not capture the wave replicas of the diodes and they disappear.

Figure 4.12: Shots #23 and #24 above. From shot #14 until #22 replicas disappear, they are dimly captured in the shots #23 and #24.

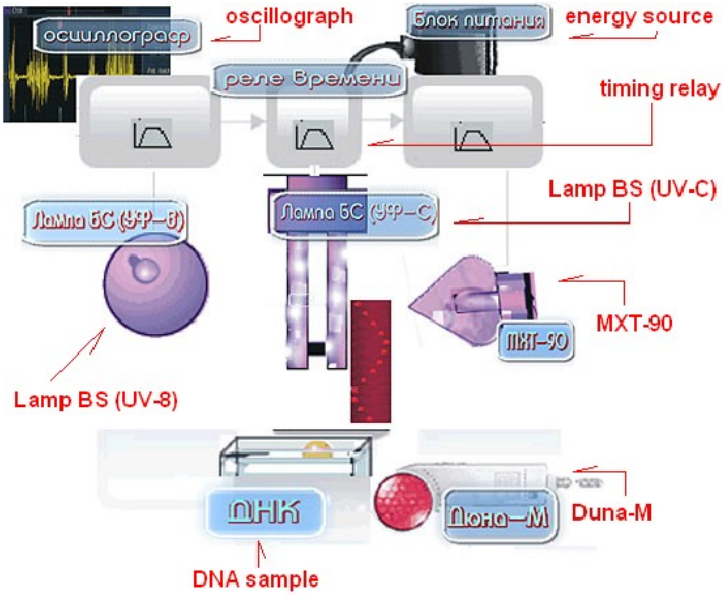


Figure 4.13: Schematic representation of the parts of the experimental apparatus

Chapter 5

Quantum Model for Remote Replication

5.1 Introduction

The idea about remote replication, transcription and translation of genes in terms of electromagnetic field patterns is very attractive and would be in accordance with the wave DNA vision. This requires a coding of DNA nucleotides. I have proposed several codings of this kind.

1. In DNA as topological quantum computer model [K3] quark and anti-quark at the ends of a flux tube connecting DNA nucleotide to a lipid of the nuclear or cell membrane takes care of the coding. Also sequences of dark nucleons giving rise to dark nuclei realize the analogs of DNA, RNA, tRNA, and amino-acids as well as vertebrate genetic code [K76], [K31]. Dark nucleons sequences could correspond to the phantom DNA discovered by Gariaev's group [I21].

2. Quantum antenna hypothesis represents one of the oldest ideas of TGD inspired quantum biology [K50]: molecules would act like quantum antennas. Frequency coding would be very natural for groups of molecules participating in the same reaction: the flux tubes connecting the molecules would carry the radiation inducing resonant antenna interaction and phase transitions reducing Planck constant would bring the reacting molecules near to each other. Magnetic flux tubes connecting the molecules would be essential element of the mechanism. Remote replication would represent an example about a situation in which $\hbar$ changing phase transition does not take place. If one wants coding of individual molecules -such as DNA nucleotides- by frequency in turned coded by the value of $\hbar$ for given photon energy ($E = hf$), one is forced to make ad hoc assumptions and it is difficult to find any plausible scenario. Quantum antenna mechanism could make possible remote replication for which the findings of Montagnier's group as well as remote transcription for which the work of Gariaev's group gives some evidence.

3. One can consider also a coding by field patterns. In fact, the quark and antiquark at the ends of the flux tube generate a color magnetic field coding for the quark pair since the classical color field depends on the color of the quark and its antiquark. Gariaev's group has proposed that the change of polarization direction could provide a possible mechanism of coding of DNA sequences to radiation patterns [I20]. The proposal is discussed from TGD point of view in [K75]. The mechanism changing the polarization direction should reduce to different propagation velocities for the two circular polarizations. The other polarization should act more strongly with the DNA related structures and this should cause the slowing down of propagation since it would correspond to sequence of absorptions and emissions. The constraint that this occurs coherently for DNAs and codes the DNA sequence is very powerful condition. It is however difficult to imagine how this mechanism alone could give rise to remote replication of DNA or similar processes: the coding from radiation pattern to DNA sequences is the bottle neck. Therefore this mechanism will not be discussed in the following.

5.1.1 The original model of remote replication

In the sequel a model for the coding of DNA in terms of radiation patterns is discussed. There are three experimental guidelines: the phantom DNA [I21] identified as dark nucleon sequences in TGD framework and the evidence for remote activation of DNA transcription [I20] - both discovered by Gariaev's group - are assumed as the first two key elements of the model. The remote replication of DNA suggested by the experimental findings of Montagnier's group serves as a further guideline in the development of the model. Also the results of the latest experiment of Gariaev's group in many respects similar to that of Montagnier's experiment but differing in certain crucial aspects from it are used as input.

Polymerase chain reaction (PCR) (see `http://tinyurl.com/ybv6mn5l`) is the technique used in the experiments of Montagnier's group [I8] and later in somewhat modified experiment by Gariaev's group involving irradiation of the second test tube by laser light. DNA polymerase catalyzes the formation of DNA from existing DNA sequences serving as a template. Since the catalytic interaction of DNA polymerase takes place with already existing DNA sequence, the only possibility is that first some conjugate DNA sequences are generated by remote replication after which DNA polymerase uses these sequences as templates to amplify them to original DNA sequences. Whether the product consists of original DNA or its conjugate can be tested.

The model inspires the proposal that the magnetic body of a polar molecule codes for it using dark nucleon sequences assignable to the hydrogen bonds between the molecule and surrounding ordered water layer. Quantum antenna mechanism would allow the immune system to modify itself by developing ordinary DNA coding for amino-acids attaching to and thus "catching" the polar molecule. The mechanism could be behind water memory and homeopathic healing. The most general option is that every polar molecule in living matter would be 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 also with the magnetic body of DNA so that DNA-dark DNA association would be automatic. Same applies to mRNA and tRNA and amino-acids.

Remark: The first part of the chapter is essentially the article published together with Peter Gariaev in DNA Decipher journal [L62]. The considerations described below reflect the more recent views about remote replication.

5.1.2 Further developments of the model for remote replication

A more detailed model for the remote replication inspired by the findings of Luc Montangier's group

The findings of Montagnier *et al* [I27] (`http://arxiv.org/abs/1012.5166`) raise the possibility of remote replication of DNA. Montangier's experiment involves two chambers A and B. A contained water and genes and B water and 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. I have written articles about Montagnier's findings [L14, L18]. Gariaev has reported a similar phenomenon already before Montagnier *et al*: we wrote together with Peter Gariaeb an article discussing the TGD based model for the finding [L62].

The model for remote replication discussed below is a modification of a model developed earlier together with Peter Gariaev on basis of his findings and involves the following basic building bricks.

1. In TGD inspired vision about quantum biology relying on the notion of magnetic body (MB) carrying dark matter as phases of ordinary matter with effective Planck constant $h_{eff} = n \times h_0$ one ends up with the notion of dark DNA realized as sequences of dark protons and to the surprising finding that dark proton triplets realize vertebrate genetic code and basic biomolecules DNA,RNA,tRNA, and amino-acids [L22, L28].

2. Second realization of the genetic code is using dark photon 3-chords [L20, L21, L17]. The allowed 3-chords of icosahedral code realized as a Hamiltonian cycle define a harmony with 20 chords and having as a symmetry subgroup Z_6, Z_4 or Z_2 of icosahedral geometry. The harmony is fixed by a Hamiltonian cycle of icosahedron defining a 12-note scale. Tetrahedral

harmony has 4 chords and is unique. The symmetry group acts on the frequencies of the chord as a scaling and this is realized if the scale is obtained by quint cycle using octave equivalence.

The fusion of 3 icosahedral codes with different symmetries with tetrahedral code gives rise to bio-harmony with 64 chords. Genetic codons are identified as allowed 3-chords and amino-acids as orbits of codons. The number of codons at the orbit of given codon would correspond to the number of DNA codons coding for amino-acid and the predicted numbers are correct for the vertebrate code under rather general assumption although also the variants of the code can be understood as being due to the failure of exact mimicry of dark photon code by the chemical realization. The identification of bio-photons as decay products of dark cyclotron photons with large value of h_{eff} having universal energy spectrum due to the condition $h_{eff} = h_{gr}$ [K53].

A model for the radiative coding of DNA creating 1-1 correlation between ordinary and dark DNA codons and between two dark DNA codons.

3. TGD explanation [L19] for the fourth phase of water discovered by Pollack [L19, I46] and characterized by negatively charged exclusion zones EZs generated by radiation.

Galois confinement and (remote) replication in codon-wise way

TGD predicts two dark variants of genetic code realized as dark codons (DDNAs) identified either as dark proton triplets or dark photon 3-chords. The objection against dark photon 3-chords (3-photon states) is that the simultaneous emission of 3 dark photons is extremely non-probable. The proposed solution of the problem is that dark photons carry a number theoretic color associated with a Z_3 sub-group of the Galois group. Number theoretic color confinement would imply that only 3-chords can appear as asymptotic states analogous to baryons as 3-quark states. If also the dark protons form a number-theoretic color triplet, dark codons must consist of 3 protons and therefore also ordinary codons would have 3 letters.

The findings of Gariaev's group and Montagnier *et al* suggest the possibility or remote replication of DNA. The fact that dark codons do not decompose into letters like chemical codons poses strong constraints on the replication and transcription if one assumes DDNA-DNA-pairing. These constraints strongly suggest that the nucleotides in the water environment of DNA are not actually free but form loosely bound triplets representing codons bound with DDNAs. Replication is predicted to occur in a codon-wise way: this has been observed to be possible for RNA. It might be that the loose nature of exotic DNA codons allows this to occur quite generally.

Remote replication in this framework reduces to ordinary replication in TGD sense if also dark genes are present and formed by attaching flux tubes characterizing dark codons to a long flux tube associated with a gene. Remote replication requires that the portion of dark gene accompanying the ordinary gene is transferred from chamber A to chamber B in the experiment of Montagnier.

Codon-wise replication of RNA in lab

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 acid 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 way. However, it has been discovered that the replication using RNA triplets - genetic codons - as a basic unit can be carried out in lab even for the folded RNA strands and with a rather low error rate. Also the ribozyme involved can thus replicate in a codon-wise way. For units longer than 3 nucleotides the replication becomes prone to errors.

The TGD based model for the findings relies on the vision that there are several realizations of the counterparts of DNA, RNA, tRNA, and amino-acids and of the genetic code so that chemical code is only one particular realization. For the dark realization in terms of entangled dark proton triplets one cannot analyze the codons to triplets of ordered letters so that codon is the smallest unit. This motivates the question whether RNA replication during the proposed RNA era happened in a codon-wise way and relied on pre-tRNA in which amino-acid catalyzed

the addition of RNA of tRNA to RNA sequence. The second possibility would be that replication occurs for dark codons basically so that ordinary letter-wise replication for DNA would actually occur codon-wise. The nucleotides in the water environment of genes would combine with scaled up dark codons to form "loose" variants of ordinary codons having no valence bonds between the nucleotides.

The crucial evolutionary step would have been analogous to the emergence of written language in which words decomposed into letters meaning a transition from RNA era to DNA era and DNA replication and transcription in a letter-wise fashion. At this step DNA and RNA polymerase and DNA helicase emerged. This picture is discussed from the point of view of the realization of the code in terms of 3-chords formed from dark photons. The 12-note scale forming the basis of the model of bio-harmony based on 64 chord harmony emerges naturally.

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` [L16].

5.2 The Findings That One Should Understand

It is good to start by summarizing the experimental findings that the model should explain.

1. One should be able to identify phantom DNA [I21]. This identification explains the findings about phantom DNA if ordinary and dark DNA have common resonance frequencies and therefore behave like resonantly interacting quantum antennae.

2. The earlier findings of Gariaev's group suggesting remote gene expression [I20], which becomes also possible if the DNAs of the sender can activate the DNA of the receiver by radiation. Direct activation could be based on electromagnetic signal between DNA of the sender and ordinary conjugate DNA of the receiver. Scattering from ordinary and possibly also phantom DNA and would generate this kind of signal. The challenge is to explain why the activation obeys genetic code in the sense that a given DNA sequence activates only similar DNA sequence.

3. The claim of Montagnier's team [I26, I27] is that the radiation generated by DNA affects water in such a way that it behaves as if it contained the actual DNA. A brief summary of experiment of Montagnier and collaborators is in order.

   (a) Two test tubes containing 100 bases long DNA fragments were studied. Both tubes were subjected to 7 Hz electromagnetic radiation. Earth's magnetic field was eliminated to prevent its possible interference (the cyclotron frequencies of Earth's magnetic field are in EEG range and one of the family secrets of biology and neuroscience since seventies is that cyclotron frequencies in magnetic fields have biological effects on vertebrate brain). The frequencies around 7 Hz correspond to cyclotron frequencies of some biologically important ions in the endogenous magnetic field of.2 Tesla explaining the findings. This field is 2/5 of the nominal value of the Earth's magnetic field.

   (b) What makes the situation so irritating for skeptics who have been laughing for decades for homeopathy and water memory is that the repeated dilution process used for the homeopathic remedies was applied to DNA in the recent case. The solution containing no detectable amounts DNA (dilution factor was 10^{-12}) was placed in second test tube whereas the first test tube contained 100 bases long DNA in the original concentration.

   (c) After 16 to 18 hours both tubes were subjected to polymerase chain reaction (PCR), which builds DNA from its basic building bricks using DNA polymerase enzyme. What is so irritating from the point of view of skeptic was that DNA was generated also in the test tube containing the highly diluted water. Water in presence of second test tube seems to be able to cheat the polymerase by mimicking the presence of the actual DNA serving in the usual situation as a template for builing copies of DNA. One could also speak about the analog quantum teleportation. Note that the presence of both test tubes - and therefore some kind of communication between the samples - is absolutely esential for the process to take place: repeated dilution is not enough.

4. Peter Gariaev's team has carried out an analogous experiment recently in which one has two test tubes containing water. Tube A contained DNA fragments and tube B contained only water and DNA nucleotides plus DNA polymerase - just as as in Montagnier's experiment. The analog of the homeopathic procedure was not however applied to tube B. The experiments use a drop of DNA in water in gamma concentration in tube A. This DNA (with length of 600 base pairs) was scanned by laser radiation from helium-neon laser. The scattered radiation having a wide spectrum of frequencies down to kHz frequencies was applied on tube B at distance of 3 m in refrigerator (+4 Celsius) containing distilled water solution of DNA nucleotides and DNA polymerase inducing polymer chain reaction PCR amplifying DNA template if present. The generation of DNA sequences in tube B with the same mass distribution as in tube A by polymer chain reaction (PCR) is observed suggesting that the necessary DNA template is generated as a direct copy or conjugate of the original in test tube A by some unknown mechanism. Nucleotide sequences have not been analyzed to see whether they are identical or conjugates of those in tube A.

5.3 The Model Of Remote Replication Consistent With DNA As Topological Quantum Computer Model

The basic assumptions are that the scattered radiation, the flux tubes of the magnetic body of DNA along which the radiation propagates, and quarks and antiquarks at the ends of the flux tubes from system able to serve as a template for the formation of conjugate of ordinary DNA. To understand how remote remote replication could take place, some further assumptions are necessary.

1. The flux tubes emanating from DNA are parallel and condensed at 2-D flux sheet having DNA at is first boundary so that DNA nucleotides can attach to the flux tubes at the second boundary. The attached nucleotides would be along the same line and would form DNA sequence in remote replication process.

2. Quantum antenna interaction takes place between group of molecules participating a given reaction so that they have common antenna frequency as resonance frequency. The frequencies characterize the radiation propagating along magnetic flux tubes connecting the molecules, and could come as sub-harmonics of the frequency of (in the case considered) visible light from the formula

$$E = h_n f, \;\; h_n = nh \;\; , \;\; n = 1, 2, 3, ... \;\; .$$

Here E is the fixed energy of photon. h_n denotes value of Planck constant which in TGD Universe can have infinite number of values coming as multiplies of the ordinary Planck constant h.

For a given photon energy E one obtains harmonics of the basic wavelength

$$\lambda = \frac{c}{f(n)} = n\lambda_0 \;\; .$$

Wave length would correspond to the length of the flux tube proportional to n. DNAs with flux tubes characterized by different values of n would correspond to different levels in the evolutionary hierarchy. In TGD inspired theory of consciousness the value of h_n serves as the measure for the time scale of planned action and memory span and neurons of frontal lobe would represent the highest level in the hierarchy,

3. If resonance frequency is same for all nucleotides, frequency cannot distinguish between DNA nucleotides. In the model of DNA as topological quantum computer the quark (u or d) and antiquark ($\overline{u}$ or $\overline{d}$) at the ends of the flux tube code for A, T, C, G. This model is the simplest one and does not require any additional assumptions about frequency coding. It also allows resonant interaction at several frequencies: the scattering of visible light from DNA indeed produces a wide spectrum of frequencies interpreted in terms of dark variants of visible photons.

One can criticize the assumption that particular quark or antiquark is associated with the flux tube ending at particular nucleotide. At this moment this assumption does not have a convincing dynamical explanation. Presumably this explanation would rely on the minimization of the interaction energy.

4. What is needed is a model explaining why the resonant antenna frequency does not depend on nucleotide: obviously the frequency should relate to something shared by all nucleotides. An energy level associated with sugar-phosphate backbone of DNA is what comes first in mind. A more exotic option is transition involved with quark-antiquark pair. Since electromagnetic field for non-vacuum extremals is accompanied by classical color field, the exchange of gluons between quark and antiquark suggests itself as the quantum antenna interaction distinguishing between nucleotides.

Quantum antenna mechanism is extremely general and flexible and might be a fundamental mechanism of bio-catalysis allowing also communication between visible and dark matter sectors. Antenna mechanism is of course central also in ordinary communications. If the biologically most relevant interactions of biomolecules via quantum antenna mechanism then also water memory and the claimed effects of homeopathically treated water might be understood [K31]. The testing of the dark photon aspect of the hypothesis would require the detection of the dark photons somehow: the decay to a bunch of n ordinary photons with same wavelength is the obvious manner to achieve this.

5.3.1 Identification Of Phantom DNA

The observed residual coherent scattering from a chamber from which ordinary DNA is removed inspired the notion of phantom DNA [I21]. The questions are what phantom DNA is and is it relevant to remote replication of the ordinary DNA.

Phantom DNA observed in the scattering experiments could correspond to dark nucleon sequences realizing vertebrate genetic code with dark nucleons consisting of three quarks representing both DNA, RNA, tRNA, and amino-acids as particular nucleon states [L2, K31]. The resonant interaction between ordinary and dark DNA would explain why light at same frequencies scatters also from dark DNA in phantom DNA experiments. In Montagnier's experiments it could give rise to a positive feedback amplifying the radiation from second sample containing DNA. Water would be living in the sense that it contains "dark DNA" and dark DNA might allow remote transcription to ordinary DNA sequences in presence of ordinary DNA codons (triplets) and vice versa.

Skeptic can of course ask whether one could explain the experimental findings without assuming phantom DNA.

1. In Gariaev's experiments [I21], which inspired the notion of phantom DNA part of DNA could "drop" to parallel space-time sheets and have the same effect on the scattered radiation as the ordinary DNA. This explanation would however require the many-sheeted space-time of TGD - probably equally abominable to skeptic as phantom DNA.

2. In Montagnier's experiment and also in the recent experiment of Gariaev the ordinary DNA contained by water droplet could diffuse to dark space-time sheets and enter from flux tube A to flux tube B along the same magnetic flux tubes as radiation propagates. DNA polymerase would allow to amplify this leaking DNA and produce conjugate DNA. The irradiation of the original DNA would generate the flux sheets serving as a route for the transfer. The killer test is to check whether it is indeed conjugate of the original DNA which is produced. Again many-sheeted space-time is required.

3. For the option based on DNA as topological quantum computer hypothesis discussed above the remote replication would take place via the direct formation of conjugate DNA template and DNA polymerase produces from this copies of the *original* DNA whereas for "trivial" option conjugate DNA is produced. Phantom DNA would not be absolutely necessary. It is however questionable whether the intensity of the radiation is high enough and the resonant interaction with phantom DNA which could give rise to a positive feedback might be needed to amplify the radiation.

5.3.2 Dark DNA And Frequency Coding By Quantum Antenna Mechanism

The remote transcription of dark DNA (phantom DNA) to ordinary DNA and vice versa would have quite far reaching implications for evolution since dark DNA/RNA/tRNA/amino-acids could define a virtual world serving as $R\&D$ lab where new DNAs could be developed and if needed translated to ordinary DNA. The dark DNA could be also transferred through cell membranes without difficulty, in particular to germ cells. Also the genetic transfer between different organisms would become possible. Second possibility is that the magnetic flux tubes mediating the dark photons traverse the cell membranes so that even the transfer of dark nucleons through the cell membrane is un-necessary. The implications for genetic engineering would be obvious.

Could one generalize the quantum antenna mechanism to the interaction between dark nucleons representing DNA triplets as entangled states of three quarks and ordinary DNA codons consisting of three unentangled nucleotides? Could similar mechanism realize genetic code assigning to dark DNA dark variants of RNA, tRNA and amino-acids via the analogs of transcription and translation processes? It seems that frequency coding, which - somewhat disappointingly - did not look natural for remote replication of ordinary DNA, is ideal for these processes so that the original idea of wave DNA would be realized at the level of dark-visible and dark-dark interactions.

The flux tubes would be associated with entire codons -DNA triplets - rather than individual nucleotides. Different DNA triplets do not form interacting groups in the sense that they should be connected by flux tubes. Therefore the simplest possibility would be frequency coding with specific resonance frequency for each DNA triplet. No quarks at the ends of the flux tubes connecting codons are needed.

Remark: : A hierarchy of flux quanta is essential and must distinguish between its levels. Flux tubes associated with nucleotides at flux tubes associated with DNA codons at flux sheets traversing DNA strands.

If one assumes that octaves correspond to the same frequency this would require odd multiples

$$\lambda(n) = (2n+1)\lambda_0 \quad , \quad n = 0, ..., 63$$

of λ_0 so that the longest wavelength would be $127\lambda_0$. In the number theoretic model of the genetic code based on the notion of Combinatorial Hierarchy [K30] codons are indeed labeled by 64 integers in the range $0, ..., 127 = 2^7 - 1$. These integers are however not assumed to be odd. One can also consider the possibility that the frequencies are coded by the value of Planck constant and this option leads to an interpretation of the earlier proposed realization of divisor code [K76] to be discussed later on.

Support for this option comes from the phenomenon of phantom DNA demonstrating that resonant scattering of light from DNA and dark DNA occurs for the same frequencies.

Can one imagine remote transcription of dark DNA to ordinary DNA using *only nucleotides* as building bricks? This process would require coupling of DNA nucleotides to dark nucleons representing DNA triplets and it is not easy to imagine any simple mechanism making this possible. Already existing DNA triplets seem to be necessary.

5.3.3 Common Explanation For The Findings Of Montagnier And Gariaev

In the experiments of Montagnier's group [I27] the outcome is remote replication whereas the earlier experiments Gariaev's group [I21, I20] give evidence for phantom DNA and remote activation of DNA transcription by scattered laser light able to represented genetic code. There must be interaction between the test tubes in Montagnier's experiments and in the recent experiments of Gariaev's group observing remote replication there is explicit interaction between the test tubes due to the scattered laser radiation. Hence one expects a common underlying mechanism based on radiation between the tubes and phantom DNA.

1. The TGD based explanation [K31] of Montagnier's findings relies on the assumption that the homeopathic procedure generated a population of dark DNA nucleotides in the diluted system. The sequence of dilutions and shakings was like a series of environmental catastrophes

driving the evolution of dark DNA and also feeding metabolic energy to the system. The outcome was dark DNA population mimicking the original DNA in the test tube B. In the presence of DNA polymerase in tube B and second test tube A containing ordinary DNA the dark DNA was somehow able to generate ordinary DNA in tube B. The detailed mechanism for this remained open.

2. Could the scattered laser light have the same effect as the homeopathic procedure? This would require a direct transcription of dark DNA to ordinary DNA in the presence of DNA polymerase and nucleotides (only them!). It is very difficult to understand how this could happen. DNA polymerase very probably does not have the same catalyzing effect on dark DNA sequences as on ordinary DNA sequences. It is also difficult to imagine the build-up of ordinary DNA from nucleotides using dark nucleon sequences as templates: if frequency coded codons would serve as building bricks, situation would be simpler as already found.

3. One must not forget that the presence of the test tube A was essential in the experiment of Montagnier: communications between the test tubes crucial for the outcome must have taken place. The consistency between the two experiments could be achieved if the DNA in test tube A generated the counterpart of the scattered laser signal in Gariaev's experiments but certainly as a much weaker signal.

4. This signal should have been amplified somehow by the presence the dark DNA sequences in tube B so that it would have been able to generate critical amounts of conjugate of the original DNA amplified by DNA polymerase to the copy of the original. What suggests itself is a positive feedback loop ordinary DNA sequences $\rightarrow$ dark DNA sequences $\rightarrow$ ordinary DNA sequences..... causing the amplification of the weak signal so that it is able to induce remote replication by the proposed mechanism. This kind of feedback of signals propagating between magnetic bodies was assumed also in the model for the strange images produced by the irradiation of DNA sample by ordinary light interpreted as photographs of magnetic flux tubes containing dark matter [K1].

This model explains also the findings of the recent experiment (unpublished) of Gariaev. In this case the amplification by feedback mechanism could be present but might not be needed since the scattered laser radiation could give strong enough signal to produce the needed amount of conjugate DNA serving as a template. What is nice from TGD point of view that the consistency between the two experiments gives support also for the notion of dark DNA and its identification as phantom DNA.

5.3.4 Summing Up The Basic Assumptions Of The Mechanism

The basic assumptions of the model of remote replication deserve a short summary.

1. Bio-molecules would serve as receiving and sending quantum antennas forming populations with communications between members just like higher organisms. The molecules participating the same reaction would naturally have same antenna frequencies. Quarks and antiquarks at the ends of the flux tubes would code for different nucleotides and the frequencies associated with the nucleotides would be identical. The character of classical electromagnetic field would code for a particular nucleotide.

2. Remote replication and other remote polymerization processes would differ from the ordinary one only in that the phase transition reducing the value of Planck constant for the flux tube would not take place and bring the molecules near each other. Note that the fractal hierarchy of flux quanta: nucleotide flux tubes, codon flux tubes and flux sheets associated with DNA strands is essential.

3. The immediate product of remote replication would be the conjugate of the original DNA sequence and DNA polymerase would amplify it to the copy of the original DNA sequence. This prediction could be tested by using very simple DNAs sequences- say sequences consisting two nucleotides which are not conjugates. For instance, one could check what happens

if conjugate nucleotides are absent from the target (neither conjugate nor original DNA sequence should be produced). If the target contains conjugate nucleotides but no originals, only conjugate DNA sequences would be produced - one might hope in sufficiently large amounts to be detectable.

4. Frequency coding would be natural for quantum antenna interactions between ordinary DNA and its dark variant and also between dark variants of DNA, RNA, tRNA, and amino-acids. The reason is that dark nucleons represent the genetic code by entanglement and it is not possible to reduce the codon to a sequence of letters.

5.4 Possible Implications

The proposed realization of remote replication seems to have rather far reaching implications for the understanding of the mechanism of homeopathy and basic mechanisms of immune system as well as to the understanding of how DNA -dark nucleon sequence association. One can also interpret the proposed TGD based realization of the divisor code [K76] suggested by Khrennikov [K78] as frequency coding of DNA triplets by the value of Planck constant assignable to flux tubes emerging from DNA triplets.

5.4.1 Possible Relevance For Homeopathy And Immune System

TGD inspired vision about water memory assumes that the magnetic bodies of molecules dis-solved into water represent the molecules in terms of cyclotron frequencies characterizing its magnetic body. Molecules can lose their magnetic bodies as the hydrogen bonds connecting the molecule to the magnetic body are split. The population of these lost magnetic bodies would define a representation for the dissolved substance able to mimic it.

The hitherto unanswered questions concern the detailed structure of the magnetic body of the molecule and how it codes for the molecule. The hydrogen bonds connecting the molecule to the ordered water forming a kind of ice covering the molecule in the inactive state should be crucial aspect of the coding. If dark nucleon sequences are associated with the hydrogen bonds of this "ice layer" or generated in their splitting as I have proposed, one can ask whether dark nucleon sequences could characterize the molecular magnetic body. If so, cyclotron resonance frequencies or more general frequencies associated with the dark DNA sequences could code for the molecule. DNA sequences would define a universal language allowing for the system to name for polar molecules.

Quantum antenna mechanism would in turn associate ordinary DNA sequences with the dark nucleon sequences coding for the molecule. Hence one can imagine a development of a mechanism allowing the organism to modify its DNA by adding to it genes coding for proteins characterized by the same resonance frequencies as the magnetic bodies of the invader molecules. These proteins would couple strongly to the invader molecules via quantum antenna mechanism and the phase transition reducing Planck constant would allow them to catch the invader molecules by attaching to them. The fact that the DNA of immune system evolves very rapidly conforms with this vision.

5.4.2 Frequency Coding For DNA Sequences By The Value Of Planck Constant As A Realization Of Divisor Code

The realization of dark magnetic bodies of polar molecules in terms of dark nucleon sequences allows to understand the association of dark DNA with ordinary DNA, RNA, and tRNA making among other things possible the transcription of dark DNA to DNA and vice versa. Dark nucleon sequences would be associated with the magnetic bodies of DNA, mRNA, and tRNA. This would apply also to amino-acid sequences. Dark DNA would separate from ordinary DNA as it loses its magnetic body in the splitting of hydrogen bonds and suffers denaturation. Similar mechanism would cause denaturation of other biomolecules and would mean that they "lose their names" and thus information content and become mere organic molecules instead of living bio-molecules. This kind of association would make the emergence of the genetic code and its generalization to the naming of molecules by DNA sequences trivial.

Genetic code can be understood from the proposed natural correspondence between dark nucleon sequences and DNA, RNA, tRNA, and acmino-acids). I have however developed also another realizaton based on TGD based realization of so called divisor code first suggested by Khrennikov and Nilsson [K78] and the following argument allows to interpret in terms of frequency for fixed value of photon energy with frequencies coded by the value of Planck constant.

1. The observation of Khrennikov and Nilsson is following. Consider the integers n in the range 1, ..., 21 and obviously labeling amino-acids and let $k(n)$ the number of divisors of n. Define $B(k)$ as the number of integers n for which the number of divisors is k. It turns out that the numbers $B(k)$ are rather near to the numbers $A(k)$ of amino-acids coded by k codons. This suggests that given amino-acid A is coded by a product of prime $p(A)$, which alone characterizes it, and integer $n(A)$ in the range $1, ..., 21$. The product of integers characterizing the codon coding for A would be characterized by the product of $p(A)$ and some factor $r(A)$ of $n(A)$. With these assumptions given codon would code for only single amino-acid and the number of DNAs coding for amino-acid A is the number of the factors $r(A)$ of $n(A)$. The codons coding for A would be coded by integers $p(A)r(A)$ such that $r(A)$ divides $n(A)$. The safest assumption would be that the primes $p(A)$ satisfy $p(A) > 19$ so that $p(A)$ does not divide $n(A)$ for any A. If $p(A)$ is as small as possible the value spectrum of $p(A)$ is

$$\{23, 29, 31, 37, 41, 43, 47, 53, 59, 61, 67, 71, 73, 79, 83, 89, 97, 101, 103, 107, 109\} \ .$$

   If one assumes that the two additional amino-acids coded in some cases by non-vertebrate genetic code correspond to primes also the primes $113, 127$ are included.

   What is interesting is that Mersenne prime $M_7 = 2^7 - 1 = 127$ appears in the model of genetic code based on the notion of Combinatorial Hierarchy [K30]. This model assumes that DNA codons correspond to 64 integers in the range $1, ..., 127$. This realization of the genetic code cannot however be consistent with the divisor code realized in the proposed manner since it would require that the integers $n(A)p(A)$ belong to the range $1, .., 127$. The prime factors of these integers can however belong to this range.

2. The TGD inspired proposal [K76] was that the flux tube assignable to amino-acid A corresponds to $\hbar = p(A) \times n(A)\hbar_0$ whereas the DNA triplet (for quark-antiquark coding nucleotide rather than triplet) coding for it is characterized by $\hbar = p(A) \times r(A)\hbar_0$ such that $r(A)$ divides $n(A)$.

3. This proposal could be interpreted in terms of frequency coding by quantum antenna mechanism. For a given photon energy E wave length would be coded by the value of $\hbar$ and one would have $\lambda_n = n\lambda_0$, $n = p(A)n(A)$ for amino-acids and $n = p(A)r(A)$ for codons. The condition that flux tube lengths are same for different DNA triplets would be satisfied if the common length of the flux tubes is an integer multiple of λ_0 proportional to the product of all integers appearing as factors in the integers coding for amino-acids. The common length of the flux tubes would be therefore proportional to the product $\prod_A p(A) \prod_A r_A$.

5.5 More Precise View About Remote DNA Replication

Both Luc Montagnier [I26, I27] and Peter Gariaev [I31] have found strong evidence for what might be called remote replication of DNA. I have developed a TGD inspired model for remote replication using the data from Peter Gariaev [K82], who has developed the notion of wave DNA [I20] supported by Montagnier's findings.

Polymer chain reaction (PCR) [I8] provides a way to build copies of piece of DNA serving as template. Once single copy is produced, it serves as a template for a further copy so that exponential amplification is achieved. Montagnier's and Gariaev's works suggest however that the synthesis of DNA could also occur without a real matrix DNA as remote replication. According to the proposal of Gariaev [I20, I45] DNA template would be remotely represented as what he calls wave DNA. Montagnier [I27] uses 7 Hz ELF radiation to obtain the effect whereas Gariaev [I31] uses scattering of laser light into large interval of frequencies to achieve the effect.

In TGD approach magnetic body containing dark matter with large Planck constant, the associated cyclotron radiation for which energy scale is proportional to effective Planck constant $h_{eff} = n \times h$ having large values implying conjectured macroscopic quantum coherence of living matter, dark analog of DNA represented as dark proton sequences at magnetic flux tubes and accompanying ordinary DNA, plus reconnection of U-shaped magnetic flux tubes assignable to the magnetic bodies of biomolecules and allowing them to recognize each other, are the basic elements. The model has evolved from the attempts to understand water memory and homeopathy in TGD framework [K31].

Both 7 Hz ELF radiation and scattering of laser light would both generate dark photon (large Planck constant) spectrum with a wide spectrum of frequencies but with the same energy which in Gariaev's experiments would naturally be the energy of scatter laser light. The dark photons would provide representation for DNA codons. If 7 Hz frequency radiation involves dark photons with energies of visible photons transforming to ordinary photons before scattering from DNA the outcome would be same as in Gariaev's experiments.

This picture conforms with Gariaev's hologram idea and also with TGD based vision about living matter as a conscious hologram [K8]. The laser beam that Gariaev has used and the 7 Hz irradiation (involving dark ELF photons at bio-photon energies) would act as a reference beam allowing to read a biohologram coded by DNA and its magnetic body. The outcome is dark photons with same energy but with varying values of Planck constant and thus with varying frequencies propagating along magnetic flux tubes to the target, which could be exclusion zone (EZ). Flux tubes are characterised by h_{eff} and magnetic field strength B_{end} determining cyclotron frequency (coded by the transversal area by flux quantization if monopole flux is in question). Metabolic energy is needed to create EZ and could be provided either by the radiation itself or by the repeated heating. Negentropic entanglement is generated and creates the correlation between dark (phantom) DNA codons and ordinary DNA codons.

The following involves same elements as the model discussed in [K82] but there are also new elements due to the developments in the model of dark DNA allowing to imagine a detailed mechanism for how water can represent DNA and how DNA could be transcribed to dark DNA. The transcription/association represents a rule and rules are represented in terms of negentropic entanglement in TGD framework with pairs of states in superposition representing the instances of the rule. Transition energy serves as a characterizer of a molecule - say DNA codon - and the entangled state is a superposition of pairs in which either molecule is excited or dark DNA codon is excited to higher cyclotron state with same energy: this requires tuning of the magnetic field and sufficiently large value of h_{eff} at the flux tube. Negentropic entanglement is due to the exchange of dark photons: this corresponds to wave DNA aspect. Dark cyclotron photons also generate negatively charged exclusion zones (EZs) discovered by Pollack and in this process transform part of protons to dark ones residing at the magnetic flux tubes associated with EZs and forming dark proton sequencies.

5.5.1 Some Background

The model for remote replication involves the following basic building bricks.

1. Dark variant of DNA realized as dark proton strings representing dark nuclei.

2. The identification of bio-photons as decay products of dark cyclotron photons with large value of h_{eff} having universal energy spectrum due to the condition $h_{eff} = h_{gr}$.

3. TGD explanation for the fourth phase of water discovered by Pollack [L19] and characterized by negatively charged exclusion zones EZs generated by radiation.

4. A model for the radiative coding of DNA creating 1-1 correlation between ordinary and dark DNA codons and between two dark DNA codons.

Dark DNA as dark proton strings

TGD leads to a model of nuclei as nucleons strings [L2]. The model generalizes to the dark matter sector [L2, K31].

1. I have proposed the notion of dark DNA realized as dark proton sequences (3 quark states), which I have argued ton basis of a simple model to form representations for DNA, RNA, amino-acids and even tRNA is central for TGD inspired biology. Biochemistry would define only a secondary representation for more fundamental realization of genetic code and analogs of basic biomolecules in terms of dark nuclear physics.

   I have conjectured that translations, transcription, etc generalize and apply to pairs of ordinary and dark and dark and dark DNA and amino-acids. One could even consider that dark DNA would make possible induction of genetic changes: transfer dark DNA inside germ cells and transform them to ordinary DNA and attach to existing DNA. If dark DNA can be generated by radiation as wave DNA notion suggests then radiation from other cells to germ cells could induced genetic changes. Living systems would have kind of Research and Discovery apartment developing new candidates for genes. Evolution would be the opposite for blind random trials.

2. I have also proposed that immune system could have developed from what is basic mechanism of homeopathy and water memory. The magnetic bodies of water clusters mimic invader molecules - or rather their magnetic bodies. What is needed is a representation for cyclotron frequencies so that radiation would emerge in this phase. Cyclotron frequency spectrum would represent the invader and the simplest mimicry of invader molecule would be water structure with magnetic body characterized by same cyclotron frequency spectrum: water memory in short. Also the braiding of the magnetic body of the invader might be mimicked.

   Protein folding might be a chemical representation for this braiding and the proteins of immune system might mimic the braidings of the magnetic bodies of the invader molecules. DNA in turn would give a symbolic representation of proteins allowing to construct them when needed. Ordinary DNA and proteins would have been preceded by dark DNA and dark proteins. I have even proposed an interpretation of genetic code based on the idea that it represents the dynamical evolution of braiding of the magnetic body - or 2-braiding [K57].

   The basic mechanism of directed attention or sensing the presence of the invader molecule would be reconnection of U shape flux tubes of the magnetic bodies of the two system. Also resonant interaction by cyclotron radiation inducing cyclotron transitions is expected to be an essential piece of the mechanism. Magnetic body of water cluster could tune the thickness of flux tube so that the magnetic field is same as that in the flux tube of invader molecule so that primitive consciousness and act of free will would be involved.

3. Suppose that DNA codes for proteins, their cyclotron frequency spectrum and their braiding and knotting in protein folding in turn representing invader molecule. Is the frequency spectrum all that is needed to represent DNA and construct its dark variant? The experiments of Benveniste and followers [I18, I19] suggest that invader molecules are indeed represented by the cyclotron frequency spectrum alone. This would suggest connection with wave DNA concept.

Universality of cyclotron energy spectrum and bio-photons as decay products of dark photons

There are good empirical motivations [K53] to expect that the cyclotron energy spectrum is universal and in the range of bio-photon energy spectrum. This is achieved if h_{eff} is proportional to the mass m of the charged particle so that cyclotron energy $\hbar_{eff}eB/m$ is independent of mass and same for all charged particles.

Universality follows also from the condition that gravitational and biological Planck constants are identical: $h_{gr} = h_{eff}$, where $\hbar_{gr} = GMm/v_0$ is the gravitational Planck constant introduced by Nottale and assigned with the flux tubes mediating gravitational interaction in TGD Universe. The condition states that electromagnetic and gravitational flux tubes have same the value of effective Planck constant meaning that also gravitation would become a key player in biology.

Fourth phase of water, EZs, and metabolic role of cyclotron radiation

The experiments of Pollack [L19] suggest a partial answer to the question. in terms of what he calls fourth phase of water containing negatively charged regions, exclusion zones (EZ) of size up to 200 micrometers.

1. Irradiation of water by visible light generates negatively charged regions which he calls exclusion zones (EZs). The energy goes to the formation of electric voltage between exterior and interior and is analogous to cell membrane potential. Predecessor of cell could be in question. Some fraction of protons must go outside the system and my proposal is that it goes to magnetic flux tubes and forms dark proton sequences defining the analogs of basic bio-molecules. The $H_{1.5}O$ stoichiometry of EZs [L19] characterizing also earlier findings suggesting that one fourth of protons of water are dark in attosecond time scale (not visible in electron scattering and neutron diffraction) suggests that every fourth proton disappears from EZ. This anomaly was one of the strong motivations for taking the idea about dark matter as large h_{eff} phases seriously [K26].

   These structures would be involved also with water memory and homeopathy and immune system would have emerged from these. Free energy researchers know these regions quite well [H1] (no-one of course takes them seriously!) and they can be generated by just feeding energy to system used as metabolic energy. In homeopathy the mechanical agitation would do this and induce replication and perhaps even evolution of the resulting primitive lifeforms. Cavitation, use of strong electric field, maybe even heating used in PRC, etc... are possible mechanisms of energy feed.

2. The cyclotron radiation at cyclotron frequencies associated with flux tubes emanating from DNA codons could provide the energy needed to induce the formation of EZs. This would be the first function for the radiation.

3. If the DNA end of flux tube contains dark proton in state which corresponds to the DNA in one-one manner then the mass of the dark proton state would assign to it a unique cyclotron frequency distinguishing between DNA codons. The challenge is to understand the mechanism of DNA dark DNA pairing and dark DNA-dark DNA pairing and one expects resonant binding by exchange of dark cyclotron photons.

Pairing ordinary and dark DNA codons and two identical dark DNA codons by negentropic entanglement

One should understand the pairing of ordinary and dark DNA. As a matter fact, this pairing defines a realization of the genetic code as a physical 1-1 correlation of DNA codons with some physical states. I have consider this kind of realizations also in the model of DNA as topological quantum computer. The following realization relies on resonant interaction by exchange of dark cyclotron photons and can be seen as radiation based.

1. The most natural association between ordinary and dark DNA would via energy resonance. The energy for some molecular transition of DNA (in bio-photon energy range by argument below) would be same as cyclotron energy for the codon with large value of $h_{eff} = n \times h$ making cyclotron energy large.

2. By suitably tuning the value of the magnetic field B associated with the flux tube accompanying ordinary DNA codon the dark cyclotron energy can be tuned to be equal to the value of some biochemical transition energy of DNA, which is in visible and UV range typically - that is in the energy range of bio-photons.

3. Classically DNA codon and its dark variant can be thought of as exchanging forth and back dark photon at resonance frequency and become strongly correlated in this manner like tennis players during game. Quantum mechanically one has quantum entangled Schrödinger cat like state in which state pairs have same total energy but individual states do not have well-defined energy.

4. The correlation between dark proton states at two ends of flux tube would be realized as formation of bound state via resonant exchange of dark cyclotron photons. Negentropically entangled [K42] superposition for which simplest the possible form is $|n\rangle|n+1\rangle + |n+1\rangle|n\rangle$ of paired cyclotron states would be generated. DNA and dark DNA codons would pair to a negentropically entangled state in similar manner. Recall that in TGD framework negentropic entanglement (NE) carries potentially conscious information: the state represents a rule whose instances correspond to the state pairs in the superposition [K42].

5. One can consider also 3-particle NE of DNA codon and 2 dark DNA codons which is superposition of three 3-particle states with one particle excited to higher energy state with the same energy. DNA codon would be excited chemically and dark codons excited to cyclotron state ($n \to n+1$). 3-dimensional permutation symbol defines this kind of state. Also NE for larger number of particles is possible.

The tuning of the flux tube magnetic field to make cyclotron energy equal to chemical transition energy is possible for arbitrary biochemical transition energies and the association of dark proton states to arbitrary biomolecules is in principle possible via same mechanism. This would be essentially a symbolic representation of biomolecule, a name for molecule. If one has some number of different molecules able to form sequences, these sequences can be remotely reconstructed by using the cyclotron frequencies and transversal flux tubes associated with the template to generate the EZs and the name of the polymer to which the building bricks bind resonantly.

If the condition $h_{eff} = h_{gr}$ holds true, one can use instead of dark proton sequences sequences of *any* dark charged particles - say electrons and ions. Hence almost an unlimited repertoire of representations arises. These correspondences need not to be one-one. For instance, DNA-amino-acid 64-to-20 correspondence is possible to realize with the help of dark variants of DNA codons and amino-acids and also the partially or totally dark variants of this correspondence are possible.

This pairing mechanism would allow resonant interactions of the ordinary DNA codons in water and dark DNA codons induced by the dark cyclotron radiation and could play key role also in ordinary DNA replication and also in the remote replication reported by Montagnier [I27] and Gariaev [K82]. A phase transition reducing h_{eff} would bring ordinary and dark codon together and ordinary biochemistry would take care of the rest. Clearly, this mechanism would also allow biomolecules connected by magnetic flux tubes to find each other in molecular soup with pairing following by a phase transition reducing h_{eff}.

5.5.2 Does Remote Replication Apply Same Mechanism As MimicryOf Invader Molecules In The Case Of Water Memory?

Somehow the irradiation of water sample with the cyclotron radiation generated by real DNA should induce or be involved with the generation of dark DNA representing the ordinary DNA and the PCR process would use this dark DNA as template an involves pairing of ordinary and dark DNA nucleotides. How this could happen in TGD Universe?

The mechanism of remote DNA replication without chemical template would be essentially the same as in the TGD based model of water memory [K31] underlying also the model of homeopathy circumventing the ultra-naïve skeptic argument that homeopathy is not possible because the density of molecules dissolved in water is practically zero.

The cyclotron frequency spectrum allows to create EZ whose magnetic body mimics the invader molecule. Resonant formation of negentropically entangled pairs would define a realization of genetic code based on radiation and dark cyclotron radiation would give rise to the formation of EZs and accompanying dark proton sequences.

In the recent case invader molecule would be replaced with DNA expressing its presence using dark cyclotron radiation propagating along the flux tubes transversal to codons and forming part of the magnetic body of DNA. The magnetic flux tube of ordinary DNA codon realizing dark proton sequence as dark variant of DNA codon would generate its own representation by generating EZs in water.

The rules would be following.

1. Magnetic fields at U-shaped flux tubes associated with codons and dark codons must be equal so that also cyclotron frequencies coding for dark proton masses and therefore for dark proton

states would be equal so that frequency and energy resonance is possible and negentropically entangled state is formed. This assigns by resonance mechanism to the second end of flux tube same dark proton state as to the end near ordinary DNA. Recall that U-shape is essential for bio-super-conductivity based on large value of h_{eff} making possible large and negative spin-spin interaction energy for electrons of pair located at parallel flux tubes [K10, K58].

As described, binding is generated by resonant exchange of dark cyclotron photons between the ends which are in superposition of different cyclotron states. Magnetic field value in turn corresponds directly to ordinary DNA codon - or rather its transition in bio-photon energy range. It is essential that the value of magnetic field codes for ordinary DNA codon via a biochemical transition energy associated with it. One can imagine that magnetic body can tune the value of field by changing the transversal area of the flux tube carrying monopole flux (possible in TGD due to the CP_2 topology). Similar tuning would be involved when the magnetic bodies assignable to EZs detect possible invader molecules. Interestingly, the impurity molecules inside EZs are removed by unknown mechanism citebbioPollackYoutube.

2. Dark DNA codons associated with DNA would have U-shaped flux tubes which for large h_{eff} would extend to the water sample containing building bricks of DNA and catalyst. The flux tubes associated with dark DNA and building bricks of ordinary DNA would reconnect resonantly and lead to remote replication of DNA strand.

This option is definitely not the only possibility one can imagine but represents the general principle. For instance, one can consider using only DNA-dark DNA complex and inducing h_{eff} increasing phase transition transferring the dark DNA strand to the volume of the water sample. The mechanism allows also to consider remote translation of genes to proteins. The possible medical applications of this in a situation in which the DNA of the patient has suffered a mutation causing a disease are obvious.

5.6 Remote replication again

In TGD inspired vision about quantum biology relying on the notion of magnetic body (MB) carrying dark matter as phases of ordinary matter with effective Planck constant $h_{eff} = n \times h_0$ one ends up with the notion of dark DNA realized as sequences of dark protons and to the surprising finding that dark proton triplets realize vertebrate genetic code and basic biomolecules DNA,RNA,tRNA, and amino-acids [L22, L28].

The objection against dark photon 3-chords (3-photon states) is that the simultaneous emission of 3 dark photons used in communications as 6-bit unit is extremely non-probable. A possible solution of the problem is that dark photons carry number theoretic color associated with Z_3 subgroup of Galois group. Number theoretic color confinement would imply that only 3-chords can appear as asymptotic states analogous to baryons. If dark protons are also number theoretic color triplet, dark codons must consists of 3 protons and therefore also ordinary codons have 3 letters.

The findings of Montagnier *et al* [I27] (`http://arxiv.org/abs/1012.5166`) raise the possibility of remote replication of DNA. Montangier's experiment involves two chambers A and B. A contained water and genes and B water and DNA nucleotides. There were channels between the chambers but so thin that DNA could not get through. Besides this there was present em field with 7 Hz frequency. Same genes as in A appeared also in B. As if remote replication of genes in A had happened in B. I have written an articles about Montagnier's findings [L14, L18]. Gariaev has reported similar phenomenon already before Montagnier *et al*: we wrote together an article discussing TGD based model for the finding [K82].

How did the genetic information pass to B and how the remote replication took place? Somehow the radiation made the remote replication possible or at least more probable. Clearly the information about gene - not only about codons but also about their order and relative positions - should have been communicated from A to B. I have already earlier considered this problem but found no satisfactory solution to it.

Concerning the role of the 7 Hz frequency, there are two hints.

1. The nominal value of the lowest Schumann frequency is 7.8 Hz, not far from 7 Hz. Could one think that macroscopic quantum coherence in the scale of Earth was involved. 7.8 Hz

correspond to wavelength equal to circumference of Earth.

"Endogenous" magnetic field $B_end = .2$ Gauss identifiable as the monopole flux part of the Earth's magnetic field $B_E = .5$ Gauss explains the findings of Blackman [J7] and others about quantal looking effects of radiation at frequencies seem to be multiples of cyclotron frequencies of biologically important ions.

The problem is that the energies of cyclotron photons are ridiculously small for ordinary value of Planck constant. This was one of the motivations for the hypothesis that dark matter corresponds to phases of ordinary matter with effective Planck constant $h_{eff} = n \times h_0$ [K57, K58, K59]. The cyclotron frequency of K ion is $f_c(K^+) = 7.1$ Hz. The flux tubes with length of corresponding cyclotron frequency are also of the order of Earth circumference.

This raises several questions.

1. Did water generate flux tubes with magnetic field with frequency equal to $f_c(K^+) = 7.1$ Hz and strengthening coupling to a radiation with Schumann frequency or K cyclotron frequency or both so that the communications with the MB of Earth or/and layer of MB corresponding to K cyclotron was strengthened? The TGD based mechanism of water memory [K31] would be involved.

2. Did this make the remote replication more probable? How?

3. What DNA actually looks like in TGD Universe? What actually happens in DNA replication? What could happen in remote DNA replication?

In the sequel the questions whether cyclotron frequency or Schumann frequency or both were involved and how their presence made possible remote replication remain without detailed answer although it is clear that the presence of dark photons with this frequency should make possible the control by MB generating coherence of ordinary matter in the scale determined by the sizes of the chambers. These questions however led to a considerable increase in the understanding of dark variants of genetic code predicted by TGD [L22, L17, L36].

1. To understand remote replication one must understand replication. Dark codons do not decompose into letters like chemical codons: this poses strong constraints on the replication and transcription if one assumes DDNA-DNA-pairing. These constraints strongly suggests that the nucleotides in the water environment of DNA are not actually free but form loosely bound triplets representing codons and bound with DDNAs. This means a new variant of genetic code realizing codons as loose triplets of nucleotides in the water environment.

2. This proposal brings in mind TGD based model for viruses, which can decompose into pieces shared between several host cells and re-combine later as also the observation that the dense states of bacteria population have resemblance to multi-cellular embryos. The common TGD inspired explanation [L40] would be that the pieces of virus and cells of bacterial population are connected by magnetic flux tubes and form a single loosely bound unit at the level of MB. The prediction is that replication occurs in codon-wise manner: this has been observed to be possible for RNA [L30]. It might be that the loose nature of exotic DNA codons allows this to occur quite generally.

3. Remote replication in this framework reduces to ordinary replication in TGD sense if also dark genes are formed by attaching flux tubes characterizing dark codons to a long flux tube associated with gene. Remote replication requires that the portion of dark gene accompanying ordinary gene is transferred from chamber A to chamber B in the experiment of Montagnier.

5.6.1 Three variants of genetic code

The notions of MB and view about dark matter leads to 3 variants of genetic code.

1. The notion of MB suggests that dark proton sequences assumed to explain Pollack effect (`http://tinyurl.com/gwasd8o`) [L19] realize dark genetic code. Dark DNA (DDNA) codon

would correspond to 3-proton triplet assignable to closed flux tubes attached to a a long flux tube by U-shaped flux tube appendix giving rise to dark gene (`http://tinyurl.com/jgfjlbe`). Attaching means formation of U-shaped appendices from long flux tube and DDNA codon which reconnect to a pair of flux tubes. 3-proton states define dark analogs of DNA, RNA, tRNA, and amino-acids (DDNA, DRNA, DtRNA, DAA) [L22, L28]. The numbers of DDNAs coding for given DAA are same as for vertebrate genetic code.

2. Second dark code is needed for communications and realizes genetic codons as dark 3-photon states - 3-chords of bio-harmony [L17, L33, L36] (`http://tinyurl.com/yad4tqwl`). The model emerged from a model of musical harmony based on icosahedron and tetrahedron. 12-note scale is identified as a Hamiltonian cycle - a path going through all 12 vertices of icosahedron - such that going from vertex to neighbor corresponds to quint. Hamiltonian cycles have cyclic group Z_n,where $n = 0, 2, 4, 6$ is the order of the group, as symmetries. $n = 0$ corresponds to chaotic orbit and disharmony. Each of the 20 faces - triangles - corresponds to a chord of given harmony.

   One identifies the orbit of given face as DAA coded by faces (DDNAs) at the orbit. By combining 3 harmonies with $n = 6$, $n = 4$ and $n = 2$ one obtains 20+20+20 chords and the numbers of DNA coding given AA are essentially those in vertebrate code. By gluing tetrahedron to one face one obtains 4 additional chords (DDNAs) and 1 additional note very near to one of the notes of Pythagorean scale, whose problem is that it does not quite close. The numbers for analogs of DNA codons coding for for given DAA are same as for vertebrate code.

   The chords would be represented as "music of light" as states of 3 dark photons. Music expresses and creates emotions and bio-harmony would provide a physical correlate for emotional states at molecular level [L31].

3. Dark codes would be fundamental and chemical code would be their mimicry. One expects DDNA-DNA pairing with DDNA codons represented as dark proton triplets. DDNA codons and dark photon chords have no decomposition to letters (chinese and western languages provide an analog). This suggests that DNA replication and transcription cannot take letter-wise but but codon-wise. Amazingly, there is evidence that DNA replicates in codon-wise manner during RNA era: I have commented this in [L30].

   Nucleotides/letters in the water environment of DNA double strand should appear as loosely bound but correlated triplets of nucleotides associated with closed flux tubes containing dark DNA codon. They would represent exotic DNA codons. This would force fixed order of nucleotides essential for the code. By absence of valence bonds between nucleotides they would be effectively free but strongly correlated. This representation of the code would be crucial for replication and transcription.

These 3 codes allow to understand replication and transcription of DNA replaced in TGD with DDNA-DNA pair. The prediction is that the replication takes place codon by codon and might kill the model.

A model of replication based on this picture generalizes to remote replication suggested by the findings of Montagnier [I27]. The DDNA codons of ordinary DNA strand would be attached with a long side of closed flux tube as dark gene. In remote replication h_{eff} of dark gene would change and dark gene would be transferred to chamber B from A. After that the replication would proceed as usual.

5.6.2 An objection against bio-harmony

There is a serious objection against the realization of dark genetic code in terms of bio-harmony. The emission of 3 dark photons simultaneously looks extremely non-probable process.

Number theoretical physics suggests a solution of the problem. Number theoretical physics [L24] (`http://tinyurl.com/zylrd7w`) is a central part of quantum TGD and quantum biology and provides physical correlates for cognition. It explains dark matter as $h_{eff} = nh_0$ phases of ordinary matter with n identified as order of Galois group of extension of rationals and as dimension of extension. This picture predicts automatically evolution as increase of n in quantum jumps.

1. There is analogy with color confinement. Baryons consist of 3 quarks. Color symmetry is a symmetry of strong interactions and quarks form color triplets. Free quarks do not appear in the final states, which givs rise to color confinement: only color singlets, in particular baryons consisting of 3 quarks and mesons consisting of quark and antiquark are possible.

   This suggests that also now there must be a symmetry such that dark photons have new quantum numbers, which vanish for physical states such as dark photon triplets.

2. What these quantum numbers could be? The only candidate, which comes in mind are discrete quantum numbers related to the Galois group of extension of rationals defining number theoretic symmetry. For ordinary $h = 6h_0$ Galois group has $n = 6$ elements and equals to $Z_6 = Z_2 \times Z_3$.

   It appears as subgroup of higher Galois groups for which $h_{eff} = n \times h = 6nh_0$ one would have extension of extension. Z_3 confinement would require 3-photon states, which are Z_3 singlets with number theoretic colors summing up to zero. One would obtain only 3-chords. Ordinary photons would be Z_3 singlets.

3. Also the 3 protons of DDNA codon could form Z_3 triplet. Number theoretic color confinement would allow only 3-proton triplets. Genetic code is predicted correctly and the number letters in the codons is predicted to be 3.

   This raises two interesting questions.

1. Quantum-classical correspondence (QCC) is a exact part of TGD. Therefore I have considered the possibility that all physical symmetries could have number theoretical space-time correlates. However, at space-time level one cannot have representations of color group with non-vanishing triality $t = 0, \pm 1$. Same applies to spin half-odd integer representations of rotation group. Could $SU(2) \times SU(3)$ representations with triality $t = \pm 1$ and spin half-odd integer have triplet representation of Z_3 and double representation of Z_2 as space-time correlates? Z_6 would be the minimal Galois group allowing to realize spin and color for quarks.

2. Number theoretical physics predicts that Galois group for any extension of rationals acts as new hidden discrete symmetry. Could number theoretical confinement implying new selection rules be true quite generally? The larger the degree n of extension (h_eff), the larger the scale in which confinement holds true, is. For instance, genes could be analogs of color singlet many particle states for a larger subgroup.

This is not the only option. I have already earlier considered with Peter Gariaev [K82] a proposal in which dark photons would communicate the genetic information from A to B. The problem is how the massless extremals (MEs) [K5] associated with them can be parallel and of same length: this would require that they form a quantum coherent entity. Could one consider a modification of the above proposal assuming that gene is an entity of N codons confined number theoretically? Could one can speak about dark photon genes as composites of N dark photon 3-chords? The information would be sent by dark photon gene representing entire music piece, as one might say. In chamber B energy-frequency resonance would generate a linear configuration of exotic codons, which would reduce to DDNA-DNA pair when h_{eff} is reduced.

5.6.3 DDNA-DNA, DDNA-DDNA, DDNA-exotic DNA pairings

The idea about MB as boss of BB suggests that DNA is accompanied by DDNA. DDNA would be the fundamental DNA and ordinary DNA emerged later as a kind of mimicry and there would be DDNA-DNA pairing.

The basic problem problem is that DDNA codons do not allow decomposition into letters like DNA codons. It seems that replication and transcription must occur codon by codon rather than letter by letter. For translation of mRNA this is indeed the case: tRNA are the basic objects. Could this be true in modified sense also for replication and transcription? In fact, RNA can replicate in codon-wise manner [L30]. Could this occur quite generally, and could the codons for replication believed to occur letter-wise be present in a latent manner?

DNA and DDNA codons

At least 3 new kind of codons are predicted (`http://tinyurl.com/yygqen5g`).

1. Also ordinary DNA codons involve flux tubes. Valence bonds between nucleotides of DNA strand and hydrogen bonds in double strand involve flux tubes or pairs of them.

2. DDNA codons are paired with ordinary DNA codons of DNA strand. DDNA codons would correspond to dark proton triplets at flux loops being analogous to tritium and ^{3}He. The model for remote replication requires that DDNA codon loops are connected to long closed dark gene flux loop by U-shaped appendages - attached to dark gene.

   If DDNA and DNA codons are paired with ordinary DNA by energy resonance there is no need for flux tube contacts between the triplets.

3. Dark codons as dark photon 3-chords are predicted. Couple to DDNA by energy-frequency resonance and to DNA by energy-resonance.

4. Exotic DNA codons are required by the model of replication. DNA nucleotides in environment would combine to exotic codons paired with DDNA codons.

What various pairings do look like?

There would be 3 kinds of pairings. This would predict that nucleotides appear as apparently free entities in the water environment.

1. DDNA-DNA pairing in DNA strand. Different values of h_{eff} do not allow flux tubes contacts. Energy resonance only.

2. DDNA-DDNA pairing in DNA double strand is not necessary in geometric sense as flux tube connections because hydrogen bonds pair DNA codons and energy resonance pairs DDNA strands to DNA codons. DDNA codons could be however located along dark gene flux tube and attached to it by flux tube pairs.

3. DDNA-exotic DNA pairing would take place in environment. Nucleotides of exotic DNA would be attached to closed DDNA codon flux tubes. h_{eff} would be larger than for DDNA codon in double strand. There would be no valence bonds between nucleotides. The ordering of letters would be forced by flux tube containing the dark codon and energy resonance. One obtains correct codon if the orientation of the flux tube matters (ABC and BCA correspond to different energies in energy resonance). Strong parity breaking allowed by TGD and realized in living matter would imply it.

   This would solve the basic problem. Codon would be secretly present since there would be no valence bonds, which together with small string tension would mean that nucleotides are effectively free.

4. It is of course not clear whether this is enough to explain experimental findings. If one can demonstrate experimentally that the build-up of DNA strand in replication really occurs in letter-wise manner, the proposed model must be modified (not of course clear whether this is possible). The codon-wise coding, which can occur for RNA [L30] could be understood if the value of h_{eff} for DRNA strand can be same or nearly the same as in RNA strand.

5.6.4 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 [I24] 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 [L28] (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 [L28] (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 [L23, L29] (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 [L31, L32, L29](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 [L17, L31] (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

$$\{T,C\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ , \quad \{A,G\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ ,$$
$$\text{or}$$
$$\{T,C\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ , \quad \{A,G\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ .$$

.

(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 [L17].

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.

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 [L25, L26]. In the recent view of quantum TGD [L53], both notions reduce to physics as number theory vision, which relies on $M^8 - H$ duality [L43, L44] and is complementary to the physics as geometry vision.

Zero energy ontology (ZEO) [L42] [K81] 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) [L42, L46] [K81] 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 [A14] 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 [A8] 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 [A4]. 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 [A19] 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 [B11] 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 [B2]. 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 [L58] 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 [B3] .

   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 [K33, K17, K63] [L47, L53].

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 [K33, K63].

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 [L27] [L47, L48, L49] 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 [A14] 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 [L53]. 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 [L53] 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 [L53] 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 [L53] 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 [L50] 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 [K43, K44]). 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 [L50], 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 [L50], 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 [L50].

3. p-Adic length scale hypothesis [L54] 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 [L53] 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 $\delta M^4_+ \times CP_2$ [K33, K17]. 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 [L52].

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 [K47, K39, K14]. The fusion of the various p-adic physics leads to what I call adelic physics [L25, L26]. Later the hypothesis about hierarchy of Planck constants labelling phases of ordinary matter behaving like dark matter emerged [K19, K20, K21, K21].

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 [L43, L44] 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 [L50, L52]. 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 [L27] 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 [A3]. 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

$$|x| \;=\; p^{-k_0(x)} \;. \tag{A-6.2}$$

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

$$x \;=\; p^{k_0}\varepsilon(x) \;, \tag{A-6.3}$$

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:

$$d(x,z) \;\leq\; max\{d(x,y), d(y,z)\} \;. \tag{A-6.4}$$

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

$$d(x,y) \;\leq\; D \;. \tag{A-6.5}$$

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 [B10]. 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

$$\begin{aligned} y \;&=\; \sum_{k>N} y_k p^k \to x = \sum_{k<N} y_k p^{-k} \;, \\ y_k \;&\in\; \{0,1,..,p-1\} \;. \end{aligned} \tag{A-6.6}$$

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 **??**) has changed considerably towards the end 2021 [L47] 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 [L47] 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 [L47] 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 [L43, L44]. 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 $X^4 \subset M^8$ [L39]. 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 [L47]. 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 [L45] 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 [L47]. 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 [L42] [K81].

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 [L42].

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 [L37] in atomic scale can be explained by the same mechanism [L37]. 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 [J4] 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 [L38]. 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 [L41, L63].

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 [L41, L63]. 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

Acknowledgements: I am grateful for Dainis Zeps for enlightnening discussions concerning CP_2 geometry.

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