Three new physics realizations of the genetic code and the role of dark matter in bio-systems

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Contents

Abstract

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

1. The first realization - proposed in the model for DNA as topological quantum computer (tqc) - maps the nucleotides A,G and T,C to dark quarks u,d and their anti-quarks assignable to the ends of magnetic flux tubes representing braid strands and connecting nucleotides to lipids of cell membrane. This requires scaled up variant of QCD made possible the hierarchy of Planck cosntants.
2. Second realization was discovered in the model of dark nuclei as strings of dark baryons. Dark baryons realize codons in terms of quantum entanglement and without decomposition to letters. Dark baryons are strings of 3 quarks connected by two color flux tubes. The neutral states of the dark baryon predicted by the model are in 1-1 correspondence with DNA, RNA, aminoacids. Candidates for the counterparts of tRNA anticodons are also obtained if one accepts that genetic code actually decomposes to 2 steps $64 \to 40 \to 20$ such that there are 40 dark baryon counterparts for tRNA anticodons. The amazing finding is that vertebrate genetic code comes out correctly.
3. The third realization would be a physical realization for the divisor code proposed by Khrennikov and Nilsson. The realization relies on two integers labeling magnetic flux tubes containing dark matter. The dark magnetic flux tubes assignable to DNA codons and amino-acids could be labeled by these integers providing a representation of the genetic code consistent with the divisor code. Also a physical mechanism implying the physical equivalence of the dark baryon code and divisor code can be imagined.
4. Proposals for two further realizations are inspired by the observation that the number of vertices of icosahedron is 12 - the number of notes in 12-note scale - and that of vertices is 20 - the number of amino-acids. This suggests a connection between music and genetic code. The second model allows to "understand" the degeneracies of the genetic code in terms of representations for discrete subgroups if icosahedral group and involves imbedding of 12-note scale as a Hamiltonian cycle to icosahedron.

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

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

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

1 Introduction

This chapter represents an attempt to integrate three different models of genetic code [K1, K14] with each other and with DNA as topological quantum computer (TQC) hypothesis [K1] as well as the general ideas behind the model of protein folding and bio-catalysis [K2]. The considerations lead to a modification of the earlier model of protein folding.

1.1 The Notions Of Dark Matter And Magnetic Body

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

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

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

1.2 Realizations Of Genetic Code

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

1. The first realization is based on the map of G,C *resp.* A,T codons to quarks u,d *resp.* their anti-quarks. This code was proposed to realize DNA as TQC with braid strands represented as flux tubes connecting nucleotides with the lipids of cell membrane [K1]. The quantum states at the ends of braid strands -would be represented by many particle states of quarks and anti-quarks in this model and entanglement of quarks and anti-quarks would be essential for TQC and affected by the braiding induced by the 2-D liquid flow of the lipids.

2. Second realization is based on the observation that the neutral states of dark baryons consisting of u and d quarks in nuclear string model can be regarded as counterparts of DNA, RNA, amino-acids and perhaps even tRNA [K7, K14]. Nuclear strings would represent DNA and other polymers at the level of dark matter.

3. Third realization is based on the interpretation of divisor code discovered by Khrennikov and Nilsson [A7] in terms of the sub-group rule for phase transitions [K14]. Second realization and this one are in 1-1 correspondence under certain prerequisites. The magnetic- interaction energy of the dark baryon depends on the projections of the total quark spin and total color flux tube spin to the direction of the magnetic field labeling both DNA codons and amino-acids. This interaction energy is a function of (n_a, n_b) and minimized for some pair (n_a, n_b). This gives 1-1 correspondence the states of dark baryon and page of the book and since the page numbering allows to interpret physically the divisor code, one might hope that this correspondence is consistent with both codes.

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

5. I have also proposed number theory based thermodynamical models for the genetic code [K3, K15] discussed also by others [A5, A3]. and a suitable modification of this kind of model could allow to model the thermodynamics based on magnetic interaction energy.

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

1.3 Questions

These ideas raise a bundle of questions.

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

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

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

The appendix of the book gives a summary about basic concepts of TGD with illustrations. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L2].

2 A Vision About Evolution And Codes

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

2.1 Basic Insights

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

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

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

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

Genetic engineering would be possible by the fact that the dark nuclear string variants of genes could be easily transferred around the biological body unlike modified DNAs. In particular, modified dark genes could be transferred to the nuclei of germ cells. Essentially the TGD inspired mechanism of homeopathy would be in question [K7].

There is analogy with the evolution of language. Both DNA codons and representation of nucleotides in terms of quarks and anti quarks (perhaps accompanying the intronic portions of DNA) mean a representation of codons as three-letter sequences. Since dark baryons represent genetic codons as indecomposable structures in terms of quantum entanglement, the emergence of both representations would be analogous to the emergence of written language when spoken words forming indecomposable units decomposed into letters having no meaning as such. The findings that there are major differences between the genomes of blood and tissue cells [I18] and that the genetic variation due to jumping genes is highest in brain and germ cells [I13] is consistent with the view about dark evolution modifying at least intron portion of the genome.

RNA world [I21, I26, I14] represents a dominating vision about pre-biotic evolution. The idea is RNA era was first and that somehow DNA and amino-acids emerged in some later stage. It has not been possible yet to reproduce replicating RNA sequences in laboratory so that there is still room for alternatives. Dark baryon realization of the genetic code predicts that the analogs of DNA, RNA, amino-acids and even tRNA anticodons might have been there all the time. This might apply also to the primitive chemical representations of DNA, RNA, tRNA, and amino-acids. It is of course possible that the chemical representation of RNA evolved first. This era could still continue inside cell nuclei and make possible genetic engineering as experimentation with dark baryon genes producing amino-acids and RNA and then possibly transforming the resulting RNAs to DNA by reverse transcription. Also a direct transcription to DNA could take place.

2.2 The Simplest Scenario

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

1. Dark matter era would replace RNA and already this era involved at least the dark counterparts of DNA, RNA, amino-acids and perhaps even $64 - 40 \to 40 - 20$ two-step realization of the genetic code with tRNA anticodons representing a particular example of 40-D realization intermediate between DNA and amino-acids. Maximum number of different tRNA codons is indeed around 40 [I11]. Without further assumptions the pairing of all dark DNA and RNA codons coding for the same amino-acid was possible. The situation changes if one assumes 1-1 correspondence between dark baryon realization and the realization of the divisor code

in terms of dark magnetic flux tubes to be discussed later. This era could still continue at magnetic bodies and make genetic experimentation and genetic engineering possible.

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

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

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

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

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

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

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

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

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

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

2.3.1 Replication

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

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

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

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

2.3.2 $DNA \to mRNA$ transcription

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

Consider next Option II:

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

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

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

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

2.3.3 Translation as a sequence of reconnections

For Option I the description of translation should be obvious on basis of previous examples. For Option II translation could be realized as a sequence of reconnections in several ways. The basic

idea is that the reconnections and their reversals transform the tRNA_1-AA pairs with $tRNA_1$ denotes $tRNA$ without amino-acid AA to a sequence of them but $tRNA_1$ connected to amino-acid by a long flux tube. In the decay of the amino-acid this long tRNA would reduce to ordinary tRNA: this serves as a killer prediction.

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

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

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Large values of Planck constant allow to imagine all kinds of quantum computations [B1, B8, B3, B7]. What makes topological quantum computation (TQC) [B4, B6, B5, B2], [C2] so attractive is that the computational operations are very robust and there are hopes that external perturbations do not spoil the quantum coherence in this case. The basic problem is how to create, detect, and control the dark matter with large $\hbar$. The natural looking strategy would be to assume that living matter, say a system consisting of DNA and cell membranes, performs TQC and to look for consequences.

There are many questions. How the TQC could be performed? Could TQC hypothesis might allow to understand the structure of living cell at a deeper level? What does this hypothesis predict about DNA itself? One of the challenges is to fuse the vision about living system as a conscious hologram with the DNA as TQC vision. The experimental findings of Peter Gariaev [I16, I20] might provide a breakthrough in this respect. In particular, the very simple experiment in which one irradiates DNA sample using ordinary light in UV-IR range and photographs the scattered light seems to allow an interpretation as providing a photograph of magnetic flux tubes containing dark matter. If this is really the case, then the bottle neck problem of how to make dark matter visible and how to manipulate it would have been resolved in principle. The experiment of Gariaev and collaborators [I20] also show that the photographs are obtained only in the presence of DNA sample. This leaves open the question whether the magnetic flux tubes associated with instruments are there in absence of DNA and only made visible by DNA or generated by the presence of DNA.

3.1 Basic Ideas Of TQC

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

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

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

In TGD framework TQC differs somewhat from the ordinary one.

1. Zero energy ontology means that physical states decompose into pairs of positive and negative energy states at boundaries of causal diamond formed by future and past directed light-

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

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

3.2 Identification Of Hardware Of TQC And TQC Programs

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

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

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

3. It is natural to require that the genetic code is somehow represented as property of braids strands. This is achieved if strands are "colored" so that A, T, C, G correspond to four different "colors". This leads to the hypothesis that flux tubes assignable to nucleotides are wormhole magnetic flux tubes such that the ends of the two sheets carry quark and anti-quark *resp.* anti-quark and quark) quantum numbers. This gives mapping A, T, C, G to u, u_c, d, d_c. These quarks are not ordinary quarks but their scaled variants predicted by the fractal hierarchy of color and electro-weak physics. Chiral selection in living matter could be explained by the hierarchy of weak physics. The findings of topologist Barbara Shipman about mathematical structure of honeybee dance led her to proposed that the color symmetries of quarks are in some mysterious manner involved with honeybee cognition and this model would justify her intuition [A4].

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

In this framework genes define the hardware of TQC rather than genetic programs. This means that the evolution takes place also at the level of TQC programs meaning that strict genetic determinism fails. There are also good reasons to believe that these TQC programs can be inherited to some degree. This could explain the huge differences between us and our cousins in spite of almost the identical genetic codes and explains also cultural evolution and the observation that our children seem to learn more easily those things that we have already learned [I25]. It must be added that DNA as TQC paradigm seems to generalizedDNA, lipids, proteins, water molecules, ... can have flux tubes connecting them together and this is enough to generate braidings and TQC

programs. Even water could be performing simple TQC or at least building memory representations based on braiding of flux tubes connecting water molecules.

Comment:

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

2. It has also turned that genetic code allows a realisation in terms of dark nucleons [K7, L1]. Note that the assignment of genetic code with braid coloring is not necessary for TQC.

3.3 How Much TQC Resembles Ordinary Computation?

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

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

2. In ordinary computers electromagnetic signalling is in key role. The vision about living matter as conscious holograms suggests that this is the case also now. In particular, the idea that entire biosphere forms a TQC web communicating electromagnetically information and control signals, looks natural. Topological light rays (MEs) make possible precisely targeted communications with light velocity without any change in pulse shape. Gariaev's findings [I16] that the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind of picture. Also the model of EEG in which the magnetic body controls the biological body also from astrophysical distances conforms with this picture.

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

   Gariaev [I16] has found that laser radiation scattering from given DNA activates only genomes which contain an address coded as temporal pattern for the direction of polarization plane. If flux tubes are super-conducting and there is strong parity breaking (chiral selection) then Faraday rotation for photons traveling through the wormhole flux tube code nucleotide to an angle characterizing the rotation of polarization plane. User id and password would define kind of immune system against externally induced gene expression.

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

$$\begin{aligned} Q_a &= [n(A)-n(T)]\tfrac{2}{3} - [n(G)-n(C)]\tfrac{1}{3} \ , \\ Q_a &= -[n(A)-n(T)]\tfrac{1}{3} + [n(G)-n(C)]\tfrac{2}{3} \ , \\ Q_a &= -[n(A)-n(T)]\tfrac{2}{3} + [n(G)-n(C)]\tfrac{1}{3} \ , \\ Q_a &= [n(A)-n(T)]\tfrac{1}{3} - [n(G)-n(C)]\tfrac{2}{3} \ . \end{aligned} \tag{3.2}$$

Table 1: Table show four possible options for em charge as sum of quark charges.

3.4 Some Predictions Related To The Representation Of Braid Color

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

3.4.1 Anomalous em charge of DNA as a basic prediction

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

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

$$Q_a \quad = \quad [n(A)-n(T)]Q(q_A) + [n(G)-n(C)]Q(q_G) \tag{3.1}$$

is predicted. The four possible options for charge are given explicitly in **Table 1**.

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

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

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

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

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

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

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

Chargaff's second parity rule states that the frequencies of nucleotides for single DNA strand satisfy the conditions $p(A) \simeq p(T)$ and $p(C) \simeq p(G)$ (I am grateful for Faramarz Faghihi for mentioning this rule and the related [**?**] [I27] to me). This rule holds true in a good approximation. In the recent context the interpretation would be as the vanishing of the net anomalous charge of the

DNA strand and thus charge conjugation invariance. Stability of DNA might explain the rule and the poly-A tail in the untranslated mRNA could relate stabilization of DNA and mRNA strands.

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

$$\begin{array}{ll} p(A) + p(C) \simeq 1/2 \ , & p(A) + p(G) \simeq 1/2 \ , \\ p(T) + p(C) \simeq 1/2 \ , & p(T) + p(G) \simeq 1/2 \ . \end{array} \tag{3.3}$$

An interesting empirical finding [I27] is that only some points at the line $p(A) + p(C) \simeq 1/2$ are realized in the case of human genome and that these points are in a good accuracy expressible in terms of Fibonacci numbers resulting as a prediction of optimization problem in which Fibonacci numbers are however put in by hand. $p(A) = p(G) = p(C) = p(T) = 1/4$ results as a limiting case. The poly-A tail of mRNA (not coded by DNA) could reflect to the compensation of this asymmetry for translated mRNA.

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

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

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

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

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

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

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

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

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

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

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

$$n(A) + n(G) \ \ mod \ \ 3 = 0 \ , \qquad n(C) + n(T) \ \ mod \ \ 3 = 0 \ . \tag{3.4}$$

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

2. General condition for integer valued anomalous charge

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

$$n(A) - n(T) + n(G) - n(C) \ \ mod \ \ 3 = 0 \ \ . \tag{3.5}$$

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

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

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

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

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

3. I have also proposed that intronic regions could obey memetic code [K5] predicting that intronic codon can be represented as a sequence of 21 3-codons (implying 2^{63} 63-codons!). Individual intronic segments need not satisfy this rule, only their union if even that. Direct experimentation with gene bank data show that neither introns nor their union correspond to integer multiples of 63 nor 3 or 2 in general.

3. Color singletness conditions for gene

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

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

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

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

4. Color singletness conditions for mRNA

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

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

$$n(A) - n(T) + n(G) - n(C) + n_{tail}(A) + 1 \ \ mod \ \ 3 = 0 \tag{3.6}$$

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

5.Chargaff's rule for mRNA

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

$$\begin{aligned}
&2\left[n(A) + n_{tail}(A) - n(T)\right] - \left[n(G) + 1 - n(C)\right] \simeq 0 \ \ , \\
&-\left[n(A) + n_{tail}(A) - n(T)\right] + 2\left[n(G) + 1 - n(C)\right] \simeq 0 \ \ , \\
&-2\left[n(A) + n_{tail}(A) - n(T)\right] + \left[n(G) + 1 - n(C)\right] \simeq 0 \ \ , \\
&\left[n(A) + n_{tail}(A) - n(T)\right] - 2\left[n(G) + 1 - n(C)\right] \simeq 0 \ \ .
\end{aligned} \tag{3.7}$$

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

6. Moving genes and repeating elements

Transposons [I10], [**?**] are moving or self-copying genes. Moving genes cut from initial position and past to another position of double strand. Copying genes copy themselves first to RNA and them to a full DNA sequence which is then glued to the double strand by cut and paste procedure. They were earlier regarded as mere parasites but now it is known that their transcription is activated under stress situations so that they help DNA to evolve. In TQC picture their function would be to modify TQC hardware. For copying transposons the cutting of DNA strand occurs usually at different points for DNA and cDNA so that "sticky ends" result ("overhang" and its complement) [I8]. Often the overhang has four nucleotides. The copied transposon have ends which are reversed conjugates of each other so that transposons are palindromes as are also DNA hairpins. This is suggestive of the origin of transposons.

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

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

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

3) The overhangs should satisfy P.

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

In the example mentioned in [I7] the overhang is $CTAG$ and has vanishing Q_a. The cut site $CCTAGG$ has also vanishing Q_a. It is known [**?**] that transposons - repeating regions themselves - tend to attach to the repeating regions of DNA [I3].

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

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

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

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

7. Tests

Some checks of the color singletness hypothesis were made for human genome [I4].

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

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

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

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

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

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

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

3.4.4 Summary of possible symmetries of DNA

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

1. Color confinement in strong form

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

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

2. Matter antimatter asymmetry at quark level

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

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

3. Isospin symmetry at quark level

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

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

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

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

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

5. Em stability

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

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

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

6. Summary of testable working hypothesis

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

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

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

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

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

5. Telomeres [I9] are of special interests as far as anomalous em charge is considered. Chromosomes are not copied completely in cell replication, and one function of telomeres is to guarantee that the translated part of genome replicates completely for sufficiently many cell divisions. Telomeres consists of 3-20 kilobases long repetitions of TTAGGG, and there is a 100-300 kilobases long repeating sequence between telomere and the rest of the chromosome. Telomeres can form can also 4-stranded structures. Telomere end contains a hair-pin loop as a single stranded part, which prevents the action of DNA repair enzymes on the chromosome end. Telomerase is a reverse transcriptase enzyme involved with the synthesis of telomeres using RNA strand as a template but since its expression is repressed in many types of human cells, telomere length shortens in each cell replication. In the case of germ cells, stem cells and white blood cells telomerase is expressed and telomere length preserved. Telomere shortening is known to relate to ageing related diseases. On the other hand, overactive telomere expression seems to correlate with cancer.

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

6. Also amino-acids could be braided. Q_a could vary and correspond to Q_a for one of the codons coding for it. The amino-acid sequences of catalysts attaching to DNA strand should have opposite Q_a for each codon-amino-acid pair so that amino-acid would attach only to the codons coding for it. The TGD based model for nerve pulse [K13] inspires the proposal that magnetic flux tubes connecting microtubules to the axonal membrane allow TQC during nerve pulse propagation when axonal membrane makes transition from gel like phase to liquid crystal phase. Amino-acids of tubulin dimers would be connected by 3-braids, smallest interesting braid, to groups of 3-lipids in axonal membrane and tubulin dimers would define fundamental TQC modules.

3.4.5 Empirical rules about DNA and mRNA supporting the symmetry breaking picture

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

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

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

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

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

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

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

Table 2 gives A, T, C, G contents (these data are from Wikipedia [I2]) provides interesting data about DNA It will be found that so called Szybalski's rules can be interpreted as saying that for coding regions there is breaking of the approximate matter antimatter asymmetry.

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

For option 2) the amount of anomalous charge is about.0057e per nucleotide and thus about $3 \times 10^7 e$ for entire human DNA having length of about 1.8 meters. The inspection of tables of [I9] shows that the anomalous em charge for the repeating sequence defining the telomere is always non-vanishing and has always the same sign. Telomeres for human chromosomes consist of

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

(3.8)

Table 2: The table gives A, T, C, G contents (these data are from Wikipedia [I2]), the amount of quark charge per nucleotide for the options 1) *resp.* 2) given by $dq_1/dn = p[2(A-T)-G-C)]/3$ *resp.* $dq_2/dn = p[A-T-2(G-C)]/3$, the amount $dI_3/dn = p(A-G+C-T]/2$ of isospin per nucleotide, the amount $d(q-\overline{q})/dn = p(A-T+G-C)$ of quark number per nucleotide, and $(A+T)/(C+G)$ ratio for *entire genomes* in some cases.

TTAGGG repetitions with anomalous em charge with magnitude $5e/3$ for all options and have a length measured in few kbases. Human genome as has 24 chromosomes so that the total anomalous em charge of telomeres is roughly $24 \times (5/18) \times x10^3 e \sim .8 \times 10^3 xe$, $1 < x < 10$. The anomalous em charge of telomeres is three orders of magnitude smaller than that of entire DNA but if DNA is quantum critical system the change the total anomalous em charge and quark number due to the shortening of telomeres could induce instabilities of DNA (due to the approach to vacuum extremal) contributing to ageing. Note that the small net value of quark number in all the cases considered might be necessary for overall stability of DNA. Telomeres are also known to prevent the ends of chromosomes to stick to each other. This could be partially due to the Coulomb repulsion due to the anomalous em charge.

According to [I2] Chargaff's rules do not apply to viral organellar genomes (mitochondria [I6], plastids) or single stranded viral DNA and RNA genomes. Thus approximate matter antimatter symmetry fails for DNA: s of organelles involved with metabolism. This might relate to the fact that the coding portion of DNA is very high and repeats are absent. Chargaff's rule applies not only to nucleotides but also for oligonucleotides which corresponds to DNA or RNA sequences with not more than 20 bases. This means that for single strand oligonucleotides and their conjugates appear in pairs. Matter antimatter asymmetry would be realized as presence of matter blobs and their conjugates. This might relate to the mechanism how the sequences of oligonucleotides are generated from DNA and its conjugate.

8. Breaking of matter antimatter symmetry for coding regions

As noticed, one can consider three type of symmetry breaking parameters for DNA in DNA as TQC model. There are indeed three empirical parameters of this kind. Chargaff rules have been already discussed and correspond to approximate matter antimatter symmetry. The second asymmetry parameter would measure the asymmetry between $u\overline{u}$ and $d\overline{d}$ type matter. $p(G+C)$ corresponds to the fraction of $d\overline{d}$ type quark matter for option 1) and $u\overline{u}$ matter for option 2). It is known that G+C fraction $p(G+C)$ characterizes genes [I23] and the value of $p(G+C)$ is proportional to the length of the coding sequence [I5, I23].

Besides Chargaff rules holding true for entire genome also Szybalski's rules [I2] hold true but only for coding coding regions. The biological basis of neither rules is not understood. The interpretation of Chargaff's rules would be in terms of approximate matter antimatter symmetry and the vanishing of net isospin at the level of quarks whereas Szybalski's rule would state the breaking of these symmetries non-coding regions. Hence all the three basic empirical rules would

have a nice interpretation in DNA as TQC picture.

Consider now Szybalski's rules in more detail.

1. In most bacterial genomes (which are generally 80-90 % coding) genes are arranged in such a fashion that approximately 50 % of the coding sequence lies on either strand. Note that either strand can act as a template (this came as a surprise for me). Szybalski, in the 1960s, showed that in bacteriophage coding sequences purines (A and G) exceed pyrimidines (C and T). This rule has since been confirmed in other organisms and known as Szybalski's rule [I2, I24]. While Szybalski's rule generally holds, exceptions are known to exist.

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

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

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

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

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

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

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

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

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

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

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

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

3.4.6 Genetic codes and TQC

TGD suggests the existence of several genetic codes besides 3-codon code [K6, **?**]. The experience from ordinary computers and the fact that genes in general do not correspond to $3n$ nucleotides encourages to take this idea more seriously. The use of different codes would allow to tell what kind of information a given piece of DNA strand represents. DNA strand would be like a drawing of building containing figures (3-code) and various kinds of text (other codes). A simple drawing for the building would become a complex manual containing mostly text as the evolution proceeds: for humans 96 per cent of code would corresponds to introns perhaps obeying some other code.

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

The hierarchy of Mersenne primes $M_n = 2^n - 1$ with $M_{n(next)} = M_{M_n}$ starting from $n = 2$ with $M_2 = 3$ gives rise to 1-code with 4 codons, 3-code with 64 codons, and $3 \times 21 = 63$-code with 2^{126} codons [K6] realized as sequences of 63 nucleotides (the length of 63-codon is about $2L(151)$, roughly twice the cell membrane thickness. It is not known whether this Combinatorial Hierarchy continues ad infinitum. Hilbert conjectured that this is the case.

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

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

There are also further short Combinatorial hierarchies corresponding to Mersenne primes [A2].

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

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

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

4. The next Mersennes are M_{31} belonging to $n = 5$ hierarchy, M_{61} with $2^{60=30\times 2}$ codons represented by 30-codons. This corresponds to DNA length $L(151) = 10$ nm (cell membrane thickness). M_{89} (44-codons), M_{107} (53-codons) and M_{127} (belonging to the basic hierarchy)

are the next Mersennes. Next Mersenne corresponds to M_{521} (260-codon) and to completely super-astrophysical p-adic length scale and might not be present in the hierarchy.

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

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

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

4.1 Fermionic Representation

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

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

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

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

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

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

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

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

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

1. The problem of electron and proton options is that it does not allow realization of color qualia. There is also the well-known problem related to the stability of DNA caused by the phosphate charge of -2 units per nucleotide. Somehow this charge should be screened. In any case, the charge -2 should correspond to the electron pair at the DNA end of the flux tube for electron option. For proton option the charge would be screened completely. One could of course consider also the large $\hbar$ color excitations of ordinary protons instead of quark at its nucleotide ends. This option would however require the modification of quark wave functions inside proton and this option will not be discussed here.

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

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

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

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

4.3 Realization Of Color Qualia For Quark Option

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

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

2. Does the "external world" corresponds to another cell or to the inner lipid layers of the cell membrane containing the nucleus. In the first case flux tubes would end to another cell. If the nuclei of receptor cells are integrate to a larger structure by magnetic flux sheets traversing through them one can also consider the possibility that the polarization in the scale of cell nucleus (recall that the nucleus has also double lipid layer) is transformed to a polarization in cell scale so that similar process in cell scale gives rise to qualia.

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

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

3. Consider now how the color qualia are generated.

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

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

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

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

cell membrane is for the generation of qualia at cell level. Note also that biomolecules are quite generally polar molecules.

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

This model is not consistent with the naïve expectation that the quale is generated after state function reduction. Rather, the beginning of sensation of quale means beginning of negentropic entanglement and fusion with external world and state function usually associated with the quantum measurement would mean the end of the sensation and separation from the external world! Maybe one can say that state function reduction means that experience is replaced with a memory "I had the sensation of quale" ! Krishnamurti would certainly agree!

5 Realization Of Genetic Code In Terms Of Dark Baryons

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

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

Water memory is one of the ugly words in the vocabulary of a main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [L1, K7, K14], [L1] , [I19]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

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

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

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

1. Dark nuclear baryons are considered as a fundamental realization of DNA codons and constructed as open strings of 3 dark quarks connected by two colored flux tubes, which can be

also charged. The baryonic strings cannot combine to form a strictly linear structure since strict rotational invariance would not allow the quark strings to have angular momentum with respect to the quantization axis defined by the nuclear string. The independent rotation of quark strings and breaking of rotational symmetry from SO(3) to SO(2) induced by the direction of the nuclear string is essential for the model.

Baryonic strings could form a helical nuclear string (stability might require this) locally parallel to DNA, RNA, or amino-acid) helix with rotations acting either along the axis of the DNA or along the local axis of DNA along helix. The rotation of a flux tube portion around an axis parallel to the local axis along DNA helix requires that magnetic flux tube has a kink in this portion. An interesting question is whether this kink has correlate at the level of DNA too. Notice that color bonds appear in two scales corresponding to these two strings. The model of DNA as topological quantum computer [K1] allows a modification in which dark nuclear string of this kind is parallel to DNA and each codon has a flux tube connection to the lipid of cell membrane or possibly to some other bio-molecule.

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

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

$$\sum_q Q_{em}(q) = -\sum_{flux\ tubes} Q_{em}(flux\ tube) \ . \tag{5.1}$$

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

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

5.1.1 States in the quark degrees of freedom

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

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

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

candidate for amino-acids. Thus RNA and DNA should correspond to states of type uud and ddu and amino-acids to states of type *uuu* or ddd. What this means physically will be considered later.

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

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

5.1.2 States in the flux tube degrees of freedom

Consider next the states in flux tube degrees of freedom.

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

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

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

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

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

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

correspond to uuu states with identical color bonds with charges $(-1,-1)$, $(0,0)$, or $(1,1)$. uuu with color bond charges (-1, -1) is the only neutral state. Hence only the analogs of DNA, RNA, and amino-acids are obtained, which is rather remarkable result.

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

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

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

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

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

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

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

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

As found, dark baryon counterpart of tRNA could correspond to the multiplet of states containing 40 states. According to [I12] most organisms have fewer the 45 species of tRNA. Typical value of anticodons is around 30 and in some organisms the number is as low as 22. This means that the number of different anticodons in tRNA is not larger than 45 and could be at most 40. Unfortunately I do not know what the real situation is. The realization of mRNA-tRNA pairing is known to be based on wobble base pairing [I12]. This means that the pairing is not unique for the third nucleotide of the anticodon so that all mRNA codons can pair with tRNA in a way consistent with the genetic code.

This finding suggests that tRNA could correspond to a 40-plet of anticodons at the level of dark matter then for tRNA-amino-acid genetic code the numbers of codons $N(k)$ with given degeneracy

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

5.1.5 Objections

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

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

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

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

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

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

5.2 DNA As Topological Quantum Computer Hypothesis And Dark Genetic Code

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

1. DNA as TQC using dark baryons to represent DNA codons would require that DNA strand is accompanied by a nuclear string parallel to it. If the pairing of baryons at the ends of string requires only opposite total quark spins and total flux tube spins the map would obey genetic code rather than being 1-1. The situation changes if dark baryon states are in 1-1

correspondence with the integers (n_a, n_b) labeling the page of book at which magnetic body of the codon resides.

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

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

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

5. Only the portions of DNA having interpretation as gene have a natural decomposition to codons. Hence the dark baryon representation of codons is not attractive idea in intronic portions of the genome forming the most plausible candidates for quantum computing part of DNA since the portion of introns has been increasing during evolution and highest variation of this portion is encountered in human brain [I13]. Hence one might think that TQC as relatively late outcome of the evolution and that only this part of genome is responsible for TQC so that the mpa of nucleotides to quarks would realize genetic code. Furthermore, braiding matters in TQC much more than the colors of braid strands determined by nucleotides so that intronic portions could quite well be repeating sequences without any obvious as information carriers in standard sense and therefore interpreted as junk DNA. There would be also an analogy between emergence of written language meaning that words as holistic entities were replaced with sequences of letters having as such no meaning.

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

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

For almost two decades ago I deduced by purely dimensional considerations a formula for gravitational constant G in terms of p-adic length scale and exponent of Kähler action for CP_2 type vacuum extremal defining the line of generalized Feynman diagram representing graviton [K10]. The prediction was that G should have an entire spectrum of values and approach p-adic length scale squared $L_p^2 = pR_{CP_2}^2$ when the action of the deformed CP_2 type vacuum extremal becomes small: this happens at short length scale limit. In particular, hadronic strings would correspond to strong gravitation limit, and TGD predicts fractally scaled up variants of ordinary hadron physics so that a rich spectrum of strong gravities follows as a prediction. This means that in TGD Universe the the gravitational effects on space-time geometry can be rather dramatic even in condensed matter length scales whereas in GRT the effects are extremely small.

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

Cosmic honeycombs and their possible counterparts for water clusters modeled as consisting of icosahedral pieces of S^3 bring in mind foams (see `http://tinyurl.com/3a29pz`). Soap film foam is perhaps the most familiar example about foam. Plateau's laws (see `http://tinyurl.com/y7rrstej`) govern the structure of many foams. Mean curvature is constant for each film and physically derives from area minimization assuming constant pressure difference over the film. 3 films meet at angle of 120 degrees along a line known as Plateau border and 4 Plateau borders meet

at each vertex at tetrahedral angle of $arcos(-1/3) \simeq 109.47$ degrees (tetrahedral angle is defined as the angle between radii drawn from the center of tetrahedron to its vertices). This suggests spherical tetrahedron as a basic building brick in a model as a honeycomb built from pieces of S^3. Plateau's laws can be derived mathematically for foams, for which films are minimal surfaces (pressure difference vanishes).

The idea that icosahedral structures assignable to water clusters could define a geometric representation of some kind of code is very intriguing. Genetic code is of course the code that comes first in mind. The observation that the number of faces of tetrahedron (icosahedron) is 4 (20) raises the question whether genetic code might have a geometric representation and the following piece of text is inspired by this question. In TGD framework also a second code emerges: I have christened it memetic code [K6]. Also memetic code could have a geometric realization. Another purely TGD-based notion is that of dark DNA allowing to assign the states of dark protons with DNA, RNA, tRNA and amino-acids and to predict correctly the numbers of DNA codons coding for a given amino-acid in vertebrate genetic code [L1].

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

6.1 The Notions Of Memetic Code And Dark Genetic Code

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

6.1.1 The notion of memetic code

The notion of memetic code introduced for more than 20 years ago allows to interpret the sequences of 21 DNA codons as memetic codons [K6]. The starting point is so called Combinatorial Hierarchy [A6]. Mersenne integers are defined as numbers $M_n = 2^n - 1$. For some values of n, which belong to a subset of primes, one obtains Mersenne primes. In particular the lowest members in the hierarchy defined by the recursive formula $M(n+1) = M_{M(n)}$ with $M(1) = 1$, one obtains the sequence $M(1) = 1$, $M(2) = 3$, $M(3) = 7$, $M(4) = 127$, $M(5) = 2^{127} - 1$, ... All the explicitly listed Mersenne integers $M(n)$, $n > 1$, are Mersenne primes. An unproven conjecture by Hilbert is that all numbers $M(n)$, $n > 1$ in the sequence are Mersenne primes.

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

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

6.1.2 The notions of dark nucleus and dark genetic code

The notions of dark nucleus and dark genetic code belong to the most speculative ideas of TGD inspired quantum biology. The original motivation for the notion of dark proton came from the observations suggesting that in atto-second time scale 1/4: th of protons of water molecules are dark in the sense that are not visible in electron scattering and neutron diffraction [D2, D1, D3].

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

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

The recent work of Persinger's group [**?**, **?**, **?**] combined with the observation of Hu and Wu [**?**] that the magnetic interaction energy between protons assigned to the opposite sides of cell membrane corresponds to frequency in EEG range led to the conjecture that the pair of cell membrane lipid layers is accompanied by a pair of dark proton strings analogous to DNA double strand and indeed representing double DNA strand. There is also a close connection with the model of DNA as topological quantum computer [K1]: in this model magnetic flux tubes connecting nucleotide with lipids are responsible for braiding defining the quantum computer programs.

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

Consider first the intriguing observations suggesting that tetrahedral and icosahedral geometries relate to genetic code and its generalization to memetic code [K6]

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

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

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

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

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

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

   For instance, the areas of the faces could be different and if the amino-acid is glued only to the face which it "fits" (recall the analogy with lock and key mechanism) one would have the desired 1-1 correspondence with amino-acids and icosahedrons. The outcome could be that only single amino-acid can be glued to a given face. Note that magnetic flux tubes could realize the correspondence between amino-acids and icosahedral outer faces in very concrete manner: this mechanism is proposed as a general mechanism of bio-catalysis making it possible for two reacting molecules to find each other in the thick molecular soup [K1, K4].

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

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

6.4 Icosahedral Realization Of The Memetic Code?

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

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

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

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

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

From the net representation (see `http://tinyurl.com/yatsguy5`) of icosahedron obtained by cutting the icosahedron open, it is clear that there are at least two paths of this kind but differing only by orientation. Each of them can be regarded as a union of 5 4-triangle paths of the net combining to form a connected triangle path at the surface of icosahedron when appropriate identifications of the edges are made. The step between neighboring triangles corresponds to reflecting with respect to the common edge. Each 4-triangle path corresponds to a path containing vertices of "big" tetrahedron (not one of the twenty tetrahedrons with one vertex at the center of icosahedron) shared also by icosahedron. This sequence corresponds to the orbit of the icosahedral isometry group, which is the alternating group A_5 (60 even permutations of 5 letters) acting transitively so that the orbit visits all triangles at the isosahedral surface. A good guess is that these two oppositely oriented orbits and their images under A_5 define the only ways to fill the icosahedral surface by single path. The number of images is 12 since each of the 12 vertices of icosahedron defines one tetrahedron. Note that this identification for the folded DNA sequence allows also to think that it traverses the surface of the icosahedron rather than filling the entire icosahedron.

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

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

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

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

6.5 Geometric Representation Of Dark DNA Codons

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

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

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

A couple of remarks are in order.

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

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

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

6.6 Could Water Clusters Represent Memetic Code?

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

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

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

2. It is however known that known (see `http://tinyurl.com/yb9waklg`) that 14 water molecules indeed combine to form tetrahedral structures (see `http://tinyurl.com/ybl9eqt9` [D2], and that these in turn combine to form icosahedral structures. The size scale of the 14 molecule cluster is nearer to the size scale of single DNA nucleotide so that perhaps this option is more realistic. If these structures provide a representation of memetic codons with tetrahedral structure of 14 water molecules representing single DNA codon or amino-acid, there are 14 water molecules per single dark proton representing dark DNA codon.

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

The view about evolution as a random process suggests that genetic code is pure accident. My own view is that something so fundamental as life cannot be based on pure randomness. TGD has led to several proposals for genetic code, its emergence, and various realizations based on purely mathematical considerations or inspired by physical ideas. One can argue that genetic code is realized in several ways just like bits can be represented in very many ways. Two especially interesting proposals have emerged. The first one is based on geometric model of music harmony involving icosahedral and tetrahedral geometries. Second model has two variants based on dark nuclear strings: the original version maps codons do dark nucleons, the more recent version maps

codons to dark 3-nucleon states. Both models predict correctly the numbers of DNA codons coding for a given amino-acid but the model based on dark 3-nucleon triplets is favoured by some recent findings suggesting a pairing between DNA nucleotides and dark nucleons. Also the counterparts of RNA,tRNA, and amino-acids are predicted. In the sequel the updated nuclear string variant is summarized and also its connection with the model of harmony is discussed.

7.1 Background

The view about evolution as a random process suggests that genetic code is pure accident. My own view is that something so fundamental as life cannot be based on pure randomness. TGD has led to several proposals for genetic code, its emergence, and various realizations based on purely mathematical considerations or inspired by physical ideas (see chapters of [K5] and [L1, K7]). One can argue that genetic code is realized in several ways just like bits can be represented in very many ways.

Two especially interesting proposals have emerged. The first one is based on geometric model of music harmony [L3] involving icosahedral and tetrahedral geometries. Second one having two variants is based on dark nuclear strings. Both models predict correctly the numbers of DNA codons coding for a given amino-acid. In the sequel the nuclear string variant and also its connection with the model of harmony is discussed in detail.

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

7.1.1 Genetic code and Combinatorial Hierarchy

The first proposal [K6] was purely mathematics inspired and in terms of so called Combinatorial Hierarchy consisting of certain Mersenne primes $M_k = 2^k - 1$ via the formula $M(n+1) = M_{M(n)}$ having interpretation in terms of abstraction. The list beginning from $M(1) = 2$ is $2, M_2 = 3, M_3 = 7, M_7 = 127, M_{127} = 2^{127} - 1$: it is not known whether subsequent integers are Mersenne primes. The idea is that the $2^k - 1$ points define almost full Boolean algebra spanned by k bits- one visualization is as a polygon. The algebra defined $k - 1$ bits is maximal full Boolean sub-algebra having interpretation as maximal number of mutually independent statements, which can hold true simultaneously. For M_7 ($k = 3$) one would have 2 bits and 4 codons. For M_7 one would have $k = 7$ and 6 bits and genetic code. For M_{127} one would have 126 bits and one would have "memetic" code realizable in terms of sequences of 21 DNA codons.

7.1.2 Geometric theory of harmony and genetic code

The idea that the 12-note scale could allow mapping to a closed path going through all vertices of icosahedron having 12 vertices and not intersecting itself is attractive. Also the idea that the triangles defining the faces of the icosahedron could have interpretation as 3-chords defining the notion of harmony for a given chord deserves study. The paths in question are known as Hamiltonian cycles and there are 1024 of them [A1]. There paths can be classified topologically by the numbers of triangles containing 0, 1, or 2 edges belonging to the cycle representing the scale. Each topology corresponds to particular notion of harmony and there are several topological equivalence classes.

In the article [L5] I introduced the notion of Hamiltonian cycle as a mathematical model for musical harmony and also proposed a connection with biology: motivations came from two observations. The number of icosahedral vertices is 12 and corresponds to the number of notes in 12-note system and the number of triangular faces of icosahedron is 20, the number of amino-acids. This led to a group theoretical model of genetic code and replacement of icosahedron with tetra-icosahedron to explain also the 21st and 22nd amino-acid and solve the problem of simplest model due to the fact that the required Hamilton's cycle does not exist. The outcome was the notion of bioharmony.

All icosahedral Hamilton cycles with symmetries(Z_6,Z_4, Z_2^{rot} and $Z_2 refl$ turned out to define harmonies consistent with the genetic code. In particular, it turned out that the symmetries of the Hamiltonian cycles allow to to predict the basic numbers of the genetic code and its extension to include also 21st and 22nd amino-acids Pyl and Sec: there are actually two alternative codes -

maybe DNA and its conjugate are talking different dialects! One also ends up with a proposal for what harmony is leading to non-trivial predictions both at DNA and amino-acid level.

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

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

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

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

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

3. TGD based model of bio-superconductivity assumes that flux tubes appear as pairs with members of Cooper pair at parallell flux tubes [K11, K12]. This suggests that electron pairs at in spin 1 and spin 0 states could realize the code. The spin of the electrons would matter and one would obtain 4 states - two qubits in correspondence with A,T,C,G.

Also the model of dark nuclear strings allows to imagine letter-wise representations of the genetic code. The model for cold fusion based on the findings of Prof. Holmlid and his group [C1, L9] leads to the idea that Pollack's EZs [L4] are accompanied by dark nuclear strings consisting of dark protons connected by color flux tubes analogous to mesons [L6, L9]. Color bonds would have quark and antiquark at their ends [L1]. This leads to non-trivial predictions and nuclear anomalies giving support for the notion of nuclear string have emerged, the latest anomaly is so called X boson with mass of 17 MeV [L10, C3] having identification as p-adically scaled analog of pion.

Dark protons could also decay to neutrons by dark weak decays rapidly since dark weak bosons are effectively massless below dark Compton length. Furthermore, proton plus negatively charged color bond could behave like neutron as far as chemistry is considered. The X boson anomaly of nuclear physics [L10] suggests that the flux tubes in the ground state correspond to pion-like states which can be colored: this could bind the nucleons to form a nucleus. The evidence for the occurence of cold fusion in living matter gives support for the role of dark nuclear strings [K8] [L9].nOne can consider several representations of the genetic code in this framework.

Consider first models for which letters are represented separately.

1. Dark protons and neutrons have 4 spin states and could correspond to letter A,T,C,G. In this case dark color bonds would not matter. A rather convincing proposal for a pathway leading to a selection purines as DNA nucleotides has been proposed [I15]. TGD based model [L7] suggests that acidic solutions contain dark protons and purine results when the precursor amine combines with dark proton such that the proton remains dark. Could DNA nucleotide pair with dark protons and neutrons (resulting in dark beta decay from dark proton strings yielded by Pollack's mechanism)?

2. Also the 4 states of dark color bonds between dark nucleons (3 pion-like states and one eta meson like state: spin 1 bonds would be analogous to ρ and ω mesons and have higher mass) correspond to letters A,T,C,G. Now the dark protons and neutrons would not matter. This option would require that the character of the nucleotide correlates with the color flux tube attached to the dark proton. They would have at their ends charge conjugate color bonds.

The states would be of form $u\overline{u}, d\overline{d}, u\overline{d}, d\overline{u}$ with the ordering of q and $\overline{q}$ correlating with the direction in which transcription and replication take place being thus same or opposite). For conjugate strand the direction of strand would be opposite in the sense that one would have $\overline{u}u, \overline{d}u, \overline{d}\overline{u}, \overline{u}u$.

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

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

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

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

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

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

3. This model can be modified by replacing u and d by dark nucleon states p and n without any change in predictions related to genetic code. The evidence that DNA codons indeed couple to dark nucleon states [L7] supports this option.

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

7.2 Codons as dark quark-triplet strings

Water memory is one of the ugly words in the vocabulary of the main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [K7, K14], [I19]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

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

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

The dark model emerged from the attempts to understand water memory [K7]. The outcome was a totally unexpected finding [L1, K7]: the states of dark nucleons formed from three quarks connected by color bonds can be naturally grouped to multiplets in one-one correspondence with

64 DNAs, 64 RNAS, 20 amino-acids, and tRNA and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

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

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

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

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

1. The original model identifying codons to dark nucleon states assumed the overall charge neutrality of the dark proton strings: the idea was that the charges of color bonds cancel the total charge of dark nucleon so that all states uuu, uud, udd, ddd can be considered. The charge itself would not affect the representation of codons. Neutrality assumption is however not necessary. The interpretation as dark nucleus resulting from dark proton string could quite well lead to the formation the analog of ordinary nucleus via dark beta decays [L9] so that the dark nucleus could have charge. Isospin symmetry breaking is assumed so that neither quarks nor flux tubes are assigned to representations of strong $SU(2)$.

   There is a possible objection. For ordinary baryon the mass of Δ is much larger than that of proton. The mass splitting could be however much smaller for linear baryons if the mass scale of excitations scales as $1/h_{eff}$ as indeed assumed in the model of dark nuclear strings [L6, L9].

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

   The rejection of spin 0 pionic bonds looks strange. These could however occur as bonds connecting dark codons and could correspond to different p-adic length scale as suggested by the successful model of X boson [L10].

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

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

4. Genetic code would be defined by projecting DNA codons with the same total quark and color bond spin projections to the amino-acid with the same (or opposite) spin projections. The

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

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

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

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

7.2.2 Objections against the identification of codons as dark quark triplets

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

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

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

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

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

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

7.3 Codons as dark nucleon-triplet strings?

The assumption that entire codon rather than letter corresponds to a state of dark proton does not conform with the model for the origin of purines as DNA nucleotides [L7] assuming that purines, and in fact all nucleotides, are combined with dark proton unless one assumes that 3 nucleotides combine with the same dark proton. This looks somewhat artificial but cannot be excluded.

The arguments of the model involve only the representations of rotation group and since p and n have same spin as u and d, the arguments generalize to 3- nucleon states (ppp, ppn, pnn, nnn) connected by two color bounds and organized to linear structures. Concerning genetic code, exactly the same predictions follow in the recent formulation of the model. In this case quark color is not present. One could however use the 1-dimensionality and the ordering of dark nucleons as already described.

The model with linear quark triplets generalizes by replacing dark u and d quarks with dark nucleons p and n. The analogs of ρ mesons would correspond to 2 bonds also now. Irrespective of changes of nucleons, all states would have decomposition $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ corresponding to the degrees of freedom associated with 3 nucleon spins and 2 neutral ρ meson spins.

ppp could correspond to DNA and RNA and proton charges would neutralize the negative charges of ordinary DNA codons. The singlet formed by bonds would be neglected. nnn triplets could correspond to amino-acids and trNA. Amino-acids could correspond to $4 \times 5 = 20$ and the remaining states $4 \otimes 3 \oplus (2 \oplus 2) \otimes 5 \oplus 3$. could correspond to 44 tRNAs. Also other options are possible and have net charges 2 and 1.

This variant has several nice features. The model is consistent with the model for dark nucleon strings consisting of nucleons and color bonds between them. There is no need to introduce Δ type nucleon states and colored states are not needed in fermionic sector. Color bonds must be colored if one wants ordinary bosonic statistics for flux tubes but here braid statistics might help. Colored bonds could of course have some important function.

7.3.1 Could dark DNA, RNA, tRNA and amino-acids correspond to different charge states of codons?

If dark codons correspond to dark nucleon triplets as assumed in the following considerations there are 4 basic types of dark nucleon triplets: ppp, ppn, pnn, nnn. Also dark nucleons could represent codons as uuu, uud, udd, ddd: the following discussion generalizes as such also to this case. If strong isospin/em charge decouples from spin the spin content is same independently of the nucleon content. One can consider the possibility of charge neuralization by the charges assignable to color flux tubes but this is not necessarily. In any case, one would have 4 types of nucleon triplets depending on the values of total charges.

Could different dark nucleon total charges correspond to DNA,RNA, tRNA and amino-acids? Already the group representation content - perhaps correlating with quark charges - could allow to distinguish between DNA, RNA, tRNA, and amino-acids. For amino-acids one would have only 4×5 and ordinary statistics and color singlets. For DNA and RNA one would have full multiplet also color non-singlets and for tRNA one could consider $(4 \oplus 2_1 \oplus 2_2) \times 5$ containing 40 states. 31 is the minimum number of tRNAs for the realization of the genetic code. The number of tRNA molecules is known to be between 30-40 in bacterial cells. The number is larger in animal cells but this could be due to different chemical representations of dark tRNA codons.

If the net charge of dark codon distinguishes between DNA,RNA, tRNA, and amino-acid sequences, the natural hypothesis to be tested is that dark ppp, ppn, pnn, and nnn sequences are accompanied by DNA,RNA, tRNA, and amino-acid sequences. The dark beta decays of dark protons proposed to play essential role in the model of cold fusion [**?**]ould transform dark protons to dark neurons. Peptide backbones are neutral so that dark nnn sequence could be also absent but the dark nnn option is more natural if the general vision is accepted. There is also the chemically equivalent possibility that only dark protons are involved: dark proton + neutral color bond would represent proton and dark proton + negatively charged color bond would represent neutron. At this moment it is not possible to distinguish between these two options.

Is this picture consistent with what is known about charges of amino-acids DNA,RNA, tRNA, and amino-acids? Consider first the charges of these molecules.

1. DNA strand has one negative charge per nucleotide. Also RNA molecule has high negative

charge. This conforms with the idea that dark nucleons accompany both DNA and RNA. DNA codons could be accompanied by dark ppp implying charge neutralization in some scale and RNA codons by dark ppn. The density of negative charge for RNA would be 2/3 for that for DNA.

2. Arg, His, and Lys have positively charged side chains and Asp,Glu negative side chains (see `http://tinyurl.com/jsphvgt`). The charge state of amino-acid is sensitive to the pH value of solution and its conformation is sensitive to the counter ions present. Total charge for amino-acid in peptide however vanishes unless it is associated with the side chain: as in the case of DNA and RNA it is the backbone whose charge is expected to matter.

3. Amino-acid has central C atom to which side chain, NH_2, H and COOH are attached. For free amino-acids in solution water solution $NH_2 \to NH_3^+$ tends to occur pH=2.2 by receiving possibly dark proton whereas COOH tends to become negatively charged above pH= 9.4 by donating proton, which could become dark. In peptide OH attach to C and one H attached to N are replaced with peptide bond. In the pH range 2.2-9.4 amino-acid is zwitterion for which both COOH is negatively charged and NH_2 is replaced with NH_3^+ so that the net charge vanishes. The simplest interpretation is that the ordinary proton from negatively ionized COOH attaches to NH_2 - maybe via intermediate dark proton state.

4. The backbones of peptide chains are neutral. This conforms with the idea that dark amino-acid sequence consists of dark neutron triplets. Also free amino-acids would be accompanied by dark neutron triplets. If the statistics is ordinary only 4 dark nnn states are possible as also 5 dark color flux tube states.

5. tRNA could involve dark pnn triplet associated with the codon. An attractive idea is secondary genetic code assigning RNA codons to tRNA-amino-acid complex and projecting $8 \otimes (5 \oplus 3)$ containing 64 dark RNA spin states to $8 \otimes 5$ containing 40 dark tRNA spin states with same total nucleon and flux tube spins. Dark tRNA codons would in turn be attached to dark amino-acids by a tertiary genetic code projecting spin states $8 \otimes 5$ to $4 \otimes 5$ by spin projection. In the transcription dark tRNA would attach to dark mRNA inducing attachment of dark amino-acid to the growing amino-acid sequence and tRNA having only dark tRNA codon would be left. The free amino-acids in the water solution would be mostly charged zwitterions in the pH range 2.2-9.4 and the negative charge of COO^- would be help in the attachement of the free amino-acid to the dark proton of tRNA codon. Therefore also the chemistry of free amino-acids would be important.

   An interesting question is why pnn triplets for tRNA would only 5 in flux tube degrees of freedom entire 8 in nucleon degrees of freedom. For RNA consisting of ppn triplets also 3 would be possible. What distinguishes between ppn and pnn?

The model should explain the widely different properties of DNA, RNA, tRNA, and amino-acids. There are two options.

1. DNA/RNA/amino-acid codons could correspond to ppp/ppn/nnn and tRNA would correspond to pnn (order is not necessarily this). Different charge or dark codons explain why DNA (RNA) has H (OH) in $2'$ position. The repulsive Coulomb energy between dark codons would be stronger for DNA and the compensation of this forces by the magnetic tension associated with the flux tube pair connecting codon and anticodon this might have something to do with the stability of DNA double strand.

   (a) The instability of RNA as compared to DNA would result from the instability of the ribose in RNA (deoxiribose in DNA) as indeed believed. The absence of RNA double strands could be due to the instability of the flux tube pair assignable to n-n. This trivially implies absence of replication and transcription if it is based on same mechanism as in the case of DNA.

   (b) pnn structure could explain why tRNA does not form sequences and allow to understand wobble pairing, which states that the third mRNA codon does not correspond to unique tRNA anticodon but one has C,A,U $\to$ I and U$\to$ I. Due to the symmetries of the third

letter of the codon, this is consistent with the genetic code. The physical explanation for wobble base pairing could relate to pnn structure of tRNA. If the charge ordering is random one would have nnp,npn,pnn and C,A,U $\to$ I could correspond to these 3 situations whereas for U$\to$ I the correspondence would not depend on the ordering. Also for RNA one would have ppn,pnp, npp degeneracy but in this case one would have charge independence.

A possible charge pairing between RNA and tRNA would be p$\leftrightarrow$n. The charge pairing between DNA and RNA could be p $\to$ n for the third least significant letter of DNA. This would minimize the coding errors possibly induced this pairing.

(c) One can criticize the charge assignment ppn (possibly allowing permutations) for RNA codons. Could dark weak beta decays give rise to 1-D lattice like structure? Could the repetitive structure be due to energy minimization.

2. Could the correspondence be letterwise? For DNA A,T,C,G would correspond to p, and for RNA A,C,G to p and U to n. Codons not containing U wold be ppp type codons and one can wonder why the oxiribose for them is not replaced with de-oxiribose. The possible presence of n in dark codons could explain why RNA sequences are highly unstable and why they do not replicate and transcribe.

7.3.2 Objections based on group theory and statistics

The quark-triplet model and its generalization replacing u, d with nucleon states p, n works nicely but is better to try to invent objections against the proposal and try to find inconsistencies. Fermi and Bose statistics are the most obvious providers of killer arguments.

1. The basic objection is that if the quarks are organized in linear structures, one cannot talk about representation of 3-D rotation group since symmetry breaking to SO(2) acting along common axis which could be either the local axis along dark DNA helix of the axis of the entire helix. The linear ordering of the quarks is not consistent with the full harmonics. Rather, harmonics restricted to half space $0 \leq \theta \leq \pi/2$ ($\pi \geq \theta \geq \pi/2$) should characterize the "upper" ("lower") flux tube direction at the position of quark in the middle.

   If reflection along quantization axis and SO(2) generate the symmetries one still has labelling of the states by angular momentum projection and states form doublets $(m, -m)$. The representations of SO(3) split into these representation and the numbers of states with given spin projection remain the same. Therefore the predictions for the numbers of DNA codons coding given aminoacid are not changed. It is quite possible that braid statistics made possible by 1-dimensionality is needed to realize the idea about ordering and this would allow to have full DNA multiplets.

2. In quark model one forms tensor product of tensor products of 3 quark spin states and 3 quark isospin states and by color singletness requires that the state is completely antisymmetric in quark degrees of freedom. The state is completely symmetric in the non-colored degrees of freedom. One obtains only two representations $\Delta \leftrightarrow (3/2, 3/2)$ and $N = (1/2, 1/2)$ with positive parity. In quark model context the presence of other tensor products in $(4 \oplus 2_1 \oplus 2_2)_S \otimes (4 \oplus 2_1 \oplus 2_2)_I$ is forbidden. One reason is that spatial wave function is assumed to be symmetric in ground state. This forbids 2_2 in spin degrees of freedom. Symmetrization leaves only the Δ and N (Note that the total number of these state is 20!). Now strong isospin is broken and it is natural to not include it to the tensor product.

3. The presence of 2_2 would be forbidden in quark model since it would require antisymmetric spatial wave function to compensate for the antisymmetry of 2_2. In the recent case the situation is 1-dimensional and the ordering along nuclear string forces localization of quarks and one cannot have identical wave functions for quarks.

   1-D situation also suggests strongly braid statistics. Perhaps the situation could be understood in terms of fermionic oscillator operators along nuclear string having anti-commutation relations corresponding to non-trivial braid statistics - maybe making the statistics commutative. This could naturally allow anti-symmetrization along nuclear string for 2_2 states.

4. If one assumes ordinary statistics, one could one take care of the statistics of the 16 states in $2_2 \otimes (5 \oplus 3)$ by assuming that for 2_2 the color state is symmetric and thus 10-D representation of $SU(3)$. The state associated with color flux tubes cannot compensate this color (triality is 1) since it must correspond to triality zero representation. If the colors of DNA strand and conjugate correspond to 10 and $\overline{10}$ and color entanglement could guarantee color singletness for the codon pairs. This would however require anti-quarks for the conjugate strand.

   3 10:s associated with 3 codons contains in their tensor product a singlet (see `http://tinyurl.com/zjxxqhj`). Minimal color singlet dark DNA sequence would requite 3 color codons. One can of course wonder whether the presence of 3 decouplet codons - 2 at the beginning and 2 at end and one in the middle could define genes as basic units.

5. The statistics problem is encountered also for the flux tubes. 5 (and 1) as symmetric representation is allowed by statistics but triplet is antisymmetric and thus not allowed. Again braid statistics might help. If one assumes that the flux tubes are colored - say color octets - and color wave function for flux tube pairs is antisymmetric, one can achieve Bose statistics for 3. Flux tube pair would correspond to $8 \in \{8 \times 8\}$ and minimum of two flux codons would be needed for color singletness in flux tube degrees of freedom.

6. For the counterparts of amino-acids one has only $4 \otimes 5$ allowed also by statistics considerations assuming color singlets. Could distinction between DNA/RNA and amino-acids related to statistics, perhaps braid statistics. The suggested role of braid strands possibly connecting DNA double strands and DNA double strands and lipid layers of cell membrane encourages the question whether the DNA strand and its conjugate entangle via via the reconnection of the color flux tubes defining U-shaped "tentacles" to a flux tube pair connecting the strands. For amino-acids they would not be needed. Same could happen in the transcription process of DNA to mRNA and in the translation process for mRNA tentacles and those associated with tRNA.

7.3.3 Ordinary or braid statistics?

There are four options to consider: ordinary/braid statistics (1/2) and dark nucleon as dark quark/nucleon triplet as representation of DNA codon (a/b). One has options 1a,1b,2a,2b. Options 1b and 2b are at this moment the only options, which can be taken seriously: the reason is that dark protons would neutralize the negative charges of ordinary DNA nucleotides.

1. Option 1a: codons as quark-triplets with ordinary statistics. For the ordinary statistics amino-acid like dark nucleons are color singlets. Part of DNA codons are represented as dark nucleons and would be colored and 10-D representation of SU(3). Dark amino-acids need not have color bonds with dark parts of other colored biomolecules like DNA,RNA, with exception possible formed by dark tRNA. DNA double strand could realize color confinement via the reconnection of color flux tubes.

2. Option 1b: codons as nucleon-triplets with ordinary statistics. Option 1b requires in ordinary statistics for antisymmetric doublet and antisymmetric wave function for the 3 nucleons not allowing constant valued wave function also disfavored by the linear ordering. This condition might have the same implications as braid statistics.

3. Options 1a and 1b. DNA is the only molecule that appears as double strands. A possible explanation is that codons and anticodons are paired by U-shaped flux tubes associated with the color bonds of dark DNA to form color singlets. Nucleonic colors would sum up to zero along the strand.

4. Option 2a. For braid statistics it could be possible to avoid colored states of nucleon and flux tubes.

5. Option 2b. The 3-nucleon codons would have no color and amino-acids could obey braid statistics reducing to ordinary statistics. This would not be the case for DNA/RNA.

It must be admitted that the situation is unsatisfactory as far as statistics is considered. For the option 1b) with codons identified as dark proton triplets one can however consider the following variant to satisfy statistics requirement.

1. Years after writing the above comments it has become clear that adelic physics [L11] brings in additional discrete degrees of freedom assignable to the group algebra of Galois group of extension of rationals inducing the extensions of p-adic number fields appearing in the adele.

2. Galois group acts on the space of space-time surfaces, and one can say that one has wave function at the orbit of the Galois group consisting of space-time sheets. At quantum level quantum states correspond to wave functions in the group algebra of Galois group of extension.

3. The role of color in helping to achieve correct statistics could be taken by Galois degrees of freedom. One can even consider the notion of Galois confinement as a generalization of color confinement [L12] binding codons as dark proton triplets to dynamical units. Even genes as sequences of codons could be bound to dynamical units as Galois singlets.

7.4 Further considerations

7.4.1 Replication, transcription, translation

The formation of flux tube pairs between molecules would be central in replication and transcription and in all bio-catalysis. Dark DNA would replicate first to dark DNA or mRNA. This requires that the building bricks of dark DNA and mRNA emerge from environment perhaps by mechanism involving reconnection for the magnetic tentacles and reduction of h_{eff} bringing the molecules near each other. Flux tube pairs between dark DNA codonsandtheir conjugates (individual dark RNA codons) would be formed during replication (transcription). The formation of flux tube pair between mRNA and dark tRNA part of tRNA would bring tRNA to mRNA, where amino-acid would associate with the growing amino-acid sequence.

For options 1a and 1b based on ordinary statistics color singletness condition could play an important role in the replication and transcription.

1. If the value of h_{eff} before reconnection and contraction of flux tube dictating the scale of color confinement is large enough, colored dark nucleons could float as free - possibly colored states - in the environment for option 1a). For option 1b dark nucleons could be present in environment - this could relate directly to the ionization in electrolyte. For options 1a and 1b dark codons representing dark tRNA molecules would accompany them.

2. For options 1a) and 1b) color confinement in flux tube degrees of freedom by forming dark color flux tube pairs between dark DNA and its conjugate in codon-wise manner could give rise to DNA double strands as chemical shadows of dark double strands. The coupling between codon and anticodon would be defined by the condition that the total color bond spins of paired codons are opposite. Quark color could be compensated for option 1a along DNA strand: 3 10:s give singlet. One can of course ask whether dark DNA RNA sequences exist rather than being built during replication and transcription.

7.4.2 Are sound-like bubbles whizzing around in DNA essential to life?

I got a link to a very interesting article [I17] about sound waves in DNA (see `http://tinyurl.com/z7hod9b`). The article tells about THz de-localized modes claimed to propagate forth and back along DNA double strand somewhat like bullets. These modes involve collective motion of many atoms. These modes are interpreted as a change in the stiffness of the DNA double strand leading to the splitting of hydrogen bonds in turn leading to a splitting into single strands. The resulting gap is known as transcriptional bubble propagating along double strand is the outcome. I do not how sound the interpretation as sound wave is.

It has been proposed that sound waves along DNA give rise to the bubble. The local physical properties of DNA double strand such as helical structure and elasticity affect the propagation of the waves. Specific local sequences are proposed to favor a resonance with low frequency vibrational

modes, promoting the temperary splitting of the DNA double strand. Inside the bubble the bases are exposed to the surrounding solvent, which has two effects.

Bubbles expose the nucleic acid to reactions of the bases with mutagens in the environment whereas so called molecular intercalators may insert themselves between the strands of DNA. On the other hand, bubbles allow proteins known as helicases to attach to DNA to stabilize the bubble, followed by the splitting the strands to start the transcription and replication process. The splitting would occur at certain portions of DNA double strand. For this reason, it is believed that DNA directs its own transcription.

The problem is that the strong interactions with the surrounding water are expected to damp the sound wave very rapidly. Authors study experimentally the situation and report that propagating bubbles indeed exist for frequencies in few THz region. Therefore the damping deo not seem to be effective. How this is possible? As an innocent layman I also wonder how this kind of mechanism can be selective: it would seem that the bullet like sound wave initiates transcription at many positions along DNA. The transcription should be localized to a region assignable to single gene. What could guarantee this?

Can TGD say anything interesting about the mechanism behind transcription and replication?

1. In TGD magnetic body controls and coordinates the dynamics. The strongest hypothesis is that basic biochemical process are induced by those for dark variants of basic bio-molecules (dark variants of DNA, enzymes,...). The belief that DNA directs its own transcription translates to the statement that the dark DNA consisting most plausibly from sequences of dark proton triplets ppp at dark magnetic flux tubes controls the transcription: the transcription/replication at the level of dark DNA induces that at the level of ordinary DNA.

2. If the dark DNA codons represented as dark proton triplets (ppp) are connected by 3 flux tube pairs, the reverse of the reconnection should occur and transform flux tube pairs to two U-shaped flux tubes assignable to the two dark DNA strands. Dark proton sequences have positive charge +3e per dark codon giving rise to a repulsive Coulomb force between them. There would be also an attractive force due to magnetic tension of the flux tubes. These two forces would compensate each other in equilibrium (there also the classical forces due to the negatively charged phosphates associated with nucleotides but these would not be so important).

   If the flux tube pairs are split, the stabilizing magnetic force however vanishes and the dark flux tubes repel each other and force the negatively charged DNA strands to follow so that also ordinary DNA strand splits and bubble is formed. The primary wave could therefore be the splitting of the flux tube pairs: whether one can call it as a sound wave is not clear to me. Perhaps the induced propagating splitting of ordinary DNA double strand could be regarded as an analog of sound wave.

   The splitting of flux tube pairs for a segment of DNA would induces a further splitting of flux tubes since repulsive Coulomb force tends to drive the flux tubes further away. The process could be restricted to DNA if the "upper" end of the split DNA region has some dark DNA codons which are not connected by flux tubes pairs. This model reason why for dark proton sequences.

3. This model does not yet explain how the propagating splitting wave is initiated. Could a quantum phase transition increasing the value of h_{eff} associated with the flux tube pairs occur for some minimal portion of dark DNA "below" the region associated with gene and lead to the propagating wave induced by the above classical mechanism? That the wave propagates in one direction only could be due to chirality of DNA double helix.

An interesting question is how the RNA world vision (see `http://tinyurl.com/gpmxcmk`) relates to this general picture.

1. There are strong conditions on the precedessor of DNA and RNA satisfies many of them: reverse transcription to DNA making possible transition to DNA dominated era is possible. Double stranded RNA exists `http://tinyurl.com/y9mex4v7` in cells and makes possible RNA genome: this would however suggest that cell membrane came first. RNA is a catalyst. RNA has ability to conjugate an amino-acid to the $3'$ end of RNA and RNA catalyzes

peptide bond formation essential for translation. RNA can self-replicate but only relatively short sequences are produced.

2. TGD picture allows to understand why only short sequences of RNA are obtained in replication. If the replication occurs at the level of dark ppn sequences as it would occur for DNA in TGD framework, long RNA sequences might be difficult to produce because of the stopping of the propagation of the primary wave splitting the flux tube pairs. This could be due to the neuron pairs to which there is associated no Coulomb repulsion essential for splitting.

3. In TGD framework RNA need not be the precedessor of DNA since the evolution would occur at the level of dark nucleon strings and DNA as the dark proton string is the simpest dark nucleon string and might have emerged first. Dark nuclear strings would have served as templates and biomolecules would have emerged naturally via the transcription of their dark counterparts to corresponding bio-polymers.

7.4.3 Is bio-catalysis a shadow of dark bio-catalysis based on generalization of genetic code?

Protein catalysis and reaction pathways look extremely complex (see `http://tinyurl.com/kp3sdlm`) as compared to replication, transcription, translation, and DNA repair. Could simplicity emerge if biomolecules are identified as chemical shadows of objects formed from dark nuclear strings consisting of dark nucleon triplets and their dynamics is shadow of dark stringy dynamics very much analogous to text processing?

What if bio-catalysis is induced by dark catalysis based on reconnection as recognition mechanism? What if contractions and expansions of U-shaped flux tubes by h_{eff} increasing phase transitions take that reactants find each other and change conformations as in the case of opening of DNA double strand? What if codes allowing only the dark nucleons with same dark nuclear spin and flux tubes spin to be connected by a pair of flux tubes?

This speculation might make sense! The recognition of reactants is one part of catalytic action. It has been found in vitro RNA selection experiments that RNA sequences are produced having high frequency for the codons which code for the amino-acid that these RNA molecules recognize (`http://tinyurl.com/kp3sdlm`. This is just what the proposal predicts!

Genetic codes DNA to RNA as $64 \to 64$ map, RNA to tRNA as $64 \to 40$, tRNA to amino-acids with $40 \to 20$ map are certainly not enough. One can however consider also additional codes allowed by projections of $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \oplus 3(\oplus 1))$ to lower-dimensional sub-spaces defined by projections preserving spins. One could also visualize bio-molecules as collections of pieces of text attaching to each other along conjugate texts. The properties of catalysts and reactants would also depend by what texts are "visible" to the catalysts. Could the most important biomolecules participating biochemical reactions (proteins, nucleic acids, carbohydrates, lipids, primary and secondary metabolites, and natural products, see `http://tinyurl.com/jlfxags`) have dark counterparts in these sub-spaces.

The selection of bio-active molecules is one of the big mysteries of biology. The model for the chemical pathway leading to the selection of purines as nucleotides [L7] assumes that the precedessor of purine molecule can bind to dark proton without transforming it to ordinary proton. A possible explanation is that the binding energy of the resulting bound state is higher for dark proton than the ordinary one. Minimization of the bound state energy could be a completely general criterion dictating which bio-active molecules can pair with dark protons. The selection of bio-active molecules would not be random after all although it looks so. The proposal for DNA-nuclear/cell membrane as topological quantum computer with quantum computations coded by the braiding of magnetic flux tubes connecting nucleotides to the lipids wlead to the idea that flux tubes being at O=-bonds [K1].

7.4.4 Comparing TGD view about quantum biology with McFadden's views

McFadden [I22] has very original view about quantum biology: I have written about his work for the first time for years ago, much before the emergence of ZEO, of the recent view about self as generalized Zeno effect, and of the understanding the role of magnetic body containing dark

matter [**?**]. The pleasant surprise was that I now understand McFadden's views much better from TGD viewpoint.

1. McFadden sees decoherence as crucial in biological evolution: here TGD view is diametric opposite although decoherence is a basic phenomenon also in TGD.

2. McFadden assumes quantum superpositions of different DNAs. To me this looks an unrealistic assumption in the framework of PEO. In ZEO it is quite possible option.

3. McFadden emphasizes the importance of Zeno effect (in PEO). In TGD the ZEO variant of Zeno effect is central for TGD inspired theory of consciousness and quantum biology. Mc Fadden suggests that quantum effects and Zeno effect are central in bio-catalysis: the repeated measurement keeping reactants in the same position can lead to an increase of reaction rate by factors of order billion. McFadden describe enzymes as quantum mousetraps catching the reactants and forcing them to stay in same position. The above description for how catalysis catches the reactants using U-shaped flux tube conforms with mousetrap picture.

   McFadden discusses the action of enzymes in a nice manner and his view conforms with TGD view. In ZEO the system formed by catalyst plus reactants could be described as a negentropically entangled sub-self, and self indeed corresponds to a generalized Zeno effect. The reactions can proceed in shorter scales although the situation is fixed in longer scales (hierarchy of CDs): this would increase the length of the period of time during which reactions can proceed and lead to catalytic effect. Zeno effect in ZEO plus hierarchies of selves and CDs would be essentially for the local aspects of enzyme action.

4. Protons associated with hydrogen bonds and electronic Cooper pairs play a universal role in McFadden's view and the localization of proton in quantum measurement of its position to hydrogen bond is the key step of enzyme catalysis. Also TGD dark protons at magnetic flux tubes giving rise to dark nuclear strings play a key role. For instance, McFadden models enzyme catalysis as injection of proton to a very special hydrogen bond of substrate. In TGD one has dark protons at magnetic flux tubes and their injection to a properly chosen hydrogen bond and transformation to ordinary proton is crucial for the catalysis. Typical places for reactions to occur are C=O type bonds, where the transition to C-OH can occur and would involve transformation of dark proton to ordinary proton. The transformation of dark proton to ordinary one or vice versa in hydrogen bonds would serve as a biological quantum switch allowing magnetic body to control biochemistry very effectively.

   What about electronic Cooper pairs assumed also by McFadden. They would flow along the flux tube pairs. Can Cooper pairs of electrons and dark protons reside at same flux tubes? In principle this is possible although I have considered the possibility that particles with different masses (cyclotron frequencies) reside at different flux tubes.

McFadden [I22] has proposed quantum superposition for ordinary codons: This does not seem to make sense in PEO since the chemistries of codons are different) but could make sense in ZEO. In TGD one could indeed imagine quantum entanglement (necessary negentropic in p-adic degrees of freedom) between dark codons. This NE could be either between additional degrees of freedom or between spin degrees of freedom determining the dark codons. In the latter case complete correlation between dark and ordinary DNA codons would imply also the superposition of their tensor products with ordinary codons.

The NE between dark codons could also have a useful function: it could determine physically gene as a union of disjoint mutually entangled portions of DNA. Genes are known to be highly dynamical units, and after pre-transcription splicing selects the portions of the transcript translated to protein. The codons in the complement of the real transcript are called introns and are spliced out from mRNA after the pre-transcription (see `http://tinyurl.com/gmphzzy`).

What could be the physical criterion telling whether a given codon belongs to exonic or intronic portion of DNA? A possible criterion distinguish between exons and introns is that exons have NE between themselves and introns have no entanglement with exons (also exons could have NE between themselves). Introns would not be useless trash since the division into exonic and exonic region would be dynamical. The interpretation in terms of TGD inspired theory of consciousness is that exons correspond to single self.

7.4.5 Is there a connection between geometric model of harmony and nuclear string model of genetic code?

There should exists a connection between the geometric model of harmony and genetic code and the model of genetic code discussed.

1. Dark DNA strands could be connected by color flux tubes to form a double strand by reconnections of U-shaped color flux tubes. What would induce a codon-wise or letter-wise pairing of DNA codons and their conjugates represented as dark quark triplets to form double DNA strand? Cyclotron resonance could accompany reconnection (magnetic field strength would be identical and reconnection could occur).

2. One has the correspondence codon $\leftrightarrow$ state of dark nucleon or codon $\leftrightarrow$ state of dark nucleon triplet. The geometric model of harmony and genetic code [L3] represents the codons as 3-chords. The 3-chord would be represented in terms of cyclotron frequencies of dark photons assignable to the 3 dark quarks (nucleons) in the state. Each quark-color bond pair (including the pion-like bond) could be in 12 states with corresponding cyclotron frequency mappable to the basic octave. The cyclotron frequency triplets would be same for codons and conjugates. The only manner to understand the scale is in terms of spectrum of magnetic field strengths for U-shaped flux tube pairs.

   This would require 3 pairs of flux tubes between the dark codons of DNA strands. If the quarks inside linear dark proton are connected by color flux tubes (like protons in the model of dark nucleus). Reconnection for U-shaped flux tube connecting quarks would give rise to the double strand formed by dark proton strings. The magnetic field strength of the 3-flux tubes would be determined by the state of dark proton and would be same for DNA and RNA codons and also for RNA codons and corresponding tRNA-amino-acid complexes. The cyclotron frequencies would define a scaled up variant of Pythagorean scale projected to the basic octave [L3]. This option does not favor the idea about separater 4-letter code.

3. The geometric model for harmony is formulated in terms of orbits of the subgroups of the isometry groups of tetrahedral and icosahedral geometries. The DNAs coding particular amino-acid correspond correspond to the orbit of the triangle of icosahedron corresponding to the amino-acid. The decomposition $60 \to 20 + 20 + 20$ suggests strongly decomposition of I to 20 Z_3 cosets containing 3 elements each other and in correspondences with the triangular faces of icosahedron.

4. The model of the genetic code just discussed relies on the model of dark nucleon based on group theory. The symmetric groups of Platonic solids are in turn associated with inclusion of hyper-finite factors and appear in Mc Kay correspondence, whose proof involves decompositions of SU(2) representations to the representations of the discrete subgroups of Platonic solids. A further observation is that the numbers of elements for isometries of icosahedron and tetrahedron are 60 and 4 respectively: the sum is 64. Could the action of Z_3 leaving face invariant could be posed as an additional condition on amino-acids and reduce the amino-acid representation to $4 \otimes 5$.

5. In the geometric model of harmony genetic icosahedral 20+20+20 part of the code involves a combination of three different Hamilton's cycles mapping 60 DNAs to 20 amino-acids: in terms of icosahedral group I and its coset space I/Z_3 these maps correspond to coset projections. Could the decomposition $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \otimes 3)$ be understood in terms of a reduction to icosahedral and tetrahedral subgroups of rotation group or of their spin coverings.

   In this process finite-dimensional representation of $SO(3)$ decomposes to a direct sum of representations of the discrete subgroup if its dimension is larger than any of the dimensions of representations of the finite sub-group (for basic facts about these see `http://tinyurl.com/ho4onbs`). One might hope that the decomposition of the representations of SO(3) appearing in the above formula under icosahedral group and or tetrahedral group could allow to understand the emergence of DNA, RNA, tRNA, and amino-acids as kind of symmetry breaking.

6. In the geometric model of harmony 64-codon code [L3] is obtained as a fusion 60-codon code assignable to icosahedron + 4 codon code assignable to tetrahedron. There are actually two codes corresponding to tetrahedron and icosahedron as disjoint entities and tetrahedron glued to icosahedron along one face. The model explains the two additional amino-acids Pyl and Sec coded for a variant of the genetic code.

How could these two successful models relate to each other? In p-adic physics of cognition Platonic solids and polygons can be seen as discrete approximation for sphere [L8] and biomolecules could be understood as cognitive representation in the intersection of real and p-adic space-time surface consisting of algebraic points. Could one assign icosahedron and tetrahedron to a codon in some concrete manner? Could the attachment of tetrahedron to icosahedron along one face have concrete meaning? The answer seems to be negative.

1. One can about the interpretation of the 12 vertices of the icosahedron - how number 12 could be assigned with the genetic code? The vertices correspond to notes perhaps represented as magnetic field strength at the flux tubes assignable to color bonds. This field strength should be determined by the spin state of dark 3-nucleon. No concrete nuclear string counterpart seems to exist for the closed Hamiltonian cycle consisting of 12 notes and in case of tetrahedral extension of 13 notes. 12 vertices of icosahedron correspond to 12 notes and 20 faces to 3-chords so that there is not need for more concrete correspondence.

2. The attachment of tetrahedron to icosahedron would bring in further note very near to one of the notes of Pythagorean scale and corresponding 3-chords. This has concrete interpretation and there is no need to make this more concrete at the level of geometry of DNA. If icosahedron and tetrahedron are disjoint one obtains four additional codons. It seems that all these 4 3-chords be assigned with the 3 color bonds, one note for each of them. What distinguishes at the level of dark nucleon string the situations in which tetrahedron is attached and non-attached to the color bond? In presence of attachment there would be 1 shared 3-chord corresponding to stop codon assignable with the shared face. The 13:th note appearing in 4 3-chords differs very little from one of the notes of the icosahedral scale: this corresponds to the fact that 12 perfect quints do not quite give 7 octaves as already Pythagoras realized. Crazy question: Could this small difference relate to the small relative mass difference $(m_p - m_n)/m_p \simeq .0014$ making itself possible visible in cyclotron frequency scale? The idea does not seem plausible: $[(3/2)^{12} - 2^7]/2^7 \simeq .014$ is 10 times larger than $(m_p - m_n)/m_p \simeq .0014$.

The conclusion is that genetic code can be understand as a map of stringy nucleon states induced by the projection of all states with same spin projections to a representative state with the same spin projections (total quark spin and total flux tube spin). Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin.

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