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

M. Pitkänen,
February 14, 2018

Email: matpitka6@gmail.com.
http://tgdtheory.com/public_html/
Recent postal address: Rinnekatu 2-4 A 8, 03620, Karkkila, Finland.

Contents

1 Introduction 5
  1.1 The Notions Of Dark Matter And Magnetic Body 6
  1.2 Realizations Of Genetic Code 6
  1.3 Questions 7

2 A Vision About Evolution And Codes 7
  2.1 Basic Insights 7
  2.2 The Simplest Scenario 8
  2.3 How Dark Baryon Code Could Be Involved With Transcription And Translation
    2.3.1 Replication 9
    2.3.2 DNA $\rightarrow$ mRNA transcription 10
    2.3.3 Translation as a sequence of reconnections 10

3 DNA As Topological Quantum Computer: Realization Of The Genetic Code In Terms Of Quarks And Anti-Quarks 11
  3.1 Basic Ideas Of TQC 11
  3.2 Identification Of Hardware Of TQC And TQC Programs 12
  3.3 How Much TQC Resembles Ordinary Computation? 13
  3.4 Some Predictions Related To The Representation Of Braid Color
    3.4.1 Anomalous em charge of DNA as a basic prediction 14
    3.4.2 Chargaff’s second parity rule and the vanishing of net anomalous charge 14
    3.4.3 Are genes and other genetic sub-structures singlets with respect to QCD color 15
    3.4.4 Summary of possible symmetries of DNA 19
4 Constraints On The Fermionic Realization Of Genetic Code From The Model For Color Qualia
4.1 Fermionic Representation ........................................... 25
4.2 Various Options For The Fermionic Representation Of A, T, C, G .......... 26
4.3 Realization Of Color Qualia For Quark Option .......................... 26

5 Realization Of Genetic Code In Terms Of Dark Baryons
5.1 Dark Nuclear Strings As Analogs Of DNA-, RNA- and Amino-Acid Sequences and Baryonic Realization Of Genetic Code? ............................................. 28
5.1.1 States in the quark degrees of freedom .............................. 29
5.1.2 States in the flux tube degrees of freedom .......................... 30
5.1.3 Analogs of DNA, RNA, amino-acids, and of translation and transcription mechanisms ......................................................... 30
5.1.4 Is the genetic code a composite of 64 → 40 and 40 → 20 codes? ...... 31
5.1.5 Objections ................................................................. 32
5.2 DNA As Topological Quantum Computer Hypothesis And Dark Genetic Code .. 32

6 Could One Find A Geometric Realization For Genetic And Memetic Codes?
6.1 The Notions Of Memetic Code And Dark Genetic Code .................. 34
6.1.1 The notion of memetic code ......................................... 34
6.1.2 The notions of dark nucleus and dark genetic code ................. 35
6.2 Could The Faces Of Tetrahedron Correspond To The Four DNA Nucleotides? 35
6.3 Could The 20 Outer Faces/Tetrahedrons Of The Icosahedron Correspond To Amino-Acids? .................................................... 36
6.4 Icosahedral Realization Of The Memetic Code? ........................... 36
6.5 Geometric Representation Of Dark DNA Codons .......................... 37
6.6 Could Water Clusters Represent Memetic Code? .......................... 38

7 Pythagoras, Music, Sacred Geometry, And Genetic Code
7.1 Could Pythagoras Have Something To Give For The Modern Musicology? 40
7.1.1 Pythagoras and transition from rational numbers to algebraic numbers .... 40
7.1.2 Pythagoras and music .................................................. 40
7.1.3 Would you come with me to icosadisco? ............................ 44
7.2 Connection Between Music Molecular Biology? .......................... 45
7.2.1 Could amino-acids correspond to 3-chords of icosahedral harmony? ... 45
7.2.2 Can one understand genetic code? .................................... 45
7.2.3 Does the understanding of stopping codons and 21st and 22nd amino-acids require fusion of tetrahedral and icosahedral codes? ................. 47
7.2.4 How could one construct the Hamiltonian cycles on icosahedron with a minimal computational work? ................................. 50
7.2.5 Icosahedral Hamiltonian cycles numerically .......................... 52
7.3 Other Ideas ................................................................. 54
7.3.1 p-Adic length scale hypothesis and music ............................ 54
7.3.2 EEG and music .......................................................... 54
7.3.3 Standing waves and music ............................................. 55
7.3.4 Emotions and 4-D character of music experience ...................... 55

8 Geometric Theory Of Harmony
8.1 What Could Be The Basic Principles Of Harmony? ........................ 56
8.1.1 Icosahedral harmonies .................................................. 58
8.1.2 Why quints are near to each other harmonically? .................... 59
8.1.3 What could be the rules for building a harmony? ..................... 60
8.1.4 More general notion of harmony ...................................... 61
1. Introduction

This chapter represents an attempt to integrate three different models of genetic code \([K5, K24, K27]\) with each other and with DNA as topological quantum computer (TQC) hypothesis \([K5]\) as well as the general ideas behind the model of protein folding and bio-catalysis \([K1]\). 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 imbedding 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 \(\mathbb{CP}^2\) 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 \(\mathbb{Z}_{n_a}\) resp. \(\mathbb{Z}_{n_b}\) acting in the fiber of singular covering space or factor space assignable \(M^4\) resp. \(\mathbb{CP}^2\) 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 \(n_a\) \((n_b)\) divides \(n_a\) \((n_b)\) 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 [K5]. 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 [K10, K24]. 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 [A9] in terms of the sub-group rule for phase transitions [K24]. 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 discussed also by others 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.

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/mansheetd.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).
2.2 The Simplest Scenario

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 [K10].

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 [I21] and that the genetic variation due to jumping genes is highest in brain and germ cells [I15] is consistent with the view about dark evolution modifying at least intron portion of the genome.

RNA world [I24, I32, I16] 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 $64 - 40 \rightarrow 40 - 20$ 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 [I13]. 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
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 (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 \(Y\). \(U\) and \(V\) or \(X\) and \(U\). \(Y\) 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 \(dX - Y\) 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 \((X \circ Y) + (U \circ V) \rightarrow X \circ U \rightarrow Y \circ V\) with reconnection taking place for the flux tubes.

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

2.3.2 \(DNA \rightarrow mRNA\) 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 \(DNA \rightarrow mRNA\) could correspond to the \((X \circ Y) + (U \circ V) \rightarrow X \circ U \rightarrow Y \circ V\) 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 manners. 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 \(U - V = tRNA_{AA} - tRNA\). 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

Large values of Planck constant allow to imagine all kinds of quantum computations [B1, B9, 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 \(h\). 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 [I19, I23] 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 [I23] 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 \(\pi\). 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 ℏ 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 [K7].

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′, d, d′. 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 [A6].

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 [30]. 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 braiding 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 [K10, 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 [I19] 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 [I19] 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?
3.4 Some Predictions Related To The Representation Of Braid Color

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

\[
Q_a = [n(A) - n(T)] \frac{1}{4} - [n(G) - n(\overline{C})] \frac{1}{4},
\]
\[
Q_a = -[n(A) - n(T)] \frac{1}{4} + [n(G) - n(\overline{C})] \frac{1}{4},
\]
\[
Q_a = -[n(A) - n(T)] \frac{1}{4} + [n(G) - n(\overline{C})] \frac{1}{4},
\]
\[
Q_a = [n(A) - n(T)] \frac{1}{4} - [n(G) - n(\overline{C})] \frac{1}{4}.
\]  

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:

\[
Q_a = [n(A) - n(T)]Q(q_A) + [n(G) - n(\overline{C})]Q(q_G)
\]  

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

Second option is obtained from the first option \((A, T, G, C) \rightarrow (u, \overline{u}, d, \overline{d})\) 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 \(\Delta L\) 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 \([?]\) [I33] 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
3.4 Some Predictions Related To The Representation Of Braid Color

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

\[
p(A) + p(C) \simeq 1/2, \quad p(A) + p(G) \simeq 1/2, \\
p(T) + p(C) \simeq 1/2, \quad p(T) + p(G) \simeq 1/2.
\] (3.3)

An interesting empirical finding [33] 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 \( \bar{u} \) at DNA space-time sheet are more favored than \( d \) and \( \bar{d} \) 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 [K7] could distinguish between different structural sub-units. For this option only gene - understood as TQC unit with un-transcribed regions included - would be color singlet.

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

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

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

\[
n(A) + n(G) \mod 3 = 0, \quad n(C) + n(T) \mod 3 = 0.
\] (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.
Some Predictions Related To The Representation Of Braid Color

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

\[ n(A) - n(T) + n(G) - n(C) \equiv 0 \mod 3. \] (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 required only 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 [K7] 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 [K8] 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

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

(3.6) to be satisfied. The knowledge of gene would thus predict $n_{\text{tail}}(A) \mod 3$. 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

$$2[n(A) + n_{\text{tail}}(A) - n(T)] - n(G) - 1 - n(C) \simeq 0,$$
$$-2[n(A) + n_{\text{tail}}(A) - n(T)] + 2[n(G) - 1 - n(C)] \simeq 0,$$
$$n(A) + n_{\text{tail}}(A) - n(T) - 2[n(G) - 1 - n(C)] \simeq 0.$$ (3.7)

Here $n_{\text{tail}}(A)$ 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 $d$ corresponding to options 1 and 4.

6. Moving genes and repeating elements

Transposons [112] 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) [10]. 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 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 [13] the overhang is $CTAG$ and has vanishing $Q_a$. The cut site $CCTAGG$ has also vanishing $Q_a$. It is known [2] that transposons - repeating regions themselves - tend to attach to the repeating regions of DNA [13].

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 [15].

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 $(a, g) \leftrightarrow (\bar{d}, \bar{\pi})$ 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 $A \rightarrow \bar{d}$, the prediction for the length of polytail for $A \rightarrow \bar{d}$ 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 $A \rightarrow \bar{\pi}$ 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 Some Predictions Related To The Representation Of Braid Color

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 ↔ antiquark). Chargaff’s rules states \(A \approx T\) and \(C \approx G\) 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: (ile, ile, 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 $I(\text{inositol})$ 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 [110] 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 $Q_{\alpha}$ for one of the codons coding for it. The amino-acid sequences of catalysts attaching to DNA strand should have opposite $Q_{\alpha}$ 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 [K19] 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 [I10] 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
3.4 Some Predictions Related To The Representation Of Braid Color

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 \( d(q - \bar{q})/dn = p(A - T + G - C) \) of quark number per nucleotide, and \( (A + T)/(C + G) \) ratio for entire genomes in some cases.

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

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 \( 24 \times (5/18) \times 10^3 e \cdot 0.8 \times 10^3 xe \), \( 1 < x < 10 \). 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 [I7], 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 already been discussed and correspond to approximate matter antimatter symmetry. The second symmetry parameter would measure the asymmetry between \( uT \) and \( d\bar{T} \) type matter. \( p(G + C) \) corresponds to the fraction of \( d\bar{T} \) type quark matter for option 1) and \( u\bar{T} \) matter for option 2). It is known that \( G + C \) fraction \( p(G + C) \) characterizes genes [I24] and the value of \( p(G + C) \) is proportional to the length of the coding sequence [I6, I26].

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 \cite{I2, I27}. 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 (\( u \bar{u} \) and \( d \bar{d} \)): 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 (\( u \bar{u} \) or \( d \bar{d} \)) 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 (\( (Q_d < 0, I_3 = -1/2) \)) or its charge conjugate \( d_c \) (\( (Q_d < 0) \). 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 \((A, G, T, C) \rightarrow (u, d, \pi, \bar{d})\) 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 [K9] [K7]. 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 Mn = 2^n − 1 with M_{n(next)} = M_{M_n} starting from n = 2 with M2 = 3 gives rise to 1-code with 4 codons, 3-code with 64 codons, and 3 × 21 = 63-code with 2^{120} codons [K9] 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^n + 1 = 5 with M5 = 2^5 − 1 = 31 gives rise to a code with 16 codons realized as 2-codons (2 nucleotides). Second level corresponds to Mersenne prime M31 = 2^{31} − 1 and a code with 2^{30=15×2} 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 M13. The code would have 2^{12=6×2} 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 M17 and the code would have 2^{16=8×2} codons representable as sequences of 8 nucleotides.

3. n = 19 defines Mersenne prime M19 and code would have 2^{18=9×2} codons representable as sequences of 9 nucleotides or three DNA codons.

4. The next Mersennes are M31 belonging to n = 5 hierarchy, M61 with 2^{60=30×2} 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 $\bar{q}$ 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 $q\bar{q}$ 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 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 as identical bosons with 3+1 spin states and 3 x 3 color states. They form formally super-multiplet of \(N = 2\) 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 \url{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 naive 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 $udubarbar$ 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, K10, K24, L1, I22]. 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 [K5] 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:

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

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 $\Delta$ 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 $j_1 \times j_2 = j_1 + j_2 \oplus j_1 + j_2 - 1 \oplus \ldots \oplus |j_1 - j_2|$ 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 \((J, I) = (3/2, 3/2)\) (\(\Delta\) 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 \(2_{\text{odd}}\) - has wrong parity in the sense that it would require \(L = 1\) ground state for two identical quarks (\(uu\) or \(dd\) pair). Dropping \(2_{\text{odd}}\) and using only \(4 \otimes 2\) for the rotation group would give degeneracies \((1, 2, 2, 1)\) and 6 states only. All the representations in \(4 \otimes 2 \oplus 2_{\text{odd}}\) 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 \(J_z = 3/2\) are \((1, 2, 3, 2)\). Genetic code means spin projection mapping the states in \(4 \otimes 2 \oplus 2_{\text{odd}}\) 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 \(\pi\) meson (pion) with spin 0 and \(\rho\) 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 \((1, 2, 2, 2, 1)\). 8x 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 \(uud\) type states serving as candidates for the counterparts of amino-acids bosonic statistics allows only 5 states \((J = 2)\). Hence 20 counterparts of amino-acids are obtained for \(uud\). 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
5.1 Dark Nuclear Strings As Analogs Of DNA-, RNA- and Amino-Acid Sequences and Baryonic Realization Of Genetic Code?

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 $4 \times 5$. 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 $D_h \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_h$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of amino-acids coded by $D$ codons would be

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

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

4. Stopping codons would most naturally correspond to the codons, which involve the $L_z = -1$ relative rotational excitation of $uu$ or $dd$ type quark pair. For the 3-plet the two candidates for the stopping codon state are $|1/2, -1/2\rangle \otimes |[2, k]\rangle$, $k = 2, -2$. The total spins are $J_z = 3/2$ and $J_z = -7/2$. The three candidates for the 4-plet from which two states are thrown out are $|1/2, -3/2\rangle \otimes |[2, k], [1, k]\rangle$, $k = 1, 0, -1$. 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 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 tube predicts similar non-uniqueness.

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

As found, dark baryon counterpart of tRNA could correspond to the multiplet of states containing 40 states. According to [14] 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 [14]. 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 manner 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
5.2 DNA As Topological Quantum Computer Hypothesis And Dark Genetic Code

$k$ would be $(N(1), N(2), N(3)) = \{5, 10, 5\}$. The interpretation would be as $DNA \rightarrow tRNA$ 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 $\Delta$ resonance and the analogs (and only the analogs) of spin $1$ mesons known as $\rho$ 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 $\Delta$ and $N$ resp. $\rho$ and $\pi$ are large in ordinary hadron physics and this makes the decays of $\Delta$ and $\rho$ 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 $\alpha_s$ 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 \([I15]\). 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 maps 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 \([K13]\).

The prediction was that \(G\) should have an entire spectrum of values and approach p-adic length scale squared \(L_p^2 = p R_{CP^2}^2\) 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. With this background philosophy I have discussed the possible differences between General Relativity and TGD-based view about gravitation in \([K34]\). This chapter should help also to understand the discussion of this section.

The starting point for the considerations of \([K34]\) was the question whether the flat geometry for a piece of \(E^3\) could be modified by gravitational effects so that it becomes a piece of \(S^3\) allowing the decomposition of icosahedron to 20 regular tetrahedra (in \(E^3\) geometry the tetrahedra cannot be regular). This kind of decomposition is actually possible for much more general deformations of \(E^3\) geometry and one ends up with the vision about quasi-lattice like structures having piece of \(S^3\) or hyperbolic space \(H^3\) as a basic building brick. This notion makes sense in condensed...
matter length scales only if gravitational constant can be of order \( G \sim L_p^2 \) since Schwartschild radius \( r_S = 2GM \) is the natural scale for the radius of \( S^3 \).

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 icosaedral 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 icosaedral pieces of \( S^3 \) bring in mind foams (see \( \text{http://tinyurl.com/3a29pz} \)). Soap film foam is perhaps the most familiar example about foam. Plateau’s laws (see \( \text{http://tinyurl.com/y7rstej} \)) 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 \( \arccos(-1/3) \approx 109.47 \) 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 that icosaedral 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 (icosaederal) 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 \([K9]\. 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 codes \([K9]\. The starting point is so called Combinatorial Hierarchy \([AS]\. 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 \( M(n+1) = M_{2^n} \) 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
6.2 Could The Faces Of Tetrahedron Correspond To The Four DNA Nucleotides

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 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 \[K5\]: 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 \[K9\].

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 \(6\pi\) (and to a length of 10 nm for DNA strand). For twist angle of \(2\pi\) 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 predecessor 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 imbedding 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 [K5, K3].

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 21st 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 21st 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](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 icosahedral surface. A good guess is that these two oppositely oriented orbits and their images under $A_5$ define the only manners 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 \cite{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 $H_2$ 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 \url{http://tinyurl.com/yb9waklg}) that 14 water molecules indeed combine to form 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.
7 Pythagoras, Music, Sacred Geometry, and Genetic Code

The conscious experiences generated by music demonstrate a fascinating connection between algebra and emotions. How can major and minor scale using different frequency ratios generate so different emotional experiences. This strongly suggests we experience music as entire time interval, 4-D patterns - rather than time=constant snapshots. Also the ability remember the key and the tension lasting as long as the return to the basic key has not taken place, is example of this. One of the key questions is why octaves - that is powers of 2 of the basic note of the scale - are experienced as equivalent? One can also wonder what is behind consonance and dissonance.

I have already earlier tried to understand music experience and considered some ideas inspired by p-adic numbers fields - such as the idea that Pythagorean scale coming as powers of 3 for the basic note modulo octave equivalence might relate to 3-adicity. Reading of a book titled "Interference: A Grand Scientific Musical Theory" by Richard Merrick [?] re-stimulated my interest. In particular, I found the idea about a connection between music scale and harmonies with Platonic solids (3-D “sacred geometry”) as highly inspiring. The basic question was whether the 12-tone scale could be mapped to a curve going once through each point of icosahedron having 12 vertices and whether the 20 faces of icosahedron, which are triangles could define the basic chords in 12-tone scale. These curves are known as Hamiltonian cycles and in the case of icosahedron there are $2^{10}$ of them: those obtained from each other by rotation leaving icosahedron invariant are however equivalent.

A given triangle of icosahedron can contain 0, 1 or 2 edges of the cycle and the numbers of the triangles corresponding to these triangle types classify partially the notion of harmony characterized by the cycle. Quint cycle suggests the identification for the single edge of curve as quint interval so that triangles would represent basic 3-chords of the harmony with 0, 1, or 2 quints.

One can make same questions also for other Platonic solids- tetrahedron (4 vertices), octahedron and cube which are duals of each other and have (6 and 8 vertices respectively, and dodecahedron which is dual of icosahedron having 20 vertices and 12 faces. Arabic music uses half intervals and scales with 19 and 24 notes are used. Could 20-note scale with harmony defined by 5-chords assigned to the pentagons of dodecahedron have some aesthetic appeal? Nowadays it is possible to develop electronically music based on this kind of scale and this kind of experimentation might be a fascinating intellectual and artistic adventure for a young composer.

I have also played with the idea that the 20 amino-acids could somehow correspond to the 20 triangles of icosahedron. The combination of this idea with the idea of mapping 12-tone scale to a Hamiltonian cycle at icosahedron leads to the question whether amino-acids could be assigned with the equivalence class of Hamiltonian cycles under icosahedral group and whether the geometric shape of cycle could correspond to physical properties of amino-acids [11]. The identification of 3 basic polar amino-acids with triangles containing no edges of the scale path, 7 polar and acidic polar amino-acids with those containing 2 edges of the scale path, and 10 non-polar amino-acids with triangles containing 1 edge on the scale path is what comes first in mind.

The number of DNAs coding for a given amino-acid [11] could be also seen as such a physical property. The model for dark nucleons leads to the vertebrate genetic code with correct numbers of DNAs coding for amino-acids. It is not however clear how to interpret DNA codons geometrically.

It however turns out that one can understand only the role of 60 codons in the icosahedral framework. The treatment of the remaining 4 codons and of the well-known 21st and 22nd amino-acids requires the fusion of icosahedral code with tetrahedral code represented geometrically as fusion of icosahedron and tetrahedron along common face which has empty interior and is interpreted as punct coded by stopping codons. In this manner one can satisfy the constraints on the Hamiltonian cycles, and construct explicitly the icosahedral Hamiltonian cycle as (4, 8, 8) cycle whose unique modification gives (4, 11, 7) icosa-tetrahedral cycle. Remarkably, two months after writing the first version of the article I learned that the data needed to calculate the Hamiltonian cycles can be found from web and that (4, 8, 8) cycle allows at least two realizations whereas the original candidate (3, 10, 7) allows no realization with symmetries but could do so with no symmetries.
7.1 Could Pythagoras Have Something To Give For The Modern Musicology?

The ideas of Pythagorean school about music were strongly based on the number theory of that time. So called modern approaches tend to seem music scales as cultural phenomena. There are however many reasons to suspect that Pythagorean school might have been much nearer to truth.

7.1.1 Pythagoras and transition from rational numbers to algebraic numbers

Pythagoras was one of the greatest ancient mathematicians. The prevailing belief at that was that the world can be described solely in terms rational numbers. During the times of Pythagoras the ancient mathematical consciousness had entered at the verge of a profound revolution: the time had become ripe for the discovery of algebraic numbers expanding rational numbers to an infinite series of algebraic extensions of rationals containing also rational multiples for finite number of algebraic numbers emerging as roots of polynomials with rational coefficients. Euclid introduces square root geometrically as length of the diagonal of square. In ancient India it was discovered 800-500 BC, possibly much earlier. Unfortunately, the emergence of Christianity stopped the evolution of mathematics and new progress began at times of Newton when also reformation took place.

The well-known but story (good story but probably not true) tells that a pupil of Pythagoras demonstrated that the diagonal of unit square ($\sqrt{2}$) cannot be rational number and had to pay with his life for the discovery. Pythagoras himself encountered $\sqrt{2}$ through music theory. He asked what is the note exactly in the middle of the of the scale. Modern mathematician would answer half of octave corresponding to the frequency ratio $2^{1/2}$. Algebraic numbers did not however belong to the world of order of Pythagoras and he obtained to a non-satisfactory rational approximation of this number. This was very natural since only rational approximations of algebraics are possible in the experimental approach using only strings with rational number valued lengths. $\sqrt{2}$ represents the interval $C - F^\#$ known as tritone and this this interval was associated with devil and its use was denied also by church. Only after reformation $\sqrt{2}$ was accepted and this interval appears repeatedly in the compositions of Bach.

The amazing connections between evolution of mathematics and evolution of the religious beliefs inspires the question whether the evolution of consciousness could at basic level correspond to the evolution of the complexity of the number field behind the dynamics underlying consciousness. For instance, in TGD framework the vision about physics as generalized number theory allows one can to ask whether the mathematical evolution could have meant quite concretely the emergence of increasingly algebraic extensions of rationals for the coefficients of polynomials describing space-time surfaces serving as space-time correlates of consciousness.

7.1.2 Pythagoras and music

Pythagoras was both mathematician and experimentalist studying the world of musical experience experimentally. String instruments were his tool. The notion of frequency was not know at the time and length of vibrating part of string was the notion used. The experienced equivalence of notes differing by octave was known at that time and octave equivalence was understood as a fundamental symmetry of music manifesting itself as a scaling-by-2 symmetry for the length of a vibrating string.

Pythagoras developed 8 note scale CDEFGAHC (as a matter fact, 7 notes by octave equivalence) as we know as a combination of two scales EFGA and HCDE using octave equivalence and it was established as the official music scale. Pythagorean scale is expressed solely in terms of powers of the ratio 3/2 for lengths of vibrating strings correspond to an interval known and complete fifth (C-G). The series of complete fifths (C-G-D-A...) known as progression by fifths gives very nearly 7 octaves but not quite: $(3/2)^7 \approx 128 + 1.75 = 2^7 + 1.745$. It would have been very natural to build 12-note scale as powers of rational (3/2) or by octave equivalence as powers of 3. The failure to close is very small but people with absolute ear experience the transposition of a melody to different key as dissonant since the frequency ratios do not remain quite same. At the time of Bach (Well tempered Klavier) the equal tempered scale obtained by
diving the logarithmic scale to 12 equally long parts emerged and replacing powers of 3/2 with the
12 powers of algebraic number 2^{1/12} inside same octave even without octave equivalence emerged.

By octave equivalence Pythagorean scale means that all notes of the scale come in powers of 3
which strongly brings in mind 3-adicity. If one does not use octave equivalence when generalization
of p-adicity to q-adicity with q = 3/2 is highly suggestive. q-adic numbers do not in general form
number field, only an algebra.

Later more complex rational number based representations of scale using octave equivalence
have been developed. The expression of the frequency ratios of the notes of the scale in terms
of harmonic of fundamental modulo octave equivalence involving only integers consisting of
primes 2, 3, 5 is known as just intonation (http://tinyurl.com/7mc4ut).

1. Music and Platonic solids

Pythagoras was also aware of a possible connection between music scales and Platonic solids.
Pythagoras is claimed to have discovered tetrahedron, hexahedron (cube) and dodecahedron while
octahedron and icosahedron would have been documented by greek mathematician Thaletus two
hundred years later. The tetrachord and was assigned with tetrahedron and one and imagined that
Pythagorean scale could have been assigned with pair of tetrahedra somehow - cube or octahedron
which comes in mind. Note that this would require that basic note and its octave should be
regarded as different notes.

These attempts inspire the question whether the mapping music scales to the vertices of Platonic
solids could provide insights about music experience. One can also ask whether there might be a
mapping of music understood as melodies and chords in some scale to the geometries defined by
Platonic solids.

1. Since 12-note scale is used in practically all classical western music and even in atonal music
based on 12-note scale, the natural question is whether 12-note scale could be mapped to a
connected, closed, non-self-intersecting path on icosahedron going through all 12 vertices and
consisting of edges only. Closedness would mean that base note and its octave are identified
by octave equivalence.

2. This mathematical problem is well-known and curves of this kind are known as Hamilton
cycles and can be defined for any combinatorial structure defined by vertices and faces.
Hamilton proved that Hamiltonian cycles (possibly identifiable as 20-note scale) at dodecahedral
unique module rotations and reflection leaving dodecahedron invariant. Also in the case of tetrahedron and cube the Hamiltonian cycle is unique.

3. For octahedron and icosahedron this is not the case and there are both cycles containing
only faces with at least 1 edge of the path and also cycles containing no faces containing no
edges of the path. Numerical experimentation is rather straightforward manner to determine
Hamiltonian cycles and \( H = 2^{10} = 1024 \) cycles can be found. The number of topologically
non-equivalent cycles (not transformable to each other by the isometries of icosahedron) is
factor of this number. The group of orientation preserving isometries of icosahedron is the
alternating group \( A_5 \) of 60 even permutations of five letters. The full group of isometries is
\( G = A_5 \times Z_2 \) containing \( N = 120 \) elements.

4. Some subgroup of \( G \) leaves given path invariant and its order must be factor \( M \) of \( N \) so
that topological equivalence class of cycles contains \( R = N/M \) elements. The number of topologically
non-equivalent cycles in given class with \( H(\text{top}) \) elements is \( N_{\text{tot}} = H(\text{top})/R \)
so that \( R \) must be a factor of \( H(\text{top}) \).

Before continuing it is good so summarize the geometry of icosahedron shortly. There are 20
faces which are triangles, 12 vertices, and 30 edges. From each vertex 5 edges. Therefore the
construction of Hamiltonian cycles means that at each vertex on path one must select between
four options edges since one cannot return back. This gives \( 4^{12} = 2^{24} \approx 1.6 \times 10^7 \) alternatives to
be considered. Therefore the numerical search should be relatively easy. Keeping account of the
points already traversed and not allowing self intersections, the actual number of choices is reduced.
The construction requires labeling of the vertices of the icosahedron by integers 1, ..., 12 in some
manner and defining \( 12 \times 12 \) matrix \( A(i, j) \) whose element equals to 1 if vertices are neighbours
and 0 if not. Only the edges for with $A(i,j) = 1$ holds true are allowed on the path. A concrete representation of icosahedron as a collection of triangles in plane with suitable identifications of certain edges is needed. This helps also to visualize the classification of triangles to three types discussed below. This can be found in the Wikipedia article (see \url{http://tinyurl.com/ns9aa}).

2. Numbers of different triangles as characterizers of harmony

A possible interpretation for topologically non-equivalent paths is as different notions of harmony.

1. Proceeding in Pythagorean spirit, the neighboring points would naturally correspond to progression by fifths - that is scalings by powers of $3/2$ or in equal tempered scale by powers of $2^{7/12}$. This would mean that two subsequent vertices would correspond to quint.

2. The twenty triangles of the icosahedron would naturally correspond to 3-chords. Triangles can contain either 0, 1, or 1 edges of the 12-edge scale path. The triangle containing 3 edges is not possible since it would reside on a self-intersecting path. A triangle containing one edge of path the chord would contain quint which suggest a chord containing basic note, quint and minor or major third. The triangle containing two edges would contain subsequent quints - CDG is one possible example by octave equivalence. If the triangle contains no edges of the path one can say that the chord contains no quints.

The numbers of triangles classified according to the number of path edges contained by them serves as the first classification criterion for a given harmony characterized by the Hamiltonian cycle (note that one cannot exclude the possibly of non-closed paths since Pythagorean construction of the scale by quints does not yield quite precisely octave as outcome).

Fig 1. There are 3 different types of triangles characterized by the number of edges contained by them. This predicts chords with 0, 1 or 2 quints. \url{http://tgdtheory.fi/appfigures/kolmiot.jpg}

Consider now the situation in more detail.

1. The topologically equivalent cycles must have same numbers of faces containing 0, 1, or 2 edges of the Hamiltonian path since isometries do not change these numbers. Let us denotes these numbers by $n_0, n_1$ and $n_2$. The total number of faces is 20 so that one has

$$n_0 + n_1 + n_2 = 20 .$$

Furthermore, each of the 12 edges on the path is contained by two faces so that by summing over the numbers of edges associated with the faces one obtains twice the number of edges:

$$0 \times n_0 + 1 \times n_1 + 2 \times n_2 = 2 \times 12 = 24 .$$

From these constraints one can solve $n_0$ and $n_1$ as function of $n_2$:

$$n_0 = n_2 - 4 , \quad n_2 \geq 4 ,$$

$$n_1 = 24 - 2n_2 , \quad n_2 \leq 12 .$$

If these integers characterize the topological equivalence completely and if the allowed combinations are realized, one would have 12-4=8 topologically nonequivalent paths. The actual number is $N_{tot} = 2^k, k \geq 7$, so that the integers cannot characterize the topology of the path completely.

2. The number of Hamiltonian cycles on icosahedron is known to be 2560 [A1]. Numerical calculations [A3] \url{http://tinyurl.com/pmghcwd} shows that the number of Hamiltonian cyclesw with one edge fixed is $2^{10} = 1024$. Here one regards cycles with different internal
orientation as different. This would mean that the sum over the numbers \(N(n_2)\) if cycles associated with differ values of \(n_2\) satisfies

\[
\sum_{n_2=4}^{12} \sum_i N(n_2, i) = 2^{10}.
\]

\(N(n_2, i)\) is the number of paths of given topology with fixed \(n_2\). The numbers \(N(n_2, i)\) are integers which are factors of \(N = 120\) of the order of the isometry group of the icosahedron. The average of \(N(n_2, i)\) is \(2^7 = 128\).

3. Additional topological invariants characterizing the notion of harmony

The interpretation of amino-acids in terms of 20 triangles of icosahedron interpreted as allowed chords for a given notion of harmony leads to a unique identification of the integers \(n_i\) as \((n_0, n_1, n_2) = (3, 10, 7)\). The attempt to interpret this “biological harmony” leads to the identification of additional topological invariants characterizing the notion of harmony. It will be assumed that edges correspond to quints. If they would correspond to half-step the chords would contains 0, 1, or 2 subsequent half-intervals which does not conform with the usual views about harmony. In Pythagorean scale quint corresponds to \(3/2\) and in equal tempered scale quint corresponds to the algebraic number number \(2^{7/12}\).

Above the attention was paid to the properties of the triangles in relation to the Hamiltonian cycle. One can consider also the properties of the edges of the cycle in relation to the two neighboring triangles containing it. Restrict first the attention to the biological harmony characterized by \((n_0, n_1, n_2) = (3, 10, 7)\).

Fig. 2. The edge of the cycle belongs to 2 triangles, which as chords can correspond to 1 resp. 2, 1 resp. 1 and 2 resp. 2 quints.

http://tgdtheory.fi/appfigures/sivut.jpg

1. Everyone of the 12 quints \(C-G, C\#-G\#, \ldots\) would be contained to neighboring triangles tht is 3-chords containing at least one quint. Denote by \(p_{12}, p_{11}\) resp. \(p_{22}\) denote the number of edges shared by 1-quint triangle and 2-quint triangle, by 2 1-quint triangles, resp. 2 2-quint triangles. Besides \(p_{ij} \geq 0\) one has

\[
\sum p_{ij} = 12 ,
\]

since the cycle contains 12 edges. There are \(p_{12} + 2p_{11} = n_1\) 1-quint triangles and \((p_{12} + 2p_{22})/2 = n_2\) 2-quint triangles (note double counting responsible for division by two). Altogether this gives

\[
\begin{align*}
   p_{22} &= 12 - p_{11} - p_{22} , \\
   p_{22} &= p_{11} + n_2 - \frac{n_1}{2} , \\
   p_{22} &= n_2 - \frac{p_{12}}{2} .
\end{align*}
\]

2. These three Diophantine equations are for integers and would allow for real numbers only single solution and for integers it in the generic case there are no solutions at all. Situation changes if the equations are not independent which can happen if the integers \(n_i\) satisfy additional conditions. By subtracting first and second and second and third equation from each other one obtains the consistency condition

\[
n_1 = 24 - 2n_2 .
\]

This condition is however second of the conditions derived earlier so that only two equations, say the first two ones, are independent.

\[
\begin{align*}
   p_{22} &= p_{11} + n_2 - \frac{p_{12}}{2} , \\
   p_{22} &= n_2 - \frac{p_{12}}{2} .
\end{align*}
\]
7.1 Could Pythagoras Have Something To Give For The Modern Musicology?

\[ p_{11} = \frac{(n_1 - p_{12})}{2}, \]
\[ p_{22} = p_{11} + n_2 - \frac{n_1}{2} = n_2 - \frac{p_{12}}{2}. \]

One must have \( 0 \leq p_{ij} \leq 12 \) and \( p_{12} \leq n_1 \) from \( p_{11} = \frac{(n_1 - p_{12})}{2} \). Here one has \( p_{12} \in \{0, 2, ..., \text{Min}\{12, 2n_2, n_1\} \} \) so that \( \text{Min}\{7, n_2 + 1, \lfloor n_1/2 \rfloor + 1\} \) solutions are possible. The condition that the cycle has no self-intersections can forbid some of the solutions.

3. The first guess for the “biological harmony” possibly associated with amino-acids would be \((n_0, n_1, n_2) = (3, 10, 7)\): this if one neglects the presence of 21st and 22th amino-acid also appearing in proteins. It turns out that a more feasible solution fuses tetrahedral code and icosahedral codes with \((n_0, n_1, n_2) = (4, 8, 8)\) giving \((n_0, n_1, n_2) = (4, 11, 7)\) for icosatetrahedral code.

For instance, \((n_0, n_1, n_2) = (3, 10, 7)\) would give \(p_{12} \in \{0, 2, 4, 6, 8, 10\}\), \(p_{11} \in \{5, 4, 3, 2, 1, 0\}\), \(p_{22} \in \{7, 6, 5, 4, 3, 2\}\) so that one has 6 alternative solutions to these conditions labelled by \(p_{12}\). The number of neighboring triangles containing single quint is even number in the range \([0, 10]\): this brings in mind the possibility that the neighboring single quint triangles correspond to major-minor pairs. Clearly, the integer \(p_{12}\) is second topological invariant characterizing harmony.

4. Distribution of different types of edges

Also the distribution of the 12 edges to these 3-types is an invariant characterizing the shape of the curve and thus harmony as isometric invariant.

**Fig. 3.** There are different distributions of edge types characterized by the neighboring triangles of the edge.

\[ \text{http://tgdtheory.fi/appfigures/jakauma.jpg} \]

1. \(p_{12}\) 1-1 edges can be chosen in

\[ N(1 - 1, p_{12}) = \binom{12}{p_{12}} \]

manners and 1-2 edges in

\[ N(1 - 2, p_{12}) = \binom{12 - p_{12}}{p_{12}} \]

manners. The remaining 2-2 edges can be chosen only in one manner. This gives altogether

\[ N(p_{12}) = N(1 - 1, p_{12}) \times N(1 - 2, p_{12}) \]

manners for given value of \(p_{12}\).

To summarize, one obtains large number of notions of harmony are possible although one cannot expect that the absence of self-intersections does not allow all topologies for the cycle.

7.1.3 Would you come with me to icosadisco?

This map would allow one-to-one map of the notes of any music piece using icosahedral geometry. If octave equivalence is assumed, a given note would be mapped to a fixed vertex of icosahedron at which lamp is turned on and also to the wavelength of the light in question since visible light spans an octave. Chords would correspond to the turning on of lights for a group of icosahedral points. Icosahedrons with size scaled up by two could correspond to octave hierarchy: for practical purposes logarithmic scale implying that icosahedrons have same distance would be natural as in the case of music experience since piano spans 7 octaves and human ear can hear 10 octaves. Church would nowadays allow icosadiscos to use also half octaves to amplify further the audiovisual inferno effect so characteristic for discos. One could also try to realize special effects like glissandos, vibratos and tremolos.
7.2 Connection Between Music Molecular Biology?

Music affects directly emotions, and consciousness is one aspect of being living. This raises the question whether the Platonic geometries might have something to do with basic building bricks of life and with genetic code.

7.2.1 Could amino-acids correspond to 3-chords of icosahedral harmony?

The number of amino-acids is 20 and same as the number of triangular faces of icosahedron and the vertices of dodecahedron. I have considered the possibility that the faces of icosahedron could correspond to amino-acids [K5]. Combined with the idea about connection between music scale and icosahedron this inspires the following consideration.

1. For a proper choice of the mapping of the 12-note scale to the surface of icosahedron the 20 triangles could correspond to 20 amino-acids analogous to 3-chords and that the 3 types of 3-chords could correspond to 3 different classes of amino-acids. One can of course consider also the mapping of amino-acids to a unique sequence of 20 vertices of dodecahedron representing 20-note scale or 20-chord scale and replacement of the 3-chords defining the harmony with 12 5-chords.

2. Amino-acids are characterized by the non-constant side chain and these can be classified to three categories: basic polar, non-polar, and polar (http://tinyurl.com/ycvmsyjs). The numbers of amino-acids in these classes are \(a_0 = 3\), \(a_1 = 10\), \(a_2 = 7\). Could these classes correspond to the numbers \(n_i\) characterizing partially some topological equivalence classes of Hamiltonian paths in icosahedron? There is indeed a candidate: \(a_0 = n_0 = 3\), \(a_1 = n_1 = 10\), \(a_2 = n_2 = 7\) satisfies the conditions discussed above. 3 basic polar amino-acids would correspond to the triangles with no edges on the Hamiltonian cycle, 10 non-polar amino-acids to triangles containing one edge, and 7 acidic polar and polar amino-acids to those containing two edges. One can criticize the combination of polar and acidic polar amino-acids in the same class. One can also classify amino-acids to positively charged (3), negatively charged (2) and neutral (15) ones. In this case the condition is however not satisfied. Thus the proposal survives the first test - assuming of a course that these Hamiltonian cycles exist! This has not been proven and would require numerical calculations.

3. As found Hamiltonian paths have also other topological characteristics and they could correspond to physical characteristics and it would be interesting to see what they are. To proceed further one should find the total number of the Hamiltonian paths with \(n_2 = 7\) and identify the isometries of different topological equivalence class having \(n_2 = 7\).

Amino-acid sequences would correspond to sequences of 3-chords. The translation of mRNA of gene to amino-acid sequence would be analogous to the playing of a record. The ribosome complex would be the record player, the amino-acid sequence would be the music, and mRNA would be the record. Hence genes would define a collection of records characterizing the organism.

7.2.2 Can one understand genetic code?

What remains open is the interpretation of genetic code [14]. DNA triplets would correspond naturally to triangles but why their number is 64 instead of 20. They would be obviously the analogs of written notes: why several notes would correspond to the same chord?

1. Could different DNA triplets coding for the same amino-acid correspond to various octaves of the chord? The most natural expectation would be that the number of octaves so that one would have 3 DNAs would code single amino-acid and stopping codon would correspond to 4 DNAs. It is difficult to understand why some 3-chords could correspond to 6 octaves and one of them only one.

2. Could the degeneracy correspond to the ordering of the notes of the 3-chord? For the 3-chords there are 6 general orderings and 3 cyclic orderings modulo octave equivalence and characterizing by the choice of the lowest note. The simplest assumption would be that the allowed orderings - degeneracies - are characterized by a subgroup of the cyclic group \(S_3\)}
### Table 3: The number of amino acids \( N \) associated with a given degeneracy \( d \) telling the number of DNA triplets mapped to the amino acid in the genetic code. The degeneracies are always smaller than 7 as predicted by the proposed explanation of the Genetic Code.

<table>
<thead>
<tr>
<th>( d )</th>
<th>6</th>
<th>4</th>
<th>3</th>
<th>2</th>
<th>1</th>
</tr>
</thead>
<tbody>
<tr>
<td>( N )</td>
<td>3</td>
<td>5</td>
<td>2</td>
<td>9</td>
<td>2</td>
</tr>
</tbody>
</table>

yielding the allowed permutations of the notes of the chord. The subgroup orders for \( S_3 \) are 1, 2, 3, and 6. The allowed degeneracies are 6, 4, 3, 2, and 1 so that this identification fails for \( D = 4 \).

3. Could the different correspondences between DNA codons and amino-acids correspond to the different topological equivalence classes of \( n_2 = 7 \) Hamiltonian cycles. This does not seem to be the case. The number of different DNA-amino-acid correspondences obtained by choosing one representative from the set of DNAs coding for a given amino-acid (and not stopping sign) is the product of the numbers \( D(a_i) \) coding amino-acid \( a_i \). From Table 3 this number is given by \( 6^3 \times 4^5 \times 3^1 \times 2^1 \times 1^2 = 3^1 \times 2^{21} \) and clearly much larger than \( N = 2^{10} \).

4. Could the different codons coding for codon code for some additional information so that amino-acids would in some aspect differ from each other although they are chemically identical? Here the magnetic body of amino-acid is a natural candidate. This would suggest that the folding pattern of the protein depends on what DNA sequence codes it. This information might be analogous to the information contained by notes besides the frequencies. Durations of notes corresponds is the most important information of this kind: the only candidate for this kind of information is the value of \( h_{\text{eff}} = n \times h \) associated with the amino-acid magnetic body determining its size scale. Magnetic fields strength could be also code by DNA codon besides amino-acid.

Second question concerns genetic code itself. Could the DNA degeneracies \( D(a_i) \) (number of DNAs coding for amino-acid \( a_i \)) be understood group theoretically in terms of icosahedral geometry? The triangles of the icosahedron are mapped the triangles under the isometries.

1. One can start by looking the Table 3 for the genetic code telling the number \( N(d) \) of amino-acids coded by \( d \) DNA codons. One finds that one can divide DNAs to three groups containing \( n = 20 \), \( n = 20 \), resp. \( n = 21 \) codons.

(a) There are 3 amino-acids codes by 6 codons and 2 amino-acids coded by 1 DNA: \( 3 \times 6 + 2 \times 1 = 20 \) codons altogether.

**Note:** One could also consider 1 amino-acid coded by 2 codons instead of 2 coded by 1 codon \( 3 \times 6 + 1 \times 2 = 20 \).

(b) There are 5 amino-acids coded by 4 codons making \( 5 \times 4 = 20 \) codons altogether.

(c) There are 9 amino-acids coded by 2 codons and 1 by 3 codons making \( 9 \times 2 + 1 \times 3 = 21 \) codons.

**Note:** One could also consider the decomposition \( 8 \times 2 + 2 \times 1 + 1 \times 3 = 21 \) codons implied if 1 amino-acid is coded by 2 codons in the first group.

This makes 61 codons. There are however 64 codons and 3 codons code for stopping of the translation counted as punct in the table.

1. This would suggest the division to 60 + 4 codons. The identification of additional 4 codons and corresponding amino-acids is not so straightforward as one might first think. 3 of the 4 additional codons could code for punct (Ile) and 1 of them to Ile (empty amino-acid).

2. What suggests itself strongly is a decomposition of codons in 3 different manners. 3 groups of 6 codons plus 2 groups of 1 codon (1 group of 2 codons), 5 groups of 4 codons, and 10 groups of 2 codons (9 groups of 2 codons plus 2 groups of 1 codon).
This kind of decompositions are induced by the action on the triangles of icosahedron by three subgroups of the isometry group $A_5 \times Z_2$ of the icosahedron having $120 = 2 \times 2 \times 2 \times 3 \times 5$ elements and subgroups for which number of elements can be any divisor of the order. The orbit associated with a subgroup with $n$ elements has at most $n$ triangles at its orbit. This allows immediately to deduce the values of $n$ possibly explaining the genetic code in the proposed manner.

1. The 3 amino-acids coded by 6 codons must correspond to $n = 6$. This subgroup must have also two 1-element orbits (1 2-element orbit): in other words, 2 triangles must be its fixed points (form its orbit).

   (a) The non-abelian group $S_3$ permuting the vertices of is the first candidate for the subgroup in question. The triangles at the opposite sides of the icosahedron remain invariant under these permutations. $S_3$ however has two orbit consisting of 3 triangles which are “wall neighbours” of the triangles which remains fixed.

   (b) Second candidate is the abelian group $\tilde{Z}_2 \times Z_3$. Here $Z_3$ permutes the vertices of triangle and $\tilde{Z}_2$ is generated by a reflection of the triangle to opposite side of icosahedron followed by a rotation by $\pi$. This group has 3 orbits consisting of 6 triangles and 1 orbit consisting of 2 triangles (the triangles at opposite side of icosahedron). This group seems to be the only working candidate for the subgroup in question.

2. The 5 amino-acids coded by 4 codons must correspond to $n = 4$ and therefore to $\tilde{Z}_2 \times Z_2$. This is indeed subgroup of icosahedral group which permutes triangles at the vertices of inscribed tetrahedron. Now all orbits contain 4 triangles and one must have 5 orbits, which are obtained by acting on the 5 triangles emanating from a given vertex. Note that also $Z_5$ is subgroup of icosahedral group: this would give a variant of code with 4 amino-acids coded by 5 codons if it were possible to satisfy additional consistency conditions.

3. Consider next the group consisting of 9 amino-acids coded by 2 codons and Ile (“empty” amino-acid) coded by 3 codons. Since only the $\tilde{Z}_2 \times Z_3$ option works, this leaves 9 amino-acids coded by 2 codons and 2 amino-acids coded by 1 codon. The subgroup must correspond to $n = 2$ and thus $Z_2$ acting on fixed triangle and leaving it and its $\tilde{Z}_2$ image invariant. One has 9 2-triangle orbits and two single triangle orbits corresponding to the triangles at opposite sides of the icosahedron. The 9 amino-acids coded by 2 codons are all real or 8 of them are real and 1 corresponds to “empty amino-acid” coded by two codons.

   3-element orbits are lacking and this forces to consider a fusion of of icosahedral code with tetrahedral code having common “empty-acid” - common triangle of icosahedron and tetrahedron) coded by 2 icosahedron codons and 1 tetrahedral codon. Ile would be coded by 3 codons assignable to the orbit of $Z_3$ subgroup of tetrahedral symmetry group $S_3$ and would be associated with the tetrahedron. This would predict 2 additional amino-acids which could be understood by taking into account 21st and 22nd amino-acid (Sec and Pyl [III]).

   The Hamiltonian cycle is not explicitly involved with the proposed argument. Some property of the cycle respected by the allowed isometries might bring in this dependence. In Pythagorean spirit one might ask whether the allowed isometries could leave the Hamiltonian cycle invariant but move the vertices along it and induce a mapping of faces to each other.

   The amino-acid triangle at given orbit cannot be chosen freely. The choices of amino-acid triangles associated with the three groups of 20 DNAs must be different and this gives geometric conditions for the choices of the three subgroups and one can hope that the assignment of amino-acid to a given triangle is fixed about from rotational symmetries.

### 7.2.3 Does the understanding of stopping codons and 21st and 22nd amino-acids require fusion of tetrahedral and icosahedral codes?

Several questions remain. Could one also understand the additional 4 DNA codons? Could one understand also how one of them codes amino-acid (Ile) instead of stopping codon? Can one related additional codons to music?

1. **Attachment of tetrahedron to icosahedron as extension if icosahedral code**
The attachment of tetrahedron to icosahedron allows to understand both stopping codons and punct as well as the 21st and 22nd amino-acids geometrically.

1. Something is clearly added to the geometric structure, when at least 4 additional DNA codons and 2 amino-acids are brought in. The new codons could represent orbits of faces of Platonic solid with 4 faces representing punct and 3 real amino-acids: say Ile, Pyl, and Sec. The 4 faces should be triangles and actually must be so since tetrahedron is the only Platonic solid having 4 faces and its faces are indeed triangles. Tetrahedron has symmetry group $S_3$ containing $Z_3$ and $Z_2$ as subgroups. $Z_3$ leaves one of the tetrahedral triangles invariant so that one has two orbits consisting of 1 and 3 triangles respectively.

2. One amino-acid is coded by 3 rather than only 2 codons. One can indeed understand this symmetry breaking geometrically. Suppose that the tetrahedron is attached on icosahedron along one of its triangular faces and that this icosahedral face corresponds either Ile or punct coded by 2 icosahedral codons. This face remains also fixed by the action of $Z_3$ and $S_3$ subgroups of tetrahedron so that 1 tetrahedral codon codes also for the amino-acid in question.

3. The three other faces of tetrahedron $r$ should bring in three additional amino-acids. punct could correspond to either one of them or to the common base triangle which is indeed geometrically in unique position. One could even demand that this triangle is “empty” so that tetra-icosahedron would be non-singular continuous manifold. The 3-triangle orbit outside the icosahedron would correspond to Ile and base triangle to empty amino-acid. Base triangle would be coded by 1 tetrahedral codon plus 2 icosahedral codons.

4. One of the outsider triangles would thus corresponds to Ile but two other triangles to two new exotic amino-acids. In some species there indeed are 21st and 22nd amino-acids (selenocysteine (Sec) and pyrrolysine (Pyl), [http://tinyurl.com/2byr2b](http://tinyurl.com/2byr2b)) with sulphur replaced with selene. This modification does not change the polarity properties of cys and lys: cys and thus Sec is non-polar and lys and thus Pyl is basic polar implying $(n_0, n_1, n_2) = (3, 10, 7) \rightarrow (4, 11, 7)$.

5. The two other outsider tetrahedral triangles could correspond to the orbits of $Z_2$ subgroup of $S_3$ acting as reflection with respect to median of the base triangle. Outside faces form orbits consisting of 1 triangle and 2-triangles. Could these orbits correspond to 21st and 22nd amino-acids coded by 1 and 2 exotic codons?

Since Ile and Sec are non-polar, they can correspond to 1-quint triangles at tetrahedron. 2-quint triangle cannot however correspond to Pyl which should correspond 0-quint triangle. Hence the 0-quint triangle must be at the icosahedron and the 2-quint triangle must correspond to basic polar amino-acid coded by single codon: Tyr is the only possible option. Hence the tetrahedral amino-acids are fixed to be Ile, Sec, and Tyr and Pyl must correspond to some icosahedral amino-acid.

The second implication is that the icosahedral Hamiltonian cycle from which the icosa-tetrahedral cycle is obtained as deformation must correspond to $(4, 8, 8)$ since one cannot deform $(3, 7, 10)$ in such a manner that one would obtain one additional 0-quint triangle.

It should be noticed that the 2 exotic amino-acids are coded by codons which are usually interpreted as stopping codons. Something must however distinguish between standard and exotic codings. Is it “context” giving different meaning for codons and perhaps characterized by different magnetic bodies of codons [K30]? 

*Fig. 4*. tetra-icosahedron is obtained by attaching tetrahedron along one of its faces to icosahedron. The resulting structure is topological manifold if the common face is replaced with empty set and it is natural to identify it as punct.

[http://tgdtheory.fi/appfigures/tetra-icosahedron.jpg](http://tgdtheory.fi/appfigures/tetra-icosahedron.jpg)

2. How the icosahedral Hamiltonian cycle is modified?
The properties of exotic amino-acids give constraints on how the modification of the Hamiltonian cycle should be carried out. The naive expectation that the outer triangles of added tetrahedron correspond to punct and 2 exotic amino-acids is not correct. A more appropriate interpretation is as a fusion of icosahedral and tetrahedral codes having common “empty amino-acid” coded 2 icosahedral and 1 tetrahedral 1 stopping codons respectively and obtained by gluing these Platonic solids together along the triangle representing the “empty” amino-acid. That the common triangle corresponds to punct means geometrically that its interior is not included so that the resulting structure is continuous manifold having topology of sphere.

Consider now the detailed construction.

1. One should be able to modify the icosahedral Hamiltonian cycle so that the numbers \((n_0, n_1, n_2)\) charactering icosahedral cycle change so that they conform with the properties of the two exotic amino-acids. Selenocystein (Sec) is nonpolar like cys and pyrolysine (Pyl) basic polar like Lys so that \((4, 11, 7)\) seems to be the correct characterization for the extended system. One must have \((n_0, n_1, n_2) \rightarrow (4, 11, 7)\).

2. One must visit the additional vertex, which means the replacement of one edge from the base triangle with wedge visiting the additional vertex. There are several cases to be considered depending on whether the base triangle is 1-quint triangle or 2-quint triangle, and what is the type of the edge replaced with wedge. One can even consider the possibility that the modified cycle does not remain closed.

If the icosahedral cycle has \((n_0, n_1, n_2) = (3, 10, 7)\), the value of \(n_2\) is not changed in the construction. For a closed cycle edge is replaced with wedge and the only manner to preserve the value of \(n_2\) is that the process producing 1 tetrahedral 2-quint triangle transforms 1 icosahedral 2-quint triangle identified as base triangle to 1-quint triangle. If the replaced edge of base triangle is of type 2-1, one has \(n_1 \rightarrow n_1 + 1\) since one icosahedral 1-quint triangle disappears and 2 tetrahedral ones appear. Icosahedral \(n_0\) increases by 1 units. Hence the condition \((3, 10, 7) \rightarrow (4, 11, 7)\) would be met. It however seems that \((4, 8, 8)\) is more promising starting cycle as the argument below shows.

3. The number options is at most the number \(n_2\) of 2-quint triangles serving as candidates for punct. An additional condition comes from the requirement that replaced edge is of type 2-1.

Fig. 4. tetra-icosahedron is obtained by attaching tetrahedron along one of its faces to icosahedron. The resulting structure is topological manifold if the common face is replaced with empty set and it is natural to identify it as punct.

Fig. 5. The modification of \((4, 4, 8)\) icosahedral Hamiltonian cycle consistent with the constraints that icosa-tetrahedral cycle corresponds to \((4, 11, 7)\) consistent the classification of amino-acids in three classes.

http://tgdtheory.fi/appfigures/tetraikosahedron1.jpg

3. Direct construction of Hamiltonian cycle corresponding to bio-harmony

Consider bio-harmony as an example about Hamiltonian cycle taking seriously the extension of the genetic code. I have made very many unsuccessful triangles starting from the assumption that icosahedral cycle satisfies \((n_0, n_1, n_2) = (3, 10, 7)\), and the following proposal starts from different icosahedral cycle. The following is just a trial, which should be checked by a direct calculation.

1. The most obvious guess for the cycle to be modified to cycle at tetra-icosahedron having \((n_0, n_1, n_2) = (4, 11, 7)\) (the triangle corresponding to “empty” amino-acid (to be called punct) is not counted) is \((n_1, n_2, n_3) = (3, 10, 7)\). I have not found cycle with these characteristics.

2. It seems however possible to find cycle with \((n_1, n_2, n_3) = (4, 8, 8)\). From this can obtain the desired kind of extended cycle if the “empty” triangle is 2-quint triangle and the edge replaced with the wedge is of type 2-2. The replacement of icosahedral edge eliminates
two icosahedral 2-quint triangles and generates 1 tetrahedral 2-quint triangle giving \( n_2 \rightarrow n_2 - 2 + 1 = n_2 - 1 = 7 \). The disappearance of the icosahedral edge generates two icosahedral 1-quint triangles of which second one corresponds to empty amino-acid and is not counted and 2 tetrahedral 1-quint triangles giving \( n_1 \rightarrow n_1 + 3 = 11 \).

The figure below represents the construction of cycle \((4, 8, 8, .)\). The icosahedron is constructed from regions \( P(I) \) glued to the triangle \( t \) along one edge each. The arrows indicate that the one pair of edges of type 1 and 2, 1 and 3 and 3 and 2 are identified. Also the long edges \( I \) of \( T \) are identified with pairs of subsequent edges of \( P(I) \) as the arrows indicate.

**Fig. 6.** A proposal for a Hamilton cycle realizing bio-harmony \((n_1, n_2, n_3) = (4, 8, 8)\) allowing extension to cycle \((3, 11, 7)\) on tetra-icosahedron. Circled “0”, “1” and “2” indicates whether a given small triangle is 0-, 1-, or 2-quint triangle. It is relatively easy to verify that the condition \((n_1, n_2, n_3) = (4, 8, 8)\) for bio-harmony is satisfied. [http://tgdtheory.fi/appfigures/aikosahedroni.jpg](http://tgdtheory.fi/appfigures/aikosahedroni.jpg)

4. **Stopping codons and music**

What could be the interpretation of the attached tetrahedron in terms of music harmony? The attachment of tetrahedron means addition of an additional note to the 12-note scale. The scale constructed in Pythagorean spirit identifying quint as scaling by \(3/2\) contains the 12th note as scaling by \((3/2)^{12}\) of the basic frequency modulo octave equivalence. This is slightly more than scaling by \(2^9\) so that exact octave is not obtained. The attempt to solve this problem has lead to scales in which one allows a pair of notes with a very small interval between them - say \(G#\) and \(Ab\) being regarded as different notes.

This suggests that the outsider vertex of the attached tetrahedron corresponds to a note very near to some note of the 12-note scale. Which note is in question depends on which of the 10 1-quint triangles is chosen as the base triangle. This is expected to imply additional refinements to the notion of bio-harmony. 2 or three additional 3-chords emerge depending on whether empty amino-acid is interpreted as a real chord.

5. **Geometric description of DNA-amino-acid correspondence**

The mathematical structure which suggests itself is already familiar from some earlier attempts to understand genetic code [K9]. For icosahedral part of code one would have a discrete bundle structure with 20 amino-acids defining the base space and codons coding the amino-acid forming the fiber. The number of points in the fiber above based point depends on base point and is the number of codons coding the corresponding amino-acid. A discrete variant of singular fiber bundle structure would be in question.

Forgetting for a moment the 4 troublesome codons, the bundle would be the union of the orbits associated with groups \(S_3, Z_4\) and \(Z_2\) of icosahedral group, and the base would consist of 20 amino-acids, one for each orbit. The point of orbit must be selected so that the selections for orbits of two different groups are different.

The addition of the additional codons, punct and two exotic amino-acids would mean gluing of tetrahedron along one of its faces to icosahedron. This would induce extension of the singular bundle like structure. To each of the new faces one would attach the orbit of triangles representing the codons coding for the corresponding amino-acid.

To sum up, in its strongest form the model makes several purely mathematical predictions, which could easily kill it.

1. The identification of the 3-chords assignable to the triangles of the icosahedron.

2. The existence of \(n_2 = 7\) Hamiltonian cycle requiring however the lumping of acidic polar and polar amino-acids in the same class.

7.2.4 **How could one construct the Hamiltonian cycles on icosahedron with a minimal computational work?**

Although the construction of Hamiltonian cycles is known to be an NP hard problem for a general graph, one can hope that in case of Platonic solids having high symmetries, a direct construction...
1. The basic observation about one can get convinced by using paper model is following. One can decompose the surface of icosahedron to three regions $P(I)$, $I = 1, 2, 3$, with pentagonal boundary and containing 5 triangles emanating from center vertex plus one big triangle $T$ containing 4 pentagonal triangles and one lonely small triangle $t$ opposite to it. These 5 regions span the surface of icosahedron. There is clearly a symmetry breaking and there is great temptation to assume that $t$ corresponds to the triangle along which the tetrahedron is glued to the icosahedron in the model of genetic code realizing the modification of (3, 7, 10) bio-harmony.

2. The Hamiltonian cycle must visit at the centers of each $P(I)$: one enters pentagonal region $P(I)$, $I = 1, 2, 3$ along one of the five interior edges beginning at pentagonal vertex $a_{I,i}$, $i = 1, ..., 5$ and leaves it along second edge ending at vertex $b_{I,j}$, $j \neq 5$. One can call these edges interior edges. The edges at boundaries of $P(I)$ can be called boundary edges. Interior edge can correspond to $|i - j| = 0$ or $i - j > 1$. For $|i - j| = 1$ the interior edge gives rise to 2-quint triangle. For $i - j = 0$ there is no boundary edge after $b_{I,t}$. The boundary edges of small and big triangle are boundary edges of the 3 pentagonal regions so that they are not counted separately.

3. Pentagonal boundary edges come in three types. 2 of them are shared with $T$, 1 with $t$ opposite to it, and 2 with another pentagonal region $P(I)$. One can label $P(i)$ in such a manner that the $P(I)$ shares two boundary edges with $P(I + 1)$. The boundary edges of small and big triangle are boundary edges of the 3 pentagonal regions so that they are not counted separately.

4. One can assume that the cycles begins from a vertex of $T$. Since the cycle is closed it returns back to this vertex. The last edge is either at the boundary of $T$ or goes through one or two edges of the small interior triangle of $T$ so that this triangle is either 0-, 1- or 2-quint triangle. 

5. If all 3 $P(I)$ have $|i - j| > 1$, one has $n_2 = 3 \times 2 = 6$. The contribution of regions $P(I)$ is larger if some pentagon interiors have $\Delta(I) = |j(I) - i(I)| = 1$. If $|j(I) - i(I)| = 1$ gives $\Delta n_2(I) = 1$ and $\Delta n_3(I) = 0$ since 2 1-quint triangles are replaced with single 2-quint triangle. 

The interior of the $T$ can give 1 2-quint triangle.
7.2 Connection Between Music Molecular Biology?

9. The number $n_1$ of 1-quint triangles can be estimated as follows.

(a) Each pentagonal interior edge pair leading from $a(I, j)$ to $b(I, j)$ contributes 2 1-quint triangles for $\Delta(I) \neq \pm 1$, otherwise one obtains only 1 2-quint triangle. This would give maximum number of 6 1-quint triangles associated with the interior edges of 3 pentagons.

(b) $P(I)$ pentagonal boundary edges contribute $2 \times (P(I) - 1)$ additional 1-quint triangles.

(c) $T$ contributes at most 4 1-quint triangles.

(d) $t$ can correspond 1-quint triangle and would do so if the interpretation of extended code is correct.

10. The construction also breaks the rotational symmetry since the decomposition of icosahedron to regions is like gauge fixing so that one can hope of obtaining only single representative in each equivalence class of cycles and therefore less than $2^{10}$. By the previous argument related to icosatetrahedral code, $t$ and the triangle opposite to it cannot however correspond to amino-acids coded by 1 codon as one might guess first. Rather, $t$ corresponds to punct and to 1-quint triangle belonging to $Z_2$ orbit.

The number of cycles should be $2^{10}$. One can try to estimate this number from the construction. Each $b_{I,j}$ can be chosen in 4 manners at the first step but at later steps some vertices of the neighboring pentagon might have been already visited and this reduces the available vertices by $n + 1$ if $n$ subsequent edges are visited. At each vertex $b_{I,j}$ one has 4 options for the choice of the boundary edges unless some boundary edges of pentagon (shared with other pentagons) have been already visited. It is also possible that the number of boundary edges vanishes. One can start from any vertex of triangle. This gives the upper bound of $2^4$ choices giving $N < 2^{10}$ paths going through 4 pentagon-like regions. The condition that the path is closed, poses constraints on the edge path assignable to $T$ but the number of choices is roughly 24. The condition that path goes through all vertices and that no edge is traversed twice must reduce this number to $2^{10}$.

The numerical construction of Hamiltonian cycles should keep account about the number of vertices visited and this would reduce the number of candidates for $b(I, j)$ and for the choices of $P(I)$ for $I > 1$ as well as the number of edge paths associated with $T$.

7.2.5 Icosahedral Hamiltonian cycles numerically

A couple of months after writing the article I decided to look at the numerical problem of calculating the Hamiltonian cycles for icosahedron. Recall that the earlier source [A3] ([http://tinyurl.com/pmsgewd](http://tinyurl.com/pmsgewd)) telling that there are $2^{10}$ different Hamiltonian cycles when orientation is taken into account and one edge is fixed: if orientation does not matter there re $2^9$ cycles. If one does not fix one cycle one obtains 2560 cycles - not Hamiltonian paths as I had erratically concluded. The cycles were actually listed ([http://tinyurl.com/yagzozx](http://tinyurl.com/yagzozx)) and classified to five different basic classes according to their symmetries. Even better, examples of cycles with symmetries were illustrated.

Cycles can be divided to isomorphy classes within which cycles have same shape.

1. It is possible to perform a shift of the edges along the cycle. The shape of the cycle is not affected but cycle changes. Using music terms the key changes. There are 12 different keys.

2. Also the mirror image mapping $i^{th}$ edge to $(13 - i)^{th}$ edge is a symmetry which in the generic case produces a new cycle. This symmetry should be distinguished from the change of the internal orientation which does not affect the cycle.

3. Also the isometries of icosahedron leaving the fixed edge as such act as symmetries. Fixed edge belongs to a triangle and the reflection mapping the two other edges of the triangle to each other is this kind of symmetry. Therefore there are two reflection symmetries and the number of cycles of same shape in the generic case is expected to be $4 \times 12 = 48$. If some of the symmetries acts trivially or if some isometries of icosahedron act as its symmetries, the number of isomorphic cycles is reduced.
It is even possible to find illustrations of the symmetric cycles obtained using Brendan McKay’s NAUTY software! From these illustrations (see Figs. 6, 12 and 9) one can by visual inspection deduce the numbers \((n_0, n_1, n_2)\) charactering the cycle for classes involving symmetries. Also the basic chords can be deduced. If one trusts the condition \(n_1 + 2 \times n_2 = 24\), it is enough to count the number \(n_2\) triangles containing to path edges. I have also directly checked that \(n_1\) comes out correctly.

![Figure 1](image1.png)

**Figure 1:** \((n_0, n_1, n_2) = (4, 8, 8)\) Hamiltonian cycle with 2 reflection symmetries acting in vertical and horizontal directions.

![Figure 2](image2.png)

**Figure 2:** \((n_0, n_1, n_2) = (4, 8, 8)\) Hamiltonian cycle with 2-fold rotational symmetry acting as 6-quint rotation.

There are following isomorphic collections.

1. 6 asymmetric collections containing the maximal number of 48 cycles each. In this case images are not given.

2. 3 collections with 2-fold rotation symmetry containing 48/2=24 cycles each. One has \((n_0, n_1, n_2) \in \{(0, 16, 4), (0, 16, 4), (4, 8, 8)\}\).
Figure 3: \((n_0, n_1, n_2) = (4, 8, 8)\) Hamiltonian cycle with 2-fold reflection symmetry acting as horizontal reflection.

3. 5 collections with reflectional symmetry containing 48/2=24 cycles each. One has \((n_0, n_1, n_2) \in \{(2, 12, 6), (2, 12, 6), (4, 8, 8), (2, 12, 6), (2, 12, 6)\}.

4. 2 collections with 2 reflectional symmetries containing 48/4=12 cycles each. One has \((n_0, n_1, n_2) \in \{(0, 16, 4), (4, 8, 8)\}.

5. 1 collection with 6-fold rotational symmetry containing 48/6=8 cycles. One has \((n_0, n_1, n_2) = (2, 12, 6)\).

There are therefore 5 different notions of harmony and they correspond to \(n = \{6, 3, 5, 2, 1\}\) sub-harmonies. This gives altogether 6+3+5+2+1=17 different notions of harmony.

What is remarkable that the original candidate \((3, 10, 7)\) for bio-harmony is not realized as a cycle possessing symmetries (it might be realized as one of the asymmetric cycles) but that there are at least three realizations for \((4, 8, 8)\), which is forced by the condition that bio-harmony corresponds to the extended genetic code! The three \((4, 8, 8)\) cycles are illustrated in Figs. 6 and 9.

7.3 Other Ideas

The book of Merrick discusses also other ideas. The attempts to understand music in TGD framework relate to these ideas.

7.3.1 p-Adic length scale hypothesis and music

One of the key ideas is the reduction of the octave phenomenon to the p-adic length scale hypothesis predicting that octaves and half-octaves correspond to p-adic scalings allowed by the hypothesis \(p \approx 2^k\) for the preferred values of the p-adic primes, and yielding scaled variants of physical systems. This idea will not be discussed in the following: suffice it to say that Pythagorean scale coming as powers of \(p = 3\) strongly suggests approximate 3-adicity.

7.3.2 EEG and music

First of the key ideas relates to the idea that genetic code relates to the music scale.

1. Music metaphor is key element of TGD inspired view about biology and neuroscience. In particular, TGD based view about dark matter leads to the proposal that bio-photons are ordinary photons resulting as transformations of dark photons with large Planck constant
\[ h_{\text{eff}} = n\hbar \] to ordinary photons. The further hypothesis is that the energy spectrum of bio-photons is universal and contains visible photons and UV photons, which defined transition energies of biomolecules. This hypothesis follows if the value of \( h_{\text{eff}} \) assignable to a magnetic flux tube characterizes ion and is proportional to its mass number. The notion of gravitational Planck constant identified as \( \hbar_{\text{gr}} = GMm/v_0 \), where \( v_0 \) is a velocity parameter assignable to the two-particle system can be identified in the case of elementary particles and ions with \( h_{\text{eff}} \) and predicts also the universality of bio-photon spectrum.

2. In this framework bio-photons would represent music as light inducing molecular transitions. Notes that different energies of bio-photons would correspond to different magnetic field strengths at magnetic flux tubes as was proposed much earlier in the quantum model of hearing [K18]. Could the biochemical and physiological aspects involved with the generation of music experience be realized in terms of bio-photon emission induced by the listening of music?

7.3.3 Standing waves and music

Merrick consider the idea that standing waves are essential for music experience. Preferred extremals of Kähler action representing standing waves does not seem to be feasible. The known preferred extremals (with “massless extremals” (MEs) included) would represent superpositions of Fourier components with four-wave-vectors which are proportional to each other. Essentially pulse propagating in fixed direction. For more general extremals this direction can depend on position.

Although standing waves are not feasible, effects which would be explained in Maxwell’s theory in terms of standing waves are possible in many-sheeted space-time. A particle in a region of Minkowski space containing several space-time sheets touches all space-time sheets having non-vanishing Minkowski space projection to this region and the forced experience by it is sum of the forces caused by them. This leads to an operational defines of gravitational and gauge fields of Einstein-Maxwell limit of TGD as sum of the deviations of the induced metric from Minkowski metric and sum of the components of the induced spinor connection defining classical gauge potentials in TGD framework. Test particles can clearly experience the presence of standing waves. It is enough to take two massless extremals with opposite directions of three momentum but same energy with non-empty projections to same \( M^4 \) region. Particle with experience standing wave oscillating with the frequency involved. The arrangements in which photons are taken to rest effectively could correspond to this kind of situations since if it is the motion of test particles which serves as a signature. Note however that there are also vacuum extremals for which the light velocity at the space-time surface corresponds to arbitrarily low velocity at the level of imbedding space.

7.3.4 Emotions and 4-D character of music experience

Music experience involves in an essential manner time unlike visual experience which is essentially 3-dimensional. Music experience affects also emotions very directly. For instance, we somehow know the key of the piece and expect that it ends to the basic note and chord. We somehow know also the scale used (say major or minor) by the emotional response stimulated by it. All this requires information about entire time evolution of the music piece. The recent neuroscience based models of memory do not help much in attempts to understand how this is possible. The reason is that in the ordinary materialistic view in which the state of the brain at fixed time should determine the contents of consciousness.

The general vision in Zero Energy Ontology and Quantum Classical Correspondence is that space-time surface provide classical physics correlates for quantum states and also quantum jumps: the failure of the strict determinism is essential for the latter. The space-time surfaces are restricted inside causal diamond (CD) and have space-like 3-surface as their ends: the interpretation is as counterparts for the initial and final states of physical events.

The replacement of states with events makes it possible to understand mysterious looking facts about living matter such as standardized temporal patterns - say those appearing during morphogenesis. The maxima of the vacuum function defined by the exponent of Kähler function in term identified as Kähler action for Euclidian space-time regions representing analogs for the lines of Feynman graph correspond to the most probably temporal patterns.
The basic aspect of emotions is positive/negative dichotomy. An attractive identification for the physical correlated of this aspect is whether the quantum jump generating the emotion increases or decreases the negentropy of the subsystem involved. For instance, pain would correspond to a reduction of the negentropy for the body part involved. In music experience negentropy could flow between different parts of the system involved and create also sensation with local negative coloring but with overall positive coloring (by NMP [K11]). The ability of temporal patterns of music to generate negentropy flows inside the system involved could explain its effectiveness in generating emotions.

Dissonances were used by composes like Bach to generate melancholic emotions which suggests that the dissonance represent local reduction of negentropy. Also vibrato has emotional content. Physically dissonance and vibrato are assignable to the interference of frequencies which are near to each other [http://tinyurl.com/5r34ch]. The basic formula is

$$\cos(x) + \cos(y) = \cos((x + y)/2) \times \cos((x - y)/2)$$

Acknowledgements: I want to thank Tommi Ullgren for directing my attention to the book of Richard Merrick as well as for fascinating discussions about music.

8 Geometric Theory Of Harmony

For some time ago I introduced the notion of Hamiltonian cycle as a mathematical model for musical harmony and also proposed a connection with biology: motivations came from two observations [L0], [K13], [K20]. 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 and the number of basic chords for the proposed notion of harmony. This led to a group theoretical model of genetic code and replacement of icosahedron with tetra-icosahedron to explain also the 21st and 22nd amino-acid and solve the problem of simplest model due to the fact that the required Hamilton’s cycle does not exist.

This article was meant to be a continuation to the mentioned article providing a proposal for a theory of harmony and detailed calculations. It however turned out that the proposed notion of bio-harmony was too restricted: all isosahedral Hamilton cycles with symmetries turned out to be possible rather than only the 3 cycles forced by the assumption that the polarity characteristics of the amino-acids correlate with the properties of the Hamiltonian cycle. This working hypothesis had to be given up. The fuel of the minirevolution was the observation the symmetries of the Hamiltonian cycles ($Z_6$, $Z_4$, $Z_2$) are nothing but the icosahedral symmetries needed to predict the basic numbers of the genetic code and its extension to include also 12st and 22nd amino-acids. Thus icosahedral Hamiltonian cycles predict genetic code without further assumptions.

One also ends up with a proposal for what harmony is leading to non-trivial predictions both at DNA and amino-acid level.

1. 3-adicity and also 2-adicity are essential concepts allowing to understand the basic facts about harmony. The notion of harmony at the level of chords is suggested to reduce to the notion of closeness in the 3-adic metric using as distance the distance between notes measures as the minimal number of quints allowing to connect them along the Hamilton’s cycle. In ideal case, harmonic progressions correspond to paths connecting vertex or edge neighbors of the triangular faces of icosahedron.

2. An extension of icosahedral harmony to tetra-icosahedral harmony was proposed as an extension of harmony allowing to solve some issues of icosahedral harmony relying on quint identified as rational frequency scaling by factor 3/2.

This extension is kept also now. One must however give up the idea about correlation between polarity characteristics of proteins and properties of Hamilton cycles. One must allow all 11 icosahedral harmonies with symmetries as bio-harmonies: their symmetry groups $Z_6$, $Z_4$, $Z_2$ can be identified as the symmetry groups defined the decomposition of 60 DNA codons to 20+20+20 codons in the model of the genetic code. The 4 remaining DNAs and amino-acids can be assigned to both tetra-icosahedron and tetrahedron and icosahedron regarded
as defining separate genetic codes. This explains why stopping codons can code for the 21st and 22nd amino-acid under some circumstances.

Tetrahedral code is second member in the hierarchy of genetic codes inspired by the notion of Combinatorial Hierarchy \(M(n + 1) = M_M(n) = 2^{M(n)} - 1\) giving the numbers 2, 4, 7, 64, \(2^{126}\), as numbers of DNA codons. The fourth member would correspond to what I called “memetic code” allowing representation of codons as sequences of 21 DNAs. It is not known whether the Combinatorial Hierarchy of Merseprime primes continues as Hilbert conjectured.

3. The notion of bio-harmony is partially characterized by the triplet \(n = (n_0, n_1, n_2)\), characterizing the numbers of 0-, 1-, and 2-quint chords which in turn correspond to DNA codons in consistency with the observation that codons indeed correspond to triplets of nucleotides.

\(n\)-quint chord corresponds to a triangle (face of icosahedron) containing \(n\) edges of the Hamiltonian. Particular bio-harmony requires a selection of a specific Hamiltonian cycle from each class of cycles (1 \(Z_6\) symmetric cycle having \(n = (2, 12, 6)\), 2 \(Z_4\) symmetric cycles \(n \in \{(0, 16, 4), (4, 8, 8)\}\), 3 \(Z_2 = Z_2^{sod}\) with \(n \in \{(0, 16, 4), (1, 2, 12, 6), (4, 8, 8)\}\) and 5 \(Z_2 = Z_2^{refl}\) symmetric cycles with \(n \in \{(2, 12, 6), (4, 8, 8)\}\). Note that the are only three different triplets \(n\).

4. The original idea was that the rules of bio-harmony could be applied to amino-acid sequences interpreted as sequences of basic 3-chords. DNA would have represented the notes of the music. For given choice of harmony as Hamiltonian cycle meaning selection of of 4, 5 or 10 amino-acids coded by the 20 DNAs in question, the hypothesis had to be modified by replacing amino-acid sequences with DNA sequences.

These DNA sequences however define also amino-acid sequences identifiable as specific triangle at the orbit of \(Z_n\) defining the DNA codons assigned to that amino-acid (there is a singular fiber space structure). Together the three 20-plets of DNAs define an amino-acid harmony with \((4+5+10 = 19)\) chords with tetrahedral extension defining a harmony with 22 chords/amino-acids). Hence both DNA sequences and amino-acid sequences define “bio-music”.

5. The assumption that harmonic transitions between chords (DNA codons) minimize the distance between chords defined by quint-metric leads to highly non-trivial and testable predictions about both DNA sequences and amino-acid sequences. Negentropy Maximization Principle (NMP) suggests that evolution favors the generation of harmony which should thus increase in the proposed sense for DNA sequences defining particular genes or other functional units of DNA during evolution. Large quint-distances between subsequent codons/chords would tend to polished out under evolutionary pressures.

6. Could icosahedron, tetrahedron, and tetra-icosahedron have direct physical counterparts in living matter? For instance, water molecules form icosahedral clusters and the chlathrates associated with synaptic contacts have icosahedral symmetries. Tetra-icosahedron has 13 vertices with the added vertex representing one note- say E- in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more that 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.

7. Music is language of emotions and peptides are molecules of emotion as Candace Pert expressed it. Could bio-harmonies serve as direct correlates for emotions? What is bio-music? A natural TGD inspired guess is that sounds can be replaced with \(h_{eff} = n \times h\) dark photons with low frequencies and having energies in the range of bio-photons (visible and UV range maximally effective biologically) as proposed on basis of some physical facts and theoretical ideas. The frequency spectrum of dark cyclotron photons along magnetic flux tubes would define bio-music as “music of dark light” and bio-harmonies would correlate with emotions and moods.
If one can find various icosahedral Hamilton’s cycles one can immediately deduce corresponding harmonies. This would require computer program and a considerable amount of analysis. My luck was that the all this has been done. One can find material about icosahedral Hamilton’s cycles (see http://tinyurl.com/pmghcwd in web, in particular the list of all 1024 Hamilton’s cycles with one edge fixed [A1a, A2a] (this has no relevance since only shape matters). If one identifies cycles with opposite internal orientations, there are only 512 cycles. If the cycle is identified as a representation of quint cycle giving representation of 12 note scale, one cannot make this identification since quint is mapped to fourth when orientation is reversed. The earlier article about icosahedral Hamiltonian cycles as representations of different notions of harmony is helpful [L6].

The tables listing the 20 3-chords of associated with a given Hamilton’s cycle make it possible for anyone with needed computer facilities and music generator to test whether the proposed rules produce aesthetically appealing harmonies for the icosahedral Hamiltonian cycles. Biologist with access to DNA sequences could experiment with DNA codons to see whether their are harmonious in the sense that the distance between subsequent chords assignable to DNA codons tend to be small in quint metric. Note that DNA decomposes to pieces corresponding to different Hamiltonian cycles (harmonies) so that the comparison is not quite straightforward.

8.1 What Could Be The Basic Principles Of Harmony?

It indeed seems that the idea about definition of notion of harmony in terms of Hamiltonian cycles makes sense.

8.1.1 Icosahedral harmonies

1. Chords (major and minor) are labeled by their basic tones and comes either as major or minor. Harmony in classical sense requires that the transitions from key to another take place by a small number of quints and that the piece does not wander too far from the major key, say C.

If quint corresponds to a step along the edge of the cycle in the direction of its orientation, the notion of tonal closeness corresponds to the closeness in the metric of icosahedron. For instance C, F, and G are commonly used keys in same piece and correspond to 3 subsequent points along Hamiltonian cycle. Note that the number of ♯s of the key increases by one unit in standard direction and the number of ♭s by one unit in opposite direction.

2. It turns out that major and minor 3-chords and are mapped to each other in the orientation reversal for icosahedral path so that basic moods “happy” and “sad” in music have this orientation as a geometric correlate. The effect of orientation reversal does not actually depend on the icosahedral representation but is implied by quint cycle representation alone. C and half-octave F♯ defining the tritonus interval are the fixed points of the orientation reversal. Orientation reversal induces pairings (C ↔ C, F♯ ↔ F♯, G ↔ F, D ↔ B♭, A ↔ D♯, E ↔ G♯, H ↔ C♯. Quints of cycle correspond to the fourths of oppositely oriented cycle so that majors and minors are mapped to each other and one can say that the moods “happy” and “sad” have geometric correlates in the sense that majors and minors are transformed to each other in the reversal of orientation of the cycle.

The notion of harmony can be characterized in terms of numbers of basic 3-chords identified as faces of the icosahedron and their neighborhood relationship telling when corresponding chords are near to each other or vertex or face neighbours. The wall neighbours assignable to given edge are expected to be in very special relationship harmonically since they possess a common quint.

The basic classification is according to the number n = 0, 1, 2 of edges of cycle contained by them and the triplet \(n_{0}, n_{1}, n_{2}\) for the numbers of faces of various kinds gives the first rough classification. 2-quint chords have common edge and thus two common notes with two 1-quint chords and are therefore natural intermediates in transitions between them. 0-quint chords are tonal loners having no edge neighbours turns out that they involve dissonances since they consists of three notes spanning length of 1 or 3/2 steps (say EFG, EF♯G or D♯EF). Maximally symmetric harmony is an exception: 0-quint chords correspond to augmented chords of type CEG♯ with two major thirds.
8.1 What Could Be The Basic Principles Of Harmony?

The numbers of three different kinds of face neighbor pairs for the 12 edges of the path serve as an additional classification criterion in terms of the $p = (p_{1,1}, p_{1,2}, p_{2,2})$ for the numbers $p_{i,j}$ of different kind of edges. Note that the neighbor faces of an edge correspond to 3-chords, which possess two common notes and are in this sense close to each other. These numbers characterize the most natural transitions between the chords of the harmony. A further criterion is the distribution of these neighbor pairs along the cycle.

8.1.2 Why quints are near to each other harmonically?

The naive expectation would be that frequencies near to each other (using half-note as unit) are close to each other. This is not true. Their simultaneous presence is experienced as dissonance. This probably has a neurophysiological correlate: in ear the hair cell groups detecting notes which are near to each other in frequency space are overlapping. This explanation does not however tell why the conscious experience is dissonance.

The distance measure for notes could be formulated in terms of distance defined as the number of quints connecting them. For quint the distance would be minimal. This measure applies also to chords and allows to understand the basic rule of classical harmony stating that harmonic transitions take place the chords related by quint shift of the basic note (adding either one $\#\,$ or one $\flat\,$ to the scale). Also the key changes can be understood using the same rule: consider the changes $C \to G$ and $C \to F$ as examples. Note that in this case the chords have common note.

One could of course question the assumption that it is possible to choose the shortest route. The notes obtained by quint scaling are not quite same in the two directions and means that $\#\,$ is the inverse of $\flat\,$ in well tempered scale only. Could it be that people with absolute ear are able to distinguish between the two slightly differing scales and experience notes of quint $C-G$ as harmonically close when 1 quint connects them but as harmonically distant 11 quints in opposite direction connects them?

If cognition is p-adic, one can ask whether the notion of harmony can be formulated in terms of p-adic distance concept.

1. By octave equivalence the scaling by power of two means nothing so that the scalings by $3/2$ are equivalent with scalings by 3 and the distance defined by 3-adic norm having values $3^k$, where $k$ is the number of quints makes sense. The distance defined as quints could be identified the absolute value of $k$ along the quint cycle in the direction in which the distance is shorter. If so, the maximal distance is 6 units.

2. 3-adic measure of distance seems to be rather realistic. Quint corresponds to 1 unit distance. Half step corresponds to a distance of 5 units and 6 units defines the largest distance and corresponds to the tritonus interval which was forbidden by catholic church. Fourth (C-F) corresponds to 1- step in opposite direction and 11 steps in standard direction.

3. There is also a problem. Second (C-D) corresponds to 3 quints but third (C-E) corresponds to 4 quints and small third to 3 quints in opposite direction. Major third would thus correspond to a longer harmonic distance than second. This is a genuine problem, whose solution might be provided by the extension of icosahedral scale to icosatetrahedral one bringing in one additional note which is very near to one of the icosahedral notes and is major or minor third of icosahedral note.

4. Could one use the number of icosahedral edges as distance between notes but not as a minimal distance along the Hamiltonian cycle but along a minimal edge path along icosahedron? The icosahedral measure of distance would be analogous to a distance between points of object along shortest route in space that it inhabits and depends on harmony characterized by the shape of icosahedral cycle. $C$ and $E$ (and also $C$ and $F_{2\#}$) could be close to each other in some harmony and distant from each other in some other harmony. Icosahedral geometry would become an active determinant of the harmony.

To sum up, music seems to have both 2-adic (octave equivalence) and 3-adic (12-note scale by quint scalings) characters. The principle of tonal unity for classical music stating that modulations of key should not lead too many quints away from the basic chord would have 3-adic interpretation.
What could be the rules for building a harmony?

What guarantees good harmony when one has fixed the key/harmony/representation of particular Hamilton cycle?

1. One should pose conditions on the allowed transitions between chords. Are there principles would imply harmonic smoothness in geometric sense? Could the transitions occur only between chords with a common note? Or can one require a common pair of notes? Or can one require even a common quint. If so, 0-quint chords would become tonal hermits and could not be used at all. In practice their dissonant character has eliminated them in popular music and much of classical music too.

The standard quint and fourth transitions (say C to G and C to F) are basic examples in which there is only one common note between chords, and it seems that one cannot require more than this in the general case. Playing with the chords of bio-harmony however suggests that smooth bossa nova/jazz emotionally ambivalent mood is created if common pair of notes or even quint connects the neighboring chords. The rule is that only transitions between chords with same basic note are allowed. Obviously this is too stringent a condition.

2. Could 2-quint chords act as bridges between two 1-quint chords? For instance, for the maximally symmetric harmony consisting of disjoint groups of chords related by half-octave scaling the augmented chords ($F_{aug} = FAC♯$ and $G_{aug}$ mapped to each other both by half-octave scaling and reversal of orientation could serve as mediating bridges.

3. Could harmonic transitions take place only between neighboring faces of icosahedron (see http://tinyurl.com/ns9aa) or should it only tend to minimize the quint distance between subsequent chords (this distance vanishes if they have a common note)? For the 0-quint distance harmony, the harmonic movement could be seen as a path in dodecahedron which is dual of icosahedron. In the most general case the transition can take place to both wall and vertex neighbors, whose total number is 3+3=6. In this geometric picture harmony and melody could be seen as duals of each other.

Dodecahedron is dual of icosahedron and one can ask whether the harmonic motion could correspond to a path at dodecahedron. The vertex of dodecahedron is pentagon and has 3 neighbours (see http://tinyurl.com/mp5d8). The above argument gives 3 + 3 > 3 neighbors for the triangle of icosahedron. Are the wall neighbors of icosahedral triangle mapped to nearest neighbor vertices? If so then transitions between vertex neighbor triangles should correspond to longer steps at dodecahedron. By the duality triangles of icosahedron correspond to three pentagons associated with the vertex of dodecahedron. The rule that comes in mind is that steps can occur between vertices for which the 3-pentagons have one or 2 common pentagons.

Note that if the dodecahedral path is Hamiltonian cycle, it is unique apart from isometries of dodecahedron and would define a unique chord progression. One can - and of course must - allow self-intersecting harmonic paths. The condition that there exists a basic chord from which everything begins and to which everything ends implies that closed but in general self-intersecting path is in question.

4. An interesting test for the idea would a computerized generation of random chord sequences satisfying at least one common vertex rule and finding whether they are aesthetically appealing. Incidence matrix (see Appendix) for the icosahedral (and tetra-icosahedral) triangles wholes element tells how many common vertices two chords have have allows computational construction of the allowed chord sequences as random sequences.

5. For most harmonies 0-quint chords involve dissonances induced by three nearby notes (such as $CC♯D$) and spanning large number of quints (maximally symmetric harmony has 2 0-quint chords, which do not have dissonances and second harmony with 2 reflection symmetries has no 0-quint chords). Also maj7−, sus4+, and 6− 1-quint chords have half-note dissonances. Dissonances as such are however not un-sesthetical. For instance, Bach used them to create a deeply melacholic feeling.
8.1.4 More general notion of harmony

The notion of harmony discussed in previous section is rather conservative and certainly too stringent.

1. 0-quint rule is too restrictive already in chord based music. For instance, the downwards progression \( Am, G, F, E \) appearing in Spanish music and music forms like Passacaglia would have chords with 1-quint distance. Hence one must consider also a weaker notion of harmonic chord progression according to which this distance is minimized and below some maximum value \( k_{\text{max}} \). One quint would define the smallest non-vanishing maximal distance. One can define incidence matrices for chords with \( n \)-quint distance. The incidence matrices with different values of \( k_{\text{max}} \) have disjoint sets of non-vanishing elements and the total incidence matrix is their sum.

2. Even this is not enough. The direction of step matters for scales (major-minor difference) and it seems to matter also for chord harmonies. The inverse \( E,F,G,Am \) of the above mentioned progression does not sound harmonic in the same \( Am \) key. The impression of achieving the goal/ending down to something dictated by fate is lost.

Instead of \( EFGA \) one often has \( EF^*G^*A \) as a melodic progression and with \( E,B7,E7,Am \) as a chord progression having only 0-quint steps. The rule seems to be that 1-quint steps are possible only downwards in minor harmony, whereas upwards steps are 0-quint steps. Climbing slowly upwards by 0-quint steps and falling down by 1-quint steps! Could this “gravitational analogy” serve as a metaphor?

Also the number of \( n \)-quint steps between chords matters. The larger this number, the closer the chords are. Two 0-quint steps means that chords have two common notes, 1 0-quint step that they have single common note. The two 1-quint steps for downwards step \( Am \rightarrow G \) are between 3rd and 1st (\( C \rightarrow G \)) and 5th and 3rd (\( E \rightarrow H \)). For upwards 0-quint steps \( E \rightarrow H^7 \) 1-quint steps are between 5th and 5th (\( H \rightarrow F^*_7 \)) and 1st and 1st (\( E \rightarrow H \)). For \( H^7 \rightarrow E \) the reversals of these steps occur. For \( E7 \rightarrow Am \) one has 3 1-quint steps: (the reversals 1-quint steps \( E \rightarrow A \) and \( H \rightarrow E \) steps and 1 quint step \( D \rightarrow A \). The last step seems to be the smallest one in a well-defined sense.

For \( G-F \) step the number of 1-quint steps is one (\( C \rightarrow C \)): same is true for \( F-E \) step (\( A \) and \( E \)).

Using geometry language, for chords connected by 1-quint step(s) the mutual orientation of corresponding triangles with shape defined by the intervals involved matters since the number of 1-quint steps depends on the orientation.

The notion of chord harmony does not apply as such to polyphonic music with several simultaneous melodies unless on can say that it involves definite chord sequence. One could try to apply the concept of harmony for melody also in this case. The challenge is to guess what harmony for melodies could mean.

1. A conjecture inspired by the genetic code is that the codons defining the allowed melody notes associated with a given chord are in one-one correspondence with the triangles at the orbit of the triangle associated with the chord under the group \( Z_6, Z_4, \) or \( Z_2 \) characterizing the chord as a counterpart of amino-acid. In table ?? the \( Z_6 \) orbits are represented as groups of 6 similar chords (2 for 1-quint chords and 1 for 2-quint chords). In table ?? for \( Z_4 \) chords the groups consist of 4 similar chords and in the tables ?? and?? for \( Z_2 \) harmony the chord groups consist of 2 similar chords.

2. The first guess is that the union of the notes of these chords could define the chords, whose notes are compatible with chord in the time scale shorter than the duration of the chord. Note that same triangle can appear at orbits of several chords since the orbits of each group span entire icosahedron.

If the note lasts for a duration of several chords, the notes must be consistent with all the chords involved. The rule would explain why fast chromatic sequences (in the scale of chord duration) sound harmonic but slow chromatic sequences do not.
8.1 What Could Be The Basic Principles Of Harmony?

For melodies in Am key EFGA is rare and does sound harmonic being often replaced with E, F♯, G♯, A. As far as intervals are considered, this is the inversion $D^*_2, F, G, G^*_2$ of AGFE shifted upwards by 5 quints. Could one regard progressions (say Am, G, F, E) breaking the strongest rule for chord harmony as polyphonic progressions satisfying the rules for polyphonic progressions.

To conclude whether the DNA inspired notion of harmonic is realistic, one should understand how the sub-groups $Z_n, n = 6, 4, 2$ of the isometries of the icosahedron and defining the genetic code act on the Hamiltonian cycles.

1. The simplest guess is that these groups are represented as subgroups of $Z_{12}$ (also a subgroup of icosahedral group) representing quint cycle. $Z_n$ generator would shift the basic note of the chord by $12/n$ - that is 2, 3, 6 quints.

2. $Z_n$ maps chords of same type to chords of same type only if it is a rotational symmetry of the harmony. For instance, the action of $Z_6$ (see Fig. 4) on icosahedron allows doublet orbit consisting of Xang type chords, since $Z_2$ maps 2 0-quint triangles in the middle of the figure to themselves and reflection group $Z_2$ permutes them. 6-element orbits consist of either minor or major chords. More generally, the inspection of the cycles shows that the cyclic orbits of triangle under $Z_n$ correspond to the orbits of corresponding subgroups of icosahedral group.

3. $Z_2 refl$ maps the shape of the chord to its mirror images and so that the character of the chord can vary along $Z_4$ orbits. The rules are ($M \leftrightarrow m$), ($6 \leftrightarrow 7$). For other chords the character is unaffected.

4. Any subgroup of icosahedral isometry group $A_5 \times Z_2^{refl}$ having 120 elements must map chords to chords (faces to faces). In particular any $Z_n$ even if it is not a symmetry of a particular harmony. The character of the chord is not preserved and the number of quints can change. Whether these maps have interpretation in terms of music remains unclear.

These considerations forced me to finally realize that the 3 groups $Z_6, Z_4, Z_2$ that I had assigned to 20+20+20 DNA codons in the model of the genetic code are nothing but $Z_6, Z_4, Z_2$ and $Z_2$-symmetric Hamilton cycles! The numbers of amino-acids associated with various types would be $3+1=4, 5, 10$ (with empty amino-acid included). Tetrahedral extension based on gluing of tetrahedron at triangle corresponding to X6 type chord possessed by all $Z_2^{refl}$ type harmonies would give 3 additional real amino-acids giving altogether real 22 amino-acids as required. This has implications.

1. All 11 Hamilton cycles are realized separately as DNA level harmonies. Amino-acid level harmonies would correspond to selection of three Hamiltonian cycles, one for each $Z_n$.

2. To get something one must give something away. Now one must give up the idea that (4,8,8) is special via the corresponding of n-quint property with polarity properties. This is a pity, since just taking this correspondence seriously led to the extension of the icosahedral cycles to tetra-icosahedral ones. Fortunately, the extension itself makes sense for all Hamiltonian cycles.

To understand the action of symmetries one must look how the groups $Z_n$ act on C major chord.

1. $Z_2$ would induce half-octave shift and map $C = (C, E, G)$ to $F^*_2 m = F^*_2 B, D_2$. The assignment of $F^*_2$ -tritonus - with C note sounds strange in the ears of harmonic conservatives.

2. $Z_4$ would map $C = (C, E, G)$ to $A = (A, C^*_2, E), F^*_2 = (F^*_2, B, C^*_2)$ and $D_2 = D^*_2 = (D^*_2, G, B)$. These would span 8 notes since $E, G, B, C^*_2$ appear twice. Note that $C, E, G, A$ are the notes assignable to the tetrahedron in the extension of the scale and pentatonic scale corresponds to $C, D, E, G, A$. $Z^4$ orbit does not contain the notes $DFG_2H$ but the orbit of G chord does so. The orbit of C chord plus $G_7$ chord alone define the notes of C major key.

3. $Z_6$ would map C and E to the same “impressionistic” 6-note scale consisting of 6 whole notes. Together with the $Z_6$ image of G one obtains all 12 notes of the scale.
8.2 Harmony And Biology

8.2.1 Could harmonic principles be realized in biology?

The basic idea behind icosahedral harmony is connection with biology suggested by the fact that the number of icosahedral basic chords is 20 which is also the number of amino-acids. Actually there are two additional amino-acids and one ends up to an extension of genetic code by attaching to icosahedron a tetrahedron and thus adding one vertex more. The number of DNA codons increases from 60 for icosahedral code to 64 for the real code. The triangle along which icosahedral and tetrahedral amino-acids are attached together corresponds to punct coded by stopping codons. Also the following amusing observation supports the notion of bioharmony. Simple music pieces tend to begin with the basic chord CM or Am. Interestingly, mRNA starts always with a codon coding met which could correspond to CM = CEG for one of the tetrahedral faces http://tinyurl.com/3b9ymnq.

Could the application of harmonic principles to biology make sense? The triangles of icosatetrahedron correspond to amino-acids or DNA codons for the amino-acids coded by 20 codons in question.

1. The strictest rule stating that there must be common edge of Hamiltonian cycle between the amino-acids/DNAs cannot be satisfied since 0-quint amino-acids/DNA codons would be total loners and effectively eliminated from biology.

2. The weaker “common edge or vertex” rule could however make sense. A given codon in the group of 20 codons/acid could be followed only by 3+3 different nearest neighbor similar codons/acid. If the first amino-acid is fixed there would be only 6^N N-amino-acid sequences instead of 20^N sequences. This kind of symmetry would have been probably observed if exact but one can ask whether harmonic pairs could more probable than completely random pairs.

3. A more plausible formulation is obtained by restricting the rule to the level of DNA sequences and generalizing it so that it applies also to transitions between harmonies with different symmetries so that a transition between corresponding amino-acids is induces.

4. An even weaker formulations states that the transitions occur with highest probabilities between codons/amino-acids having shortest quint distance.

A natural conjecture is that evolution favors the generation of harmony even in the very concrete sense that proteins defined by harmonious chord sequences for bio-harmony are emerge as what Darwinist would call the fittest ones.

1. Icosahedral water clusters made from tetrahedra

The obvious questions concern the concrete realization of the icosahedron - or more generally icosahedral symmetries. One should also understood what the attachment of tetrahedron to icosahedron means (note that tetra-icosahedron is not the same thing as icosi-tetrahedron, which is Archimedean (not Platonic) solid http://tinyurl.com/6onvry). What comes in mind is attachment of an information molecule to the receptor of cell membrane.

Water molecules form icosahedral structures and - what is amazing to me - Plato regarded icosahedron as a symbol of water http://tinyurl.com/y7bo9omm4a3378c13bca7d93a52213a325db7db0-30. html! The page “Water structure and science” of Martin Chaplin gives illustrations about the rather complex icosahedral structures. Icosahedral structures of size 3 nm can be formed from 20 14-molecule tetrahedral water molecule clusters containing 280 water molecules altogether. They can also consists of cyclic pentamers and tricyclo-decamers and also from bi-cyclo-octomers. The 20 tetrahedrons correspond to the faces of the icosahedron and tetra-icosahedron would be formed as tetrahedron is glued to the icosahedron along one of the faces.

The bioharmonies could manifest themselves already in the structure of water molecules. Second - more plausible - option is that they differ only at the level of the magnetic body of the biomolecule. Bio-harmony suggests that 3 radial magnetic flux tubes or flux tube pairs emerge from each water tetrahedron. Hamilton’s cycle could be realized as a flux tube connecting the vertices of the icosahedron and assigning the quint cycle to the cyclotron frequencies (magnetic field strengths).
This scenario raises several questions related to the pairings between ordinary DNA/amino-acids, their icosahedral representations, and their representations as dark proton sequences.

Suppose that one takes seriously the idea that genetic code is represented as dark proton sequences with the states of dark protons formed from 3 quarks representing DNA and RNA codons, amino-acids, and even tRNA.

1. How dark proton sequences are realized? Could one regard them as icosahedral bound states of 20 dark protons? Or with a Hamiltonian cycle consisting of penta-quarks and representing dark nuclear string? Could the icosahedral representation as dark nucleus consisting of 20 dark protons and dodecahedral representation as dark nucleus consisting of 12 dark 5-proton states be dual manners to interpret the state or are they different states related duality. Equivalence of the two pictures would require that dark protons are color excited and in an entangled state.

2. Could dark proton sequences correspond to sequences of icosahedrons connected by flux tubes connecting the dark protons assignable to the dark proton states assignable to the faces of the icosahedrons? These dark nuclei would be definitely different from those possibly associated with the Hamiltonian cycle.

3. What about the tetrahedral part of the genetic code in relation to dark protons sequences? What dark proton states could tetrahedral codons and amino-acids correspond? Are they associated with water tetrahedrons representing the faces of the water icosahedron? Note the amusing numerological co-incidence that the vertices of tetrahedron have 3 quarks associated with them and those of icosahedron 5 and that the quint for icosahedral edge is replaced with third for tetrahedral edge.

4. Could the chords correspond to triplets of cyclotron frequencies for quarks associated with the three flux tubes emanating from the each face of the icosahedron? Could the breaking of the rotational symmetry from SO(3) to SO(2) - now actually $Z_3 \subset SO(2)$ - assumed to occur for dark proton states correspond to the reduction forced by the triangular geometry?

5. How DNA-amino-acid correspondence is represented at the level of dark DNA? The correspondence should be realized in terms of magnetic flux tube triplets connecting dark DNA and dark amino-acid and resonance condition would be essential. When the chords at the orbits of $Z_n$ are of same type, different DNAs correspond to the same chord but with different key. When $Z_2^{\cdot \cdot }$ is involved, the two chords at the orbit are not of same type (note the analogy with left and right-handed biomolecules). The only manner to circumvent the problem is to assume that the chord associated with amino-acids magnetic body is that of DNA. Information is not actually lost in translation, it is only transformed to different kind of information perhaps representing correlates of emotions.

6. Could the non-representability of one of the $Z_6$ codons as amino-acid have an analog?

The fiber space having icosahedron as a base and 3 copies of icosahedron assigned with 3 regions of icosahedron corresponding to $Z_n$, $n = 6, 4, 2$, defines a formal geometric representation of genetic code. Could this space represented in terms of water icosahedra?

1. Perhaps one should first try to identify the function of water icosahedrons. The first guess is that they serve as local bridges between dark DNA/amino-acid sequences and ordinary DNA/amino-acid sequences. This would suggest that dark proton of dark DNA forms a flux tube connection with the face of water icosahedron dictated by the state of the dark proton: this would take place by flux tube reconnection and cyclotron resonance. Water icosahedron in turn couples with the DNA/amino-acid like DNA conjugate codon with codon so that kind of double helix is formed.

2. What about the pairing of ordinary DNA/amino-acids and water icosahedrons? Water icosahedron has size of about 3 nm. The size of single DNA codon is about 1 nm. Single codon corresponds to a twist of $3\pi /5 \approx 36$ degrees, an angle closely related to Golden Mean. If the radius of the helix consisting of water icosahedrons is above some minimal radius which is easy to estimate from an equation for the helix. There are 10 DNAs per $L(151) = 10$ nm
and they correspond to a total twist of $3 \times 2\pi$. Therefore the twist angle is $\Delta \Phi = \pi/5 = 36$ degrees for single codon and corresponds to a distance of $L(151)/10 = 1$ nm. From this one has equation for DNA and icosahedron helices as $z = k\Phi$, $k = h/(6\pi)$, $h = L(151) = 10$ nm (radii are constant). Single codon corresponds to a distance $s = \sqrt{d^2 + R^2}d\Delta\Phi$ along the water icosahedron helix of radius $R$ accompanying DNA helix. One must have $s \geq L = 3$ nm defining the size of water icosahedron in order to avoid overlap. Deltas $\geq L = 3$ nm gives the condition $R \geq 10 \times \sqrt{2}/(3\pi)$ nm $\simeq 1.5$ nm.

3. If the representation of genetic code is possible, do the fiber icosahedrons correspond to subsets of faces of the icosahedron itself? Or do they correspond to faces of icosahedrons in some manner associated with the amino-acid icosahedron. Direct attachment is not possible but association could be achieved by connecting the icosahedrons by flux tubes with the tetrahedron at the ends of flux tubes identified as representation of the same amino-acid. This kind of structure with three icosahedra emanating from a given icosahedron could be iterated and one would obtain a fractal structure representing a binary tree. Could the water icosahedrons organize in this manner to form larger clusters?

What could be the physical correlates of Hamilton cycles representing harmonies?

1. Could $Z_6$, $Z_4$ and $Z_2$ orbits associated with the Hamiltonian cycles be realized even in the structure of water icosahedrons? Could they be realized as structures formed by the water tetrahedra and correspond to three separate regions of these icosahedral structures? Could one assign to each of the three regions of icosahedron icosahedron such that the attached icosahedron decomposes to the orbits associated with that particular region? Could the hierarchy of the icosahedral symmetry breakings have a direct counterpart at the level of the icosahedral structures formed by water molecules? My intuitive feeling is that the answer to these questions is negative.

2. Could Hamiltonian cycles be realized only at the level of dark photons as quint cycles defined by closed flux tube giving rise to dark nucleus, that is in terms of 3-chords formed by dark photons propagating along flux tubes emanating from the icosahedron? If cyclotron frequencies of dark quarks are in question then the magnetic fields associated with the flux tubes would define the notes.

3. The breaking of $Z_3$ symmetry is of special interest since it could serve as a prebiotic analog of chiral selection and could relate to dark variant of weak physics with effectively massless weak bosons in nano-scales. This would require dark magnetic body. Half-octave scaling is second broken symmetry and would have also an analog in $Z_2$ variant of icosahedron. Note that 256 variants of the bio-harmony are predicted and could be realized for magnetic body naturally. The presence of electric fields at flux tubes is possible and if the electric and magnetic fields are non-orthogonal, U(1) instanton density is non-vanishing and induces parity breaking. Is this breaking associated with $Z_2$ only?

2. Clathrin molecules as icosahedral structures

Clathrin ([http://tinyurl.com/y8ho23zf](http://tinyurl.com/y8ho23zf)) is a structure appearing at the ends of microtubules and necessary for the transmission of signals between the presynaptic and post-synaptic neurons. Clathrin consists of triskelions - kind of triangular structures with three spiral like legs and having as symmetries the rotational symmetry group $Z_3$ of equilateral triangle. Clathrins can form hexagonal planar lattices and pentagonal icosahedral lattices consisting of 12 pentagonal faces - the number of vertices of icosahedron. One can associate 3 triskelions with each pentagonal face: this makes $12 \times 3 = 36$ triskelions altogether. One can regard the centers of the 12 faces as vertices of icosahedron and assign to this structure 20 faces, which are triangles formed by 3 pentagons.

If proteins and other molecules attach to the faces of clathrin, one can ask whether each icosahedral triangle of this kind has an address formed by the three notes associated with it and serving as a password: only those molecules, which “know” this password can attach to the face. The realization would be in terms of three U-shaped magnetic flux tubes emerging from the 3 pentagonal faces representing the three notes as frequencies of dark $h_{eff} = n \times h$ cyclotron
photons with ELF frequencies but energies of bio-photons (in visible and UV range). The binding of the molecule to the face triangle would be preceded by reconnection of U-shaped flux tubes of the clathrin and molecule, by a resonant interaction by dark cyclotron photons, and by an $h_{eff}$ reducing phase transition bringing the molecule to the face.

3. **Microtubules as music instruments?**

It has become clear that microtubules have a central role in biology, neuroscience and perhaps also in consciousness theory and the evidence that they are quantum coherent systems is accumulating. Could music metaphor could help to understand microtubules?

1. Tetra-icosahedron has 13 vertices with the added vertex representing one note—say E— in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more that 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.

2. The recent TGD inspired model of microtubules [L4, K30] was inspired by the findings of the group of Bandyopadhyay ([http://tinyurl.com/ze366ny](http://tinyurl.com/ze366ny)) relies on the general vision about bio-communications and control as being based on dark cyclotron photon radiation travelling along magnetic flux tubes. These dark photons have a universal energy spectrum in the range of bio-photons (visible and UV) to which they transform as the value of $h_{eff} = n \times h$ reduces to its standard value. Frequencies would span a wide energy range but EEG frequencies would be of special importance since they would also couple to acoustic vibrations. The precise value of the energy scale of cyclotron photons would be determined by the strength of the magnetic field at flux tube.

3. Frequency modulation would be the general manner to code information in living matter: “whale’s song” would be a good metaphor for it. This is assumed in the model for cell membrane as generalized Josephson junction: the modulation would be now induced by the variations of generalized Josephson frequency by variations of the membrane potential. Also microtubules have been proposed to base their communications on frequency modulation.

4. The first possibility coming in mind is that the continually varying microtubule length codes for the frequency [L4]. The change of the frequency by say octave would however require quite fast and large variations of microtubule length. Neither does this realization conform with the idea that the state of single tubulin corresponds to frequency. Microtubule length could also code for the length of the music piece represented by the microtubule serving as a music instrument or musician at the bio-molecular level. It would also the number of microtubular units and thus the size of the orchestra consisting of 13-units.

5. Another possibility inspired by the proposal is that magnetic flux tubes form an analog of 3-D grid ideal for communication purposes using 12-note (or actually 13-note) system as a code equivalent with genetic code. Also microtubules would involve three kinds of flux tubes defining coordinate grid of cylindrical coordinates: longitudinal, radial and those which rotate along the microtubule. Radial flux tubes would be ideal for communication using 13-note system as a realization of genetic code.

6. 13-note system as cyclotron frequency spectrum for given value of $h_{eff}$ would be determined by the spectrum of the magnetic field strengths going transversally through the microtubule and each tubulin would correspond to one particular note represented as magnetic field strength. The system would be highly analogous to the system formed by hair cells in Cochlear. Note would indeed characterize single tubulin molecule rather than entire microtubule as required if one wants to code chords using the two tubulin conformations as a bit. Tubulin conformation would determine whether the tubulin serves as a sending/receiving antenna or not.
Melody in 12-note system can be interpreted as a discretized version of frequency modulation with frequency being piece-wise constant in time. Obviously the 13 bit sequences defined by tubulin conformations code for the chords of rational 12-note scale involving a representation of one particular note (the third note of the Pythagorean scale) with two slightly different frequencies in order to avoid problems caused by the rational number ratios of frequencies. 13th bit could also serve as a kind of period. Also chords could be coded up to a chord with 13 notes so that microtubules would have quite a high representative power.

The is an objection against the model.

1. One could argue that a unit consisting of 13 tubulins allows only one octave to be represented. One can of course assume that the magnetic field strengths for subsequent units differ by octave. What makes this interesting is that microtubules allow two variants, called A and B. B type microtubules appear as 13-units since microtubular surface has a gap so that the helical symmetry is broken. For variant A, which is not found in vivo or in vitro, 13-units integrate to form longer helical units. This is assumed in Penrose-Hameroff model and the experimental absence of A type microtubules is one of the basic objections against Penrose-Hameroff hypothesis.

2. The TGD inspired proposal is that A type microtubules corresponds to a critical state having therefore an enhanced symmetry and long range correlations: criticality would explain their experimental absence. The experiments of the group of Bandyopadhyay support that the critical state is induced by a resonant excitation at specific AC frequencies \[L4\]. Long range correlations would mean enchance helical symmetry - that is fusion of several 13-units to form a longer helical structure. This structure would allow an interpretation as a structure with frequency spectrum of several octaves represented coherently in terms of magnetic field strength: the 10 octave span for hearing would mean the integration of 10 microtubule units meaning length scale of order micrometer assuming that tubulin size is of order 10 nm.

3. If the field strength for subsequent units differ by octave, one can argue that for variant B various octaves play their own music without knowing of each other and thus without coherence. In state A they would play together forming something analogous to orchestra or choir.

4. Microtubules could directly couple with both DNA and clathrin molecules if they represent 12 note system as a resonant system able to receive the radiation with corresponding frequencies. 12-note system and the 3-chord system associated with it could define universal communication code allowing communications between DNA, proteins, and microtubules.

To sum up, 13-note extension of 12-note system could be seen as a realization of the genetic code in terms of frequencies. The existence of kind of realization was obvious from the beginning and I proposed it in the model of microtubules as quantum antennas during the first years of TGD inspired theory of consciousness \[K14\]. Discovering the precise realization of the proposal has however required time.

8.2.2 Could biology help in the understanding of musical harmony?

One can also ask whether biology could provide ideas about the notion of harmony. Could icosatetrahedral harmony possessing additional 13th note very near to the fourth of basic major chord provide a better view about harmony?

1. The extension of the ideas about harmony to the case of icosatetrahedron is a non-trivial task. If one assumes that the extended Hamiltonian cycle is obtained by deforming tetrahedral Hamiltonian cycle according to the proposal made earlier, one ends up with a problem since
the cycle makes a wedge while making a side track of two steps via the new vertex. The two steps must give one quint so that the new vertex must correspond to either minor or major third of note where it started from (and ended to). This would add to the scale a chord of type CGD a chord of type $CEG$ or $CEbG$ (plus two other chords containing major or minor third. Depending on the orientation of the cycle one would obtain major or minor key. The remarkable feature of icosahedral harmonies is that they often lack a unique basic chord. Could it be that the addition of tetrahedron breaks the symmetry and fixes the key?

2. The added third could be slightly different from the icosahedral third and this could allow to resolve the problems due to the fact that quint cycle does not quite close $(3/2)^{1/2} = 2^{7/12}$ does not hold true exactly. The problems can be of course solved by introducing well-tempered scale defined in terms of powers of $2^{1/12}$; for this choices the topologically induced by these scalings is same as that induced by real topology in frequency space. Algebraically this means introduction of an algebraic extension of rationals. The problem is that persons with absolute ear prefer rational number based scale and experience tempered scale as unaesthetic.

The problem with 3-adic distance of notes was already described: the distance is 4 quints for major third (C-E) and 3 quints for minor third (C−Eb). A smaller distance is suggestive for major third.

1. The proposed extension of the scale would break symmetry by bringing a third which is indeed nearest neighbor of the basic note plus two other notes, which are in corners of a 1-quint triangle in the biological realization. Thus chord CEG and chord containing EG and third note would be introduced.

2. Using the general results one can readily find the possible extensions of harmony if one assumes that both major and parallel minor with same number of ♯s or ♭s are obtained. The chord chosen for extension must be CGA, which an be seen as part of C6 or Am7. If the added vertex corresponds to E one obtains $C = CEG$, Am = CEA, and the GEA which is part of C6/Am7 as also the lost chord. In amino-acid analog CGA would become “empty” amino-acid, punct, and would be replaced with GEA contained also in C6. One can perform this kind of realization for all 11 harmonies and/or their mirror images. The modification induces symmetry breaking and defines a key which is otherwise not obvious for the icosahedral harmonies. Also half-octave symmetry is broken.

3. One can perform the modification also for the inverted harmony. The transformation to reverted harmony $X \rightarrow Y$ corresponds to $X7 \leftrightarrow Y6$ and vice versa so that the presence of $X7$ type chords in harmony guarantees the existence of the required type extension in the reverted harmony. One can of course define extension also using $X7$ type chords. This would generate besides CEG two dissonant chords of type GEE♭ and CEE♭.

4. In maximally symmetric harmony (2, 12, 6) with 6-fold rotation symmetry, there are as many as 6 manners to perform this modification so that any note of the 6-note scale spanning “impressionistic” octave can define the key. The key is either F, G, A or Dm, E, F♯m. The harmony contains however no $X7$ type chords and since the transition to the reverted harmony acts as $X6 \leftrightarrow Y7$, it does not allow a modification generating both major and parallel minor. There are also other harmonies possessing no $X6$ type chords such as (2, 12, 6) and bio-harmony (4, 8, 8) with 2-fold rotational symmetry so that the extension in the simplest form can be performed only for their reversals.

5. For the two harmonies with 4-fold reflection symmetry there are 2 manners to perform the modification and modified chords are related by half-octave shift. With the conventions of Table ?? the modification introduces key which is either A $(F^2m)$ or $D^2$ (Cm) for both harmonies (second one is bio-harmony (4, 8, 8)).

8.2.3 About the interpretation of bio-harmonies

1. How ideas about harmony evolved?

A brief summary about the evolution of the notion of bio-harmony is in order.
1. The first guess was that amino-acids could be understood as chords of icosahedral bio-harmony characterized by 3-tuples (3, 10, 7), where the integers tell the numbers of icosahedral triangles with 0, 1, or 2 edges of the Hamiltonian cycle and identifiable as 3-chords with 0, 1, or 2 quints. The interpretation was that 3 0-quint chords correspond to 3 basic polar amino-acids, 10 1-quint chords to the 10 non-polar amino-acids, and 7 2-quint triangles to the 7 polar and acidic polar amino-acids. It turned out however that (3, 10, 7) does not appear as Hamiltonian cycle although it satisfies the necessary conditions.

2. I introduced also a model of genetic code motivated by the properties of the code table suggesting that 60 DNA codons are grouped into 3 groups of 20 codons. The idea that DNA codons coding for a given amino-acid form an orbit of a subgroup of icosahedral group with order which is not smaller than the number of these DNAs and has the aminocid at it. Three subgroups $\mathbb{Z}_6, \mathbb{Z}_4, \text{ and } \mathbb{Z}_2$ would predict 3 amino-acids coded by 6 codons and two amino-acids coded by 1 codon, 5 amino-acids coded by 4 codons, and 10 amino-acids coded by 2 codons. The total number of codons would be $3 \times 6 + 2 + 4 \times 5 + 10 \times 2 = 20 + 20 + 20 = 60$ rather than 64. The number of doublets is 10 instead of 9. Could one $\mathbb{Z}_2$ orbit corresponds to punct coded by two stopping codons? But what about the codon triplet associated with Ile? Something is clearly missing.

There is also second problem: a really realistic model of genetic code should include also 21st and 22nd amino-acids (Pyl and Sec). Pyl or pyrrolysine is modification of Lys and is basic polar amino-acid so that the number 3 of basic polar amino-acids increases to 4. Contrary to the original naive extrapolation Sec (selenocystein) is acidic polar rather than non-polar so that the number 2-quint triangles increases from 7 to 8. For the properties of amino-acids see [http://tinyurl.com/y8b7fumq](http://tinyurl.com/y8b7fumq). The notion of hydrophobicity is discussed at [http://tinyurl.com/9qr8e7q](http://tinyurl.com/9qr8e7q).

3. The solution of the problems came from the extension of icosahedral code with tetrahedral code bringing 4 additional codons and 3 amino-acids assigned with the external faces of the tetrahedron (Ile, Pyl, and some standard non-polar amino-acid), and increasing the number of stopping codons from 2 to 3. This gives $60 + 3 + 1 = 64$ codons but one should code also Pyl and Sec. The solution of the problem would be that stopping codons code also these under some conditions. Are DNA codons or their mRNA counterparts pairing with tRNAs - perhaps their magnetic body - modified somehow?

For instance, Pyl and Sec could correspond to icosahedral codons before fusion. After fusion they cease to be coded - most naturally because the group orbits containing punct are replaced with those associated with tetrahedron. The 3 ordinary amino-acids represented by tetrahedron are Ile, 1-quint amino-acid and 2-quint amino-acid. As fusion is broken temporarily Pyl and Sec are coded.

4. The geometric correlate for the fusion of the codes is gluing of tetrahedron to icosahedron along one face which corresponds to “empty” face identifiable as punct coded by stopping codons. The icosahedral Hamiltonian cycle (4, 8, 8), which exists as two variants, is extended to (4, 10, 8) with two new amino-acids.

5. The music analogy for the fusion of tetrahedron is symmetry breaking bringing in a definite key by introducing the major and minor chords as 1-quint chord (but with 2-edges since tetrahedral edges correspond to major and minor thirds).

2. Understanding the misunderstanding

This was the picture as I started to work again with the notion of bio-harmony. Just when I thought that I understand the notion, I realized that something very essential is missing and even wrong.

1. One could argue that the assumption about the correlation of forms of amino-acid polarity with character of Hamiltonian cycle leading to (4, 4, 8) identification is ad-hoc: why not allow all harmonies? One can also wonder whether the group structure behind the genetic code leading to the identification of sets of DNA codons coding for a given amino-acid as
orbit of the corresponding triangle can be totally dependent on the group structure emerging from the construction of the Hamiltonian cycles.

2. The question whether the group structures associated with genetic code and with the Hamiltonian cycles might have something to do with each other leads to the realization of the obvious: the groups involved are the same: $Z_6$, $Z_4$, and $Z_2$! The symmetries of DNA are the symmetries of cycles. DNA code would be inherent to the Hamiltonian cycles, and the triangles of the icosahedron representing the harmony would correspond to DNA codons! $20+20+20$ icosahedral triangles to 60 genetic codons and 4 icosahedral triangles the remaining 4! The three 20-pls correspond to $3+1$ amino-acids coded by 6 (resp 2) codons, to 5 amino-acids coded by 4 codons, and to 10 amino-acids coded by two codons.

By direct inspection of the illustrations of the appendix one can indeed convince oneself that the groups in question map chords to chords of same type and one obtains appropriate number of orbits. This of course follows from group theory alone.

3. One must give up the assumption that the integers $n = (n_0, n_1, n_2)$ correspond to the numbers of the basic polar, non-polar, and polar and acidic polar implying that only $n = (4,4,8)$ would define bio-harmony. All Hamiltonian cycles with symmetries define bio-harmonies and both $Z_2^{cot}$ and $Z_2^{eff}$ define $Z_2$ type bio-harmonies assignable to 10 amino-acids coded by 2 codons. This is somewhat frustrating outcome, since just this correspondence served as guideline leading to the extension of the icosahedral code. The extension as such is however independent of this identification and needed in order to get the 4 missing DNA codons and to understand the coding of 21st and 22nd amino-acids Pyl and Sec.

What do the Hamiltonian triplets $n$ then correspond? Harmonies correlate with moods in music: maybe the serve as mathematical correlates for emotions and moods.

4. Harmonies are not for amino-acids but for DNAs coding them. One can however identify amino-acids as specific triangles the orbits and the chords associated with the amino-acids define much more restricted notion of harmony involving one representative of each basic type of chord. Perhaps the additional chords correspond to modulations of the harmony.

5. The rules of harmony generalize as such to transitions between DNA codons regarded as chords. If chords are near to each other with respect to the distance measured as quints, the transition between the chords respects harmony. One must think that DNA codons form a singular fiber space such that the union of fibers for type $n$ gives the space of 20 amino-acids. The ‘gauge group’ $Z_n$ acting in the fiber is different in the 3 regions of the amino-acid space and the number of elements in the fiber is factor of $n$ actually equal to $n$ for $n \neq 6$ and having values 6 and 2 for $n = 6$. Each choice for the 3 Hamilton cycles of type $Z_n$, $n = 6, 4, 2$ defines a variant of this fiber space. The distance along the fiber isomorphic to the space of amino-acids is measured as minimal quint distance.

Note that the DNA codons for two different variants of the fiber space need not define same kind of chord so that also given amino-acid can correspond to several different chords. It is enough that the notes of the chords are specified - as they indeed are. The $Z_n$, $n = 6, 4, 2$ in turn can correspond to any Hamilton cycle with symmetry $Z_n$ so that for $n = 1, 4, 2$ one can have $1, 2, 3 + 5 = 8$ different fiber spaces. The hierarchy of Fibonacci numbers is involved. A hierarchy of symmetry breakings is highly suggestive and leads to increasingly richer harmonies.

$Z_6$ has maximal symmetry but $Z_4$ is not a subgroup of $Z_6$ so that only the symmetry breakings $Z_4 \rightarrow Z_2^{cot}$ and $Z_4 \rightarrow Z_2^{eef}$ can be said to occur. Note that transition between different realizations of the covering space has interpretation as a phase transition and that it could occur at RNA rather than DNA level. These phase transitions need not relate to the bio-chemistry but to serve as correlates for emotions and moods. Also the degeneracy due to the existence of several DNAs coding given amino-acid could have similar interpretation.

One can of course play with more stringent scenarios for the transitions between DNAs or RNAs). For instance, the assumption that transitions can occur between chords of same type, leads to contradiction since the Xaug chords of $Z_6$ harmony do not appear in any other harmony.
In any case, the quint-rule in its various forms is readily testable for DNA sequences.

6. An open question concerns the change of the key. The convention of the illustrations is that 1-2 edge corresponds to C-G quint. Should one allow the DNAs at various sheets of covering space to be in different keys? Change of the key could be identified as a rotation by some number of quints. It would change the graph representing icosahedron and change the chords. $Z_{12}$ would allow to realize all keys. $Z_{12}$ is not however a subgroup of the icosahedral isometries (whereas $Z_6 = Z_3 \times Z_2^{\text{rot}}$) so that the transformation should be interpreted as a translation in quint space acting as coordinate transformation.

The active transformations induced by isometries of icosahedron do not change the graph and would map chords to new ones. The action of $Z_6$ is well-defined also for other harmonies than $Z_6$ symmetric ones. Could the modulations of the basic key correspond to $Z_{12}$ transformations. If so, one would have 6 keys. Unfortunately, the most common modulation by quint ($G \to G$) would be missing.

The change of key could correspond also the change of the chords defined by the extension to tetra-icosahedral harmony. One can choose the chord for extension in several manners for $Z_2^{\text{rot}}$ and $Z_2^{\text{refl}}$ and these choices could define the allowed modulations of the key.

7. What would be the correlates of different keys the level of DNA? An attractive assumption is that notes are realized in terms of dark photons, which could also transform to ordinary sound since living matter is piezo-electric system. The general hypothesis is that dark photons have universal energy spectrum, which is that of bio-photons. Change of key corresponds to a change of frequency scale and would correspond the change of either Planck constant or of magnetic field strength the flux tubes of the magnetic body associated with DNA codon (or amino-acid perhaps). This would mean that 12-note scale would correspond to 12-note scale for the magnetic fields strength to which cyclotron frequency is proportional or equivalently for the thickness of the flux tube since magnetic flux is quantized if monopole fluxes are in question. 12-note scale could mean in biology a standardization of frequencies used.

One must modify the extension of the icosahedral Hamiltonian cycles to tetra-icosahedral ones appropriately.

1. The $Z_6$ symmetric 20-plet contains 3 6-plets and 1 doublet and the $Z_2$ symmetric code contains 10 doublets so that here is one 11 DNA doublets in the icosahedral code. “Ordinary” amino-acids have only 9 doublets. The interpretation is that the $Z_6$ doublet corresponds to ile and the additional ile is coded by tetrahedral codon. The second surplus doublet can be identified as 2 codons coding for punct, “punct”. This gives 4+5+ 10 =19 amino-acid if “punct” is counted.

2. What is lacking is one ile, met, trp, plus Pyl and Sec. Also 4 DNA codons are needed. One of them must code ile, one met, one for punct, and one for trp. The tetrahedral codons would thus correspond to orbits of $Z_1$. This is actually the only possible subgroup since for the choices $Z_u = 2, 3, 4$ the numbers of codons and amino-acids are not correct. This exhausts all DNA codons.

3. The only manner to proceed is to assume that icosahedral and tetrahedral codes can appear also as unfused versions. This would naturally occur for $Z_2^{\text{refl}}$ for which all cycles contain $X6$ type chord but can occur also for $Z_2^{\text{rot}}$ if the completion is done for the inverse harmony and then mapped to the harmony back. The icosahedral code would be as already described. The “free” tetrahedral codes would correspond to $Z_1$ and the faces coding punct in the two codes would code for Pyl and Sec. The fusion of the tetrahedral and icosahedral codes gives just the ordinary genetic code so that the proposal is consistent with the proposal that dark proton sequences realize genetic code [K10].

4. Note that geometrically this extension means only that the amino-acid sheet of the fiber space is extended by tetrahedral sheet.

The challenge is to construct the covering space of the icosahedron representing amino-acids.
1. The has as a local fiber the orbit under $\mathbb{Z}_n$ associated with the amino-acid defining base point. The space of amino-acids decomposes to disjoint regions corresponding to the $20\times20\times20$ DNA codons. $\mathbb{Z}_n$ is the analog of gauge group and by symmetry breaking is different from three different regions of amino-acid space. There are $1 \times 2 \times 8 = 16$ variants of this space due to existence of several harmonies for given symmetries. There are actually only three different options for $n$ given by $n = (0, 16, 4), (2, 12, 6, \text{and} \ (4, 8, 8)$.

2. The $\mathbb{Z}_n$ orbits of the three disjoint amino-acid regions (containing $3+1=4$, 5, resp. 10 amino-acids) intersect each other. The challenge is to choose the representative amino-acids from the orbits of $\mathbb{Z}_n$ in such a manner that the chosen amino-acids belong to the three disjoint regions. It remains to be proven that this is possible. One must also understand how uniquely this can be done.

3. One could think of choosing a set $P_2$ of 10 representatives from the 10 orbits of $\mathbb{Z}_2$ related by 6-quint scaling along Hamiltonian cycle. The $3+1+5=9$ amino-acids associated with $\mathbb{Z}_6$ and $\mathbb{Z}_4$ would belong to the mirror images $P(S)$ of this 10-element set. $P(S)$ decomposes into set $P_0$ of 3+1 triangles and set $P_1$ of 5 triangles and there are 2-element, 4-element and 6-element orbits connecting the elements of the sets $P_2, P_3,$ and $P_6$.

The following observations lead to a rather detailed and surprisingly simple picture.

1. The key observation is that the construction of the covering space - that is identifications of amino-acids at the orbits of the groups involved - depends only on whether the choice of $\mathbb{Z}_2$ as $\mathbb{Z}_2^{\text{rot}}$ or $\mathbb{Z}_2^{\text{refl}}$! Thus the two codes (ordinary one and code with Pyl and Sec coded by stop codons) are distinguished by different DNA-amino-acid covering spaces. The details of the Hamiltonian cycle do not matter. Only the structures and mutual relationships of the groups $\mathbb{Z}_6 = \mathbb{Z}_3^3 \times \mathbb{Z}_2^{\text{refl}}$, $\mathbb{Z}_4 = \mathbb{Z}_2^{\text{rot}} \times \mathbb{Z}_2^{\text{refl}}$ and $\mathbb{Z}_2^{\text{rot}}$ and $\mathbb{Z}_2^{\text{refl}}$ matter. Furthermore, the actions of the groups $\mathbb{Z}_2^{\text{rot}}$, $\mathbb{Z}_3$ and $\mathbb{Z}_2^{\text{refl}}$ determine also the actions of $\mathbb{Z}_6$ and $\mathbb{Z}_4$. Only $\mathbb{Z}_2^{\text{rot}}$ and $\mathbb{Z}_3$ are non-commuting actions.

2. One can decompose amino-acids to 10 pairs of $\mathbb{Z}_2^{\text{refl}}$ orbits and visualize the 20 codons involved as two layers on top of each other such that two on top of each other correspond to the same 2-orbit - 2 boxes on top of each other. The choice of the two layers is not unique since one can permute the members of any vertical box pair.

3. By a suitable choice of the members of vertical box pairs one can arrange that $\mathbb{Z}_3$ and $\mathbb{Z}_2^{\text{rot}}$ act along the two layers horizontally. $\mathbb{Z}_2^{\text{rot}}$ orbits divide each layer to 5 pairs of horizontal boxes. One can also permute the vertical pairs horizontally in such a manner that the 5+5 $\mathbb{Z}_2^{\text{rot}}$ orbits correspond to neighboring horizontal boxes along upper and lower layer giving $2+3+2+2$ decomposition. This still leaves the possibility to permute these 5+5 horizontal pairs defining 4-orbits of $\mathbb{Z}_4$ horizontally with each other.

Simply by drawing one find that $\mathbb{Z}_3$ orbits divide each layer to 3 triplets and 1 singlet and by a suitable choice $\mathbb{Z}_3$ singlets correspond to the 10th box on the right for both layer. The $\mathbb{Z}_3$ orbits and $\mathbb{Z}_2^{\text{rot}}$ orbits overlap in such a manner that the middle $\mathbb{Z}_3$ orbit contains entire $\mathbb{Z}_2^{\text{rot}}$ orbit.

4. It is clear how to choose amino-acids from the orbits.

(a) Consider first the $\mathbb{Z}_2 = \mathbb{Z}_2^{\text{refl}}$ case. The lower layer corresponds to the 10 $\mathbb{Z}_2^{\text{refl}}$ amino-acids (punct included) coded by 2 codons. One must choose from each $\mathbb{Z}_4$ orbit consisting of a square of 4 boxes one upper box to represent $\mathbb{Z}_4$ amino-acid (ala, val, gly, pro, thr). Each 4-unit contains one free upper box to which one can assign 1 $\mathbb{Z}_6$ amino-acid. One cannot however put two amino-acids on 3-orbit. There are 3+1 $\mathbb{Z}_6$ amino-acids and 5 boxes so that one box remains unused. This must be the case. The used box must belong to either second or third horizontal $\mathbb{Z}_2^{\text{rot}}$-2-box: if it were filled, the middle $\mathbb{Z}_3$ 3-orbit would contain 2 $\mathbb{Z}_6$ amino-acids and the fiber space-structure would fail.

Contrary to the original intuition, the unfilled box is not at the 2-orbit of $\mathbb{Z}_6$ containing as Ile but at the middle upper 3-orbit, which would contain 2 amino-acids if filled. It is associated with one of the 10 amino-acids coded by two codons and is same for both
Table 4: The representations of the associations of amino-acids to the orbits of $Z_n$, $n = 6, 4, 2$ for $Z_2 = Z_2^{refl}$ (upper two rows) and $Z_2 = Z_2^{rot}$ (lower two rows). The integer $n$ in box tells that the amino-acid associated with that box corresponds to $Z_n$ type amino-acid. “(2)” tells that the $Z_6$ orbit in question consists of 2 codons.

<table>
<thead>
<tr>
<th></th>
<th>4</th>
<th>6</th>
<th>4</th>
<th>6</th>
<th>4</th>
<th>6(2)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>6</td>
<td>2</td>
<td>6</td>
<td>2</td>
<td>6(2)</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>4</td>
<td>2</td>
<td>4</td>
<td>2</td>
<td>4</td>
</tr>
</tbody>
</table>

$Z_2^{rot}$ and $Z_2^{refl}$. One expects that this amino-acid is somehow special: maybe it is punct. Also the corresponding 6-amino-acid (Ser, Arg, or Leu) might be somehow special.

(b) $Z_2 = Z_2^{rot}$ can be treated similarly. The upper row of boxes is filled in the same manner as in the previous case. The horizontal box pairs in the lower row contain one $Z_2^{rot}$ box and one $Z_2$ box. The difference to the previous case is that $Z_2$ boxes are now shared by the both rows: in the previous case they belonged to the lower row.

5. The assignment of amino-acids to the orbits is not unique: for $n$ similar orbits there are $n!$ different assignments. Inside orbit there is also some non-uniqueness.

Table 4 represent the two situations graphically.

3. Music and physical correlates of emotions

Peptides are regarded as molecules of emotion and also information and positive/negative coloring of emotions would naturally correlate with the increase/reduction of negentropic resources of the system as negentropy is transferred to or from it away or increases as a whole. Music induces and expresses emotions. Therefore the idea that music in generalized form - say represented by dark photons with ELF frequencies and having energy spectrum in visible and UV energy range of bio-photons- could be the fundamental correlate of emotions and whether tetra-icosahedral music could be in special role (note that one can associated Hamilton’s cycles and “music” with any graph).

There are 11 candidates for the icosahedral harmony and its extensions. The candidates have either $Z_6$ (Fig. 4), $Z_4$ reflection symmetry (Figs. 5, 6), or $Z_2$ rotation symmetry (Figs. 7, 8, 9), and $Z_2$ reflection symmetry (Figs. 10, 11, ??, ??, ??). For the first case $Z_2^{rot}$ reflection symmetry and for the second case $Z_2^{rot}$ rotation symmetry are represented as as half-octave shift. Second reflection symmetry corresponds geometrically to reflection in horizontal direction. The extension assigns to them definite key and adds to 1-quint chords minor and major chords absent for the icosahedral bio-harmonies. The question is whether one of these harmonies is selected in biology or whether all three can appear and are perhaps realized at the level of magnetic bodies of amino-acids.

The reversal of the harmony differs from the original one and major-minor transformation takes place. Could it be that both “moods” are realized at the level of magnetic body and even serve as the physical correlates of moods and emotions? Could emotions be realized at the level of amino-acid magnetic bodies as phase transitions affecting parts of organism or even entire organisms and in this manner changing the mood. Peptides are regarded as molecules of emotion: could these phase transitions occur only for peptides and other information molecules involving proteins? Could peptides also serve as seeds of these phase transitions? Could even the Hamiltonian cycle be changed for the magnetic body of the entire organism and correspond to some importance two-valued characteristic of emotional profile?

Could orientation reversal relate to time reversal, which in Zero Energy Ontology (ZEO) corresponds to state function at opposite boundary of causal diamond (CD)? This reversal would occur in volitional acts: the subsequent reduction would not affect the quantum state in positive energy but in TGD framework they affect the state at opposite boundary CD and in this manner give rise to the experience flow of time.
The simplest extension of the harmony in the proposed form requires that harmony possesses $X_6$ chord. It does not exist for for the candidate with $Z_2^{refl}$ symmetry but for its reversal 4 of them are present as images of $D7, E7$ and $G_7, B7$ which are chords of type $X^0$. One can however map the harmony to its reversal, perform the completion for it, and perform the reversal back to the original harmony. The reversal depends on what note remains invariant in the reversal. One can require that it is the basic note of the chord to itself: with this condition one would obtain $Dm, Em, Gm, Bm$ and major keys $C, F, A, H$. 4 different harmonies would result. Without the restriction the number of harmonies is different and each has different emotional characteristics.

4. Religious myths, music, and biology

These symmetries define a hierarchy of symmetry breakings. This hierarchy has amazing connections with the myths, which I believe to reflect deep facts about consciousness and biology at fundamental level expected if also consciousness is fractal. The story of genesis is a good representative in this respect.

1. The hierarchy of symmetry breakings proceeding from $Z_6$ down to $Z_2^{refl}$ brings strongly in mind evolution as loss of innocence. For $Z_6$ one as 4 orbits. One orbit contains 2 triangles (chords, DNA codons assignable to ile). The other orbits correspond to six codons assignable to amino-acids ser, arg, and leu. The chords at the orbits are major chords and 7-chords, and minor chords and 6-chords for the inverse of the harmony. There are no dissonant chords in 6-quint sector: dissonances appear only for the remaining groups as 6-quint chords. This is musical representation of paradize. This harmony is based on 6-note scale for the basic notes of the chords and used by impressionistic composers. Amino-acids correspond to selections of preferred chord from each orbit and there are only four different chords: this sub-harmony is very simple. Life in paradize is simple!

2. Next comes an intriguing observation. The number of amino-acids obtained as projections of the icosaahedral DNA orbits is 19, not 20. Could it be impossible to have 20 amino-acids as projections of the orbits and that 19 is the maximum number? The reason for 19 is that the number of amino-acid of type $Z_6$ is $3 + 1 = 4$ rather than 5. Therefore there is one "non-playable" chord - located at some "paradize orbit" - , which does not correspond to any amino-acid.

The first guess for the non-playable chord is as one of the aug type chords (say $CEG_Z$, which is the last breath in many finnish tangos telling about unhappy love end - it is something between happy CM and sad Am, "raneta" is finnish word for this manner to come to an end: "expire" might be the nearest english counterpart). This chord is located at the 2-chord orbit related to the other chord of the orbit by half-octave shift (chords could be $CEG_Z$ and $F^\#B^\#D$), the tritonus denied by church.

Unfortunately, this identification is not consistent with the argument identifying the amino-acid chords at $Z_n$ orbits (see table ?? ) the non-playable chord must belong to an intersection of 6-orbit and 4-orbit and is not completely unique without further assumptions. It belongs to a 2-orbit of $Z_2^{refl}$: if it is somehow special, it could belong to the 2-orbit assignable to punct. If the chords at the 2-orbit have basic notes differing by tritonus, the inspection of the Table ?? shows that it is possible to find a unique chord pair having this property for all 5 $Z_2^{refl}$ cycles.

One cannot avoid the associations between non-playable chord and the denied fruit hanging in the tree of good and bad knowledge in the story of Adam and Eve, and its analog in many fairy tales. The non-playable chord also brings in mind the hilarious story of Gödel-Escher-Bach about non-playable record (a truth unprovable in given axiom system).

3. The hierarchy of symmetry breakings leading from $Z_6$ to $Z_2^{refl}$ encourages one to continue with the biblical analogies. $Z^0, Z_4$ and $Z_2^{refl}$ cycles have half-octave shift as a symmetry: good and evil do not exist in paradise, but dissonances are already there for $Z_4$ and $Z_2$ harmonies - the evil snake! These states correspond to the consciousness of animals, children, and saints. Note that bio-harmony corresponds to the presence of one sub-harmony of type $Z_n$, $n = 6, 4, 2$. 

8.2 Harmony And Biology 74
4. The banishing from the paradize takes place as \( Z_2^{refl} \) symmetric harmony replaces \( Z_2^{rot} \) harmony: half-octave shift is not a symmetry anymore, and one can tell between good and evil, and eventually church decides to deny tritonus as a symbol of evil! Paradise is left as icosahedral and tetrahedral code are fused to form the tetra-icosahedral code - the ordinary genetic code leading to the breaking of \( Z_2^{refl} \) symmetry.

5. In banishment punct ("empty" amino-acid) as a counterpart of chord shared by tetrahedron and icosahedron emerges and means stopping of the music piece altogether. Death of the sinner! For unfused codes this chord is playable as Sec/Pyl and the music piece is never-ending: life is eternal in paradise! No notion of time, no sin, no death! Amusingly, impressionist music with 6-note scale is music of "now", attempt to catch this moment.

6. Also the holy trinity finds an analog as \( Z_6 - Z_4 - Z_2 \) trinity of the bio-harmony. Holy Spirit, Father, Son: perhaps in this order. Even more, \( Z_2^{rot} \) can be associated with Son in Heaven and \( Z_2^{refl} \) with Son at Earth as ordinary mortal!

5. What do DNAs/amino-acids sound like?

If DNA/amino-acid sequences correspond to chord sequences of tetra-icosahedral harmony, one can ask what they sound like. The best manner to study this question is to build concrete simulations of the DNA/amino-acid sequences.

1. This requires specification of harmony by selecting one Hamiltonian cycle from the cycles belonging to the groups of cycles with \( Z_n \), \( n = 6, 4, 2 \) symmetry and decomposing amino-acids to 3 groups correspondingly (those coded by 6, 4, and 2 codons). One must include tetrahedral codons and amino-acids.

2. The basic rule of harmony would be the minimization of quint distance between initial and final chords of the transition. One can consider probabilistic versions of this rule or pose strict form of the rules stating in the most stringent form that only transitions with vanishing quint distance (between neighboring triangles) are possible.

3. The transitions between different amino-acid regions would be governed by this rule. Also the transitions between different variants of the DNA-amino-acid space defined by different choices of the Hamilton cycles would be governed by the same rule.

4. The most plausible looking model considers only transitions between DNA codons since DNA sequences induce amino-acid sequences.

Appendix represents an example about randomly generated chord sequence assignable to bio-harmony defined as a composite of 3 harmonies - one from each symmetry type and \( Z_2^{refl} \) involving tetra-icosahedral extension. Anyone having garage band skills in guitar playing can check what these chord sequences sound like and maybe try to build a melody on the background. One could also test the proposal that codons at the orbit of amino-acid define the melody by finding a concrete representation for the orbits and building random melodies defined by DNA sequences coding for the chord sequence.

8.2.4 Magnetic body, bio-harmonies, morphogenesis, and epigenetics

What TGD can possibly give to biology is the vision about magnetic body as an intentional agent using biological body as a sensory receptor and motor instrument and about various mechanism used by magnetic body for control and communication purposes. A new element is brought in by Zero Energy Ontology: magnetic body is 4-dimensional and thus correlate for a behavioral pattern rather than 3-D state for part of organism. Also the notion of bio-harmony suggests itself as a correlate for quantum coherence at the level of basic bio-molecules. The discussion below raises and tries to answer general questions.

The finding that behavioral patterns of planaria can be remembered also by the piece of split planaria without brains is consistent with the idea that replication of magnetic body coding for behaviors is behind biochemical replication. That alleles of the same gene have different expression
could be understood if the bio-harmony assignable to gene carries additional information besides the biochemical information. An alternative explanation is that emotional memories associated with conditioning are realized at the level of the body of planaria. These notions might also provide a fresh approach to epigenetics. Histone modification and DNA methylation are believed to induce kind of geometric locking preventing transcription. They could also affect the frequency assignable to DNA codon or some key unit so that the resonance condition making possible reconnection of U-shaped flux tubes allowing biomolecules to get in contact fails and transcription cannot proceed. Epigenetic inheritance could reduce to the inheritance of bio-harmony: the magnetic bodies of cells of offspring get in tune with those of parent. To how high degree magnetic body and bio-harmony are inherited? This becomes the key question.

1. Basic ideas related to magnetic body

Recall first some key ideas of TGD inspired quantum biology.

1. In TGD framework magnetic body extends the pair formed by organism and environment to a kind of holy trinity. Magnetic flux tubes and the realization of genetic code in terms of dark proton sequences has been the key hypothesis. The model for cold fusion \( [L7] \) suggests that also more general dark nuclei must be allowed. Dark neutron sequences could correspond to genes separated by dark protons. Dark weak interactions with large value of \( h_{eff} \) effectively massless below neuron size scale would play central role and induce large parity breaking effects (chiral selection).

The chemistry would not be all that matters. DNA-nuclear/cell membrane as topological quantum computer with braided magnetic flux tubes would explain why organisms with virtually identical genomes are so different (we and our ancestors for instance). The hierarchy of magnetic bodies would be responsible for the development of intelligence and for cultural evolution. Flux tubes connecting DNA and mRNA as well as mRNA and tRNA molecules are present but it is difficult to say anything concrete.

2. Ontogeny could be seen as a kind of editing process for the text defined by the DNA. Control of control of... is involved so that situation is very complex. Who performs the editing? Does DNA edit itself and is the editing process defining evolution of genome coded by genome? Or is the editing performed by Darwinian selection at cell level (see \( \text{http://tinyurl.com/nd9a9ks} \))? Or is the magnetic body the editor using genome also as its tool as TGD would suggest? What is important that in TGD framework self-organization in 4-D sense implied by Zero Energy Ontology replaces ordinary self organization leading to asymptotic spatial patterns and select spatiotemporal patterns as asymptotic behavioral patterns defining various biological functions. The role of magnetic body is central in this process.

3. Magnetic body contains cyclotron Bose-Einstein condensates and cyclotron frequencies determined by the strength of magnetic field would give for DNA and other biomolecules additional characteristics. In TGD based model for musical harmony DNA codons would correspond quite concretely to 3-chords but played using dark photons (also ordinary music represented as sounds could be transformed to dark photon music). If one accepts the icosahedral model of bio-harmonies predicting genetic code correctly, there would be 256 fundamental harmonies characterised by the allowed collection of 3-chords and they would add to the information carried by DNA molecules. I have constructed a program building random sequences of the allowed chords using the additional harmonic rule that two subsequent chords contain at least one common note and this music sounds rather harmonic (albeit boring in absence of any other elements!)

4. Could one distinguish between different states/phases of DNAs, mRNAs, tRNAs, and amino acids in terms of harmony? Could their functioning depend on the harmony? With the inspiration coming from the connection of emotions and musical harmonies I have proposed that the harmony associated with a gene or organ could correlate with something analogous to an emotional state or mood - maybe micro-mood or microemotion could be the proper notion. Could amino-acids be happy, hilarious, melancholic, sad, depressed? Could one distinguish between different phases of DNA, RNA, tRNA, aminoacid collections characterized by the
8.2 Harmony And Biology

harmony in turn characterizing the of a cell, organelle, organ, or even organism? tRNA defines the map of the harmony associated with DNA codons to amino-acid harmony. Is the information about DNA codon and about corresponding 3-chord represented at the level of magnetic body of amino-acid- that is as the 3-chord, which it represents, and realized as the rules telling with which tRNAs amino-acid can reconnect?

In contrast to DNA codons, which represent local information, harmony could represent holistic information and characterize entire genes or their intronic portions.

2. Problem

There is however a problem. DNA codons coding for the same amino-acid correspond to different 3-chords of harmony. One of these chords corresponds to amino-acid itself and the codons coding for amino-acid correspond to the orbit of this chord under subgroup of isometries of icosahedron moving the triangles of icosahedron along the orbit. This would apply also to mRNA and maybe also to tRNA. The chords at the orbit of amino-acid are isomorphic (intervals are same) and obtained as transposes of each other.

The chords are isomorphic but not identical and this leads to the problem with resonance paradigm unless one gives up the idea that amino-acid corresponds to a unique DNA codon and assumes that there is analog of gauge invariance allowing to choose the preferred codon freely.

1. The assumption about preferred DNA codon could be given up if one can choose the preferred DNA codon freely so that also the magnetic bodies of amino-acids are characterized by 3-chords and thus carry information about what DNA codon coded them. This is possible if one has the analog of fiber space structure with DNA codons coding for amino-acid defining the fiber and amino-acids defining the base. This fiber structure with discrete gauge invariance is strongly suggestive and I have proposed it for two decades ago but it seems that it poses strong conditions on the orbits of the subgroups of isometries of icosahedron.

This condition is very restrictive. Simplifying somewhat: one considers 60 codons decomposing into 20+20+20 codings and each group of 20 codons codes for amino-acids belonging to different groups. There are twenty of them. The 20 triangles of icosahedron correspond to 3 DNA codons each and each of them corresponds to one and only one amino-acid. One has 3 subgroups of isometries corresponding to 20+20+20 decomposition.

Can one perform a global gauge transformations realized as isometries and moving triangles along the orbits of one of the 3 subgroups involved - say isometry $g_1$ of $G_1$? These transformations would move the entire orbits of 2 subgroups involved - call them $G_2$ and $G_3$. What happens to the chords of $G_2$ and $G_3$: is their character changed completely so that these harmonies would be destroyed? It seems that this cannot work. Should one replace $G_2$ and $G_3$ with their automorphs $g_1G_2g_1^{-1}$ and $g_1G_3g_1^{-1}$. Does this make sense? 3-chords defining give orbit should be invariant under automorphisms of $G_i$? This does not seem to be a realistic condition.

2. Could different automorphs correspond to different collections of chords physically just as global gauge transformations generate different physical situations? Isometries of groups $G_i$ would therefore define physically different realizations of bio-harmonies such that for each of them only one of the DNA codons coding for given amino-acid could actually perform the coding. Ordinary genetic code with many-to-one correspondence would make sense in statistical sense only. If this is true, the cyclotron frequency 3-chord assignable to amino-acid depends on the DNA coding it and implies physical distinctions.

3. One can consider also a third alternative. DNA codon with same 3-chord as coding for amino-acid is in special role in that only it can resonate with the amino-acid! Could DNA codons coding correspond to same cyclotron frequency triplet (magnetic fields) but different value of $\hbar_{eff}$ so that one would have chord with respect to energy rather than frequency. Different values of $\hbar_{eff}$ for DNA codons coding for the same amino-acid would scale their cyclotron frequencies to the same amino-acid frequency while keeping cyclotron energies invariant? Cyclotron energy ratios for codons correspond to rational valued ratios $E_i/E_j = h_{eff}(i)/h_{eff}(j) = n(i)/n(j)$. Amino-acid would correspond to fixed $h_{eff}$ and this creates a
problem: can DNA codon code for amino-acid with different value of $h_{eff}$. This option does not look attractive.

Second option looks most plausible. Of course, it is early to talk about a prediction: it might well be that I have mis-understood something.

3. Questions about bio-harmony

One can pose a lot of questions about bio-harmony.

1. It is not necessary to assign any interpretation on the harmony. Just the harmony could be enough if it is forced to be same for DNA, corresponding mRNA, tRNA, and aminoacids. One can however make questions. Is the harmony inherited invariant and could it distinguish between different personality types about which we learned in old books of psychology? Or could the harmonies correlate with our own moods?

2. Could differentiation selecting particular genes as expressed genes apply also to harmonies so that given gene would correspond only to a particular harmony and different copies of gene could correspond to different harmonies. Could this selection rely on the same mechanisms as ordinary differentiation realized in terms of epigenetic mechanisms and DNA editing? From the magnetic bodies of genes the harmony would be automatically transferred to the magnetic bodies of mRNA, tRNA and aminoacids since otherwise the transcription and translation do not work since magnetic bodies do not have common resonance frequencies and reconnection and resonant interaction is not possible.

3. Does given harmony characterize given gene or the entire cell? All basic biomolecules associated with a gene would naturally correspond to the same harmony. If the rRNAs associated with ribosomes are in harmony mutually cellular harmony seems to be the only option. If ribosomes have their own harmonies, only certain ribosomes can translate given gene. This would bring in additional control tool. The most plausible picture is that the situation depends on what happens in the self-organization process. Some organs/organisms are more harmonious, others not so harmonious. Harmony need not be given fixed to remain the same: magnetic body can have motor actions changing the cyclotron frequencies. Moods could reflect the character of harmony at gene level.

4. Does magnetic body control the differentiation by posing restrictions on gene expression or vice versa? The idea about magnetic body as intentional agent suggests that the first option is correct. There would be hierarchy of magnetic bodies with magnetic bodies at the higher level controlling bodies at the lower level. The value of Planck constant would label the hierarchy levels and also DNA codons would be characterized by "intelligence quotient" defined by $h_{eff}/h$. This would be nothing but the analog for the hierarchy of program modules and I have earlier considered the realization of this hierarchy [LS].

5. The selection of harmony could take place and be analogous to cell differentiation. This would be a self-organization process in which magnetic bodies of genes, cells, etc., tune themselves to resonance with each other by modifying their magnetic fields by controlling their thickness (for monopoles flux the flux is invariant). Something analogous to the development of social skills. This could pose resonance as a constraint on processes like replication, transcription, reverse transcription, silencing, enhancing, editing, etc.... It might induce the differentiation at gene level.

Editing processes for genome could be seen as being induced by the motor actions of the magnetic body involving reconnection and change of the value of $h_{eff}$ changing the length of the flux tube and bringing biomolecules near to each other or separating them. This selection would also apply to the intrinsic part of DNA proposed to be responsible for topological quantum computation like processes. The copies of same fragment appearing in intrinsic portion and copies of genes could correspond to different harmonies.

4. Can the notions of magnetic body and bio-harmony explain something that ordinary genetic cannot?
It would be nice to identify some biological phenomenon difficult to understand in standard framework but having an elegant explanation in terms of magnetic body.

1. The notion of harmony could manifest itself at the level of genes as different expressions for the copies of same gene if they correspond to different notions of harmony. The copies of gene are known as alleles (see [http://tinyurl.com/bpee49t](http://tinyurl.com/bpee49t)). The alleles can indeed give rise to different phenotypic traits such as different pigmentation.

2. Morphogenesis provides examples of this kind of phenomena [I28, I29, I31]. The first key idea is that DNA and cell replication is induced by the replication of magnetic bodies serving as information carriers [K30]. The second key idea is that in zero energy ontology (ZEO) magnetic body is 4-dimensional and represents behavioral patterns rather than only 3-dimensional patterns. For instance, memory as behavioral patterns can be inherited by the piece of planaria worm not containing the brain. The explanation could be that the magnetic body carries behavioral patterns replicated in the splitting of the worm.

3. Epigenetics (see [http://tinyurl.com/4xpwcm](http://tinyurl.com/4xpwcm)) studies changes of gene expression not caused by the change of DNA itself. Epigenome (see [http://tinyurl.com/y9xkfb2u](http://tinyurl.com/y9xkfb2u)) is the highly dynamic part of DNA controlling expression of the rather stable part of genome. One might regard stable part of genome as hardware and epigenome as topological quantum computer programs assignable to magnetic body and modifying gene expression epigenetically. Comment sign in computer code serves as a computer scientific metaphor for epigenetic control by repression.

The modelling of epigenesis in terms of magnetic body and bio-harmonies deserves a separate discussion.

1. The modification of transcription rate is the basic tool of epigenetic regulation. There are two basic mechanisms involved. Histone modification (see [http://tinyurl.com/y8ywse5v](http://tinyurl.com/y8ywse5v)) affects the histones of chromatin so that the transcription is repressed or activated. Histone modification takes place by several mechanisms. DNA methylation occurs for CpG pair and if it occurs for a promoter region it represses the transcription and serves as a kind of gene lock. The degree of methylation serves as a measure for the effectiveness of repression. I do not know whether the locking is absolute at the level of single gene or whether only the transcription rate is reduced. Two mechanisms are mentioned in the Wikipedia article (see [http://tinyurl.com/y9kwrvwx](http://tinyurl.com/y9kwrvwx)). Methylation can impede geometrically some step in the transcription. Methylation site can be also accompanied by proteins affecting histones in chromatin and in this manner impede transcription.

2. The notions of magnetic body and bio-harmony suggest an alternative - one might even hope fundamental - mechanism of repression. Methylation (histone modification) could affect some cyclotron frequency associated with DNA codon (histone). In the optimal situation for transcription the DNA and protein catalyzing the transcription or mRNA are in resonance. When cyclotron resonance condition is not exactly satisfied, the reconnection rate for the U-shaped flux tubes associated with the molecules involved in the process is reduced and also transcription is repressed.

I have considered also the radical possibility that the dynamics at the level of magnetic body is fundamental for biology and that magnetic body defines templates for the bio-molecular self-organization making dark matter dynamics visible. This is probably too extremist view and it would seem that biochemistry affects the cyclotron frequencies assignable to the magnetic body by affecting the strengths of magnetic fields also at dark magnetic flux tubes.

3. The notions of epigenetic code (see [http://tinyurl.com/y8ztzzza](http://tinyurl.com/y8ztzzza)) and histone code (see [http://tinyurl.com/y854w58p](http://tinyurl.com/y854w58p)) have been proposed. Epigenetic code would consist of histone modifications and additional modifications such as DNA methylation. The codeword of the epigenetic code could code for some larger unit than protein: say gene or entire cell. The hypothesis is that the chromatin-DNA interactions are induced by histone tail modifications (such as methylation, acetylation, ADP-ribosylation, ubiquitination, citrullination, and phosphorylation). There are 4 histones and the position of modification varies as well
as the modifier (the above modifications are not the only ones) so so that the number of modifications is very large.

The addition of bioharmonies to the genetic information could simplify the situation dramatically since the modifications could be seen as defining of of the 256 bio-harmonies with 64 chords each (this for fixed scale which varies if the value of magnetic field strength is varied: biophoton spectrum in visible is proposed to represent the range of values of magnetic field). The most plausible starting hypothesis is that given harmony characterizes the gene. Much simpler option would be that the harmony characterizes entire cell or even group of cells. If the modification by kicking cyclotron frequency out of harmony is enough to repress transcription, almost endless number of bio-chemical manners to achieve would exist but the epigenetic code could be very simple at the basic level as TGD would predict. Each bioharmony \( L^3 \) \( K^{18} \) would provide a representation of genetic code in terms of 3-chords predicting correctly the DNA-amino-acid correspondence (there are actually two slightly differing codes explaining the presence of 21st and 22nd amino-acid and deviations from the standard code). The states of dark protons (or neutrons) are also proposed to realize genetic code \( L^1 \) \( K^{10} \): it is an open question whether these codes imply each other as they should.

4. The understanding of transgenerational epigenetic inheritance (see \[http://tinyurl.com/h6qg64c\]) raises difficult challenges. One should understand how histone modification and DNA methylation are transferred to daughter cells in cellular division or inherited by the offspring. Transgenerational interaction of the genomes seems necessary. In TGD framework the interaction of magnetic bodies of via resonance mechanism could transfer the epigenetic programs to the offspring. Offspring could "learn" the epigenetic programs of the mother by tuning.

5. Gregory Carey (see \[http://tinyurl.com/ydyznsaq\]) gives nice real life examples about the complexities of epigenesis identified quite generally as gene regulation (see \[http://tinyurl.com/zb97cgs\]). He compares the gene regulation involved with the handling of a stressful situation to “nightmarish Rube Goldberg mousetrap” and sees the process as extremely ineffective from engineering point of view. For instance, the hormones secreted to blood circulation are distributed to the entire body. The whole thing could be carried out in brain! He also wonders why evolution is so inefficient. All cells have same genome although most of the genes are silenced. Second strand of DNA is totally un-used and most of DNA consists of introns. His explanation is that evolution does not make long term plans but finds just a solution to a particular without thinking it from a wider perspective: “If it ain’t broke, don’t fix it”.

I tend to see this differently. If entire body is coherent quantum entity, engineering based thinking does not make sense. Entire body and also magnetic body must be informed from the stress situation since the reaction is holistic. The genes which are not used for gene expression might be used for other purposes. Topological quantum computation could be this purpose in TGD framework and repressed genes could be thus used for quantum information processing. Information processing could be actually the dominating function of the DNA of higher vertebrates.

To sum up, magnetic body could be seen as the "boss" controlling the gene expression and also the evolution of genome in longer scales. Magnetic body would use bio-molecular mechanisms for its purposes. This would bring in a new kind of inheritance: bio-harmony would be inherited. The most spectacular almost-prediction would be that genetic code is many-to-one only in statistical sense.

5. **RNA is transferred between soma cells and germ cells**

The basic question of epigenesis is how the information between soma cells and germ cells is transferred. In standard genetic the transfer of RNA or DNA molecules is necessary to achieve this. In TGD dark DNA, RNA, tRNA, and aminocids consisting of dark nucleons realized as nuclear strings and accompanied by the corresponding biomolecules is one possibility. The extremist view would be that the dynamics of the dark variants of basic bio-molecules induces the dynamics of their molecular shadows making them only visible. Also the transfer of information as cyclotron
8. Harmony And Biology

Radiation can be considered in TGD framework and cyclotron resonance could serve as a fundamental mechanism of epigenetic control. The above model suggests that epigenetic control mechanisms rely on resonance mechanism for 3-chords associated with DNA codons and other biomolecules giving them “names” is also at work besides purely geometrical silencing.

The popular article “No Sex Required: Body Cells Transfer Genetic Info Directly Into Sperm Cells, Amazing Study Finds” (see http://tinyurl.com/hhdth5j) summarizing the findings discussed in the article [118] (see “Soma-to-Germline Transmission of RNA in Mice Xenografted with Human Tumour Cells: Possible Transport by Exosomes” (see http://tinyurl.com/yde7wb55) as very interesting concerning this basic question.

The abstract of the article gives for a professional a readable summary.

Mendelian laws provide the universal founding paradigm for the mechanism of genetic inheritance through which characters are segregated and assorted. In recent years, however, parallel with the rapid growth of epigenetic studies, cases of inheritance deviating from Mendelian patterns have emerged. Growing studies underscore phenotypic variations and increased risk of pathologies that are transgenerationally inherited in a non-Mendelian fashion in the absence of any classically identifiable mutation or predisposing genetic lesion in the genome of individuals who develop the disease. Non-Mendelian inheritance is most often transmitted through the germline in consequence of primary events occurring in somatic cells, implying soma-to-germline transmission of information. While studies of sperm cells suggest that epigenetic variations can potentially underlie phenotypic alterations across generations, no instance of transmission of DNA- or RNA-mediated information from somatic to germ cells has been reported as yet.

To address these issues, we have now generated a mouse model xenografted with human melanoma cells stably expressing EGFP-encoding plasmid. We find that EGFP RNA is released from the xenografted human cells into the bloodstream and eventually in spermatozoa of the mice. Tumor-released EGFP RNA is associated with an extracellular fraction processed for exosome purification and expressing exosomal markers, in all steps of the process, from the xenografted cancer cells to the spermatozoa of the recipient animals, strongly suggesting that exosomes are the carriers of a flow of information from somatic cells to gametes. Together, these results indicate that somatic RNA is transferred to sperm cells, which can therefore act as the final recipients of somatic cell-derived information.

Some background is needed to understand this rather technical summary.

1. Darwinism has dominated biology since Darwin. The rules of classical Mendelian inheritance conform with the Darwinian view and can be reduced to genetic level. Various traits are inherited genetically by sexual reproduction and genome would change during lifetime only through mutations. Genome changes extremely slowly by random changes for offspring from which selection pressures choose the survivors.

Lamarckian view in turn assumed that the external circumstances experienced by organism leave a trace, which can be inherited but it could not be formulated in terms of modern molecular biology whereas the Darwinian dogma could be formulated in terms of Weissman’s genetic barrier. Information flows from germ cells to soma but never in opposite direction. If it would do so, the soma interacting with environment could transfer information to germ cells and the experiences during lifetime could leave inheritable trace to germ cells.

An analogous dogma is that information is always transcribed from DNA to RNA to proteins but never in opposite direction. It is now known that this takes place in case of viruses and retroviruses: there are so called jumping genes which can also make copies of themselves. 5 per cent of human genome consists of endogenous retroviruses capable of doing the same. The huge genome of maize is due to this kind of process.

2. The development epigenetics has started to shatter the belief on Weissmann’s genetic barrier. Gene expression is not fixed by genome alone and can be change even when genes are unaffected. Silencing of genes by DNA methylation and histone modification allow to modify gene expression. Silencing is essentially a locking of gene preventing its expression by transcription followed by translation.

It is now known that epigenetic changes in the gene expression can be inherited. The mechanisms are still poorly understood. What seems however clear the genome is more like a
slowly changing hardware and gene expression or whatever is behind it is the software and programs can change very rapidly by just adding or deleting comment signs in the code. A deeper understanding of this software is needed.

3. Epigenetic inheritance requires that genetic information is transferred from soma cells to germ cells. If only DNA or RNA are capable of representing genetic information, then DNA or RNA must be transferred from soma cells to germ cells. No instance of direct DNA or RNA mediated information from soma to germ cells had been observed before the above mentioned experiments. One can of course challenge the assumption about DNA and RNA as the only representations of genetic information.

The basic idea of the experiment was simple. Use a marker for RNA by using plasmids (DNA strands not belonging to chromosomes) genetically engineered to code for a marker protein making itself visible by fluorescence. Then one just follows the fate of these proteins generated in soma cells and looks whether they end up inside germ cells and how this happens.

More technically: mouse model was xenografted with human melanoma cells stably expressing EGFP-coding plasmid (expressed in a manner possibly evoking emotions: human melanoma cancer tissue was implanted in mouse). EGFP-RNA is released from xenografted human cells to blood. One just looks whether it eventually ends up to the sperm cells of mice and tries to identify the transfer mechanism. Only transfer to sperm cells was studied. One might expect that the transfer of RNA can happen also to ovum. I guess that the sperm cells are easier to study.

What was observed?

1. The transfer of RNA from soma cells to sperm cells was indeed found to occur. The transferred RNA can in turn induce epigenetic effects in germ cells known to be inherited by a mechanisms, which however remain poorly understood. Epigenetic mechanisms seem to be involved in the cases considered so that DNA is not changed, only its expression.

2. The transfer mechanism was identified. The transferred RNA is contained by exosomes analogous to synaptic vesicles transferring neurotransmitters from presynaptic to postsynaptic cell. Transfer of RNA takes place via fusion of the membranes just like transfer of neurotransmitters. Maybe genetic engineering using exosomes or analogous structures to transfer the needed material to cells has been tried.

The implications of the findings are dramatic but already implied by the earlier work in epigenetics. What is important that Lamarckian view can be now defended by a concrete genetic mechanism. Lamarckism implies that the time scale of inheritance becomes the time scale for the appearence of a new generation. Nutrition, environment, lifestyle and even meditation and similar practices, are already now known to affect gene expression on daily basis: we are not victims of genetic determinism and are epigenetically responsible for our own well-being. Epigenetic information can be transferred also to germ cells so that we responsible also for the well-being of our children. Our children suffer our sins and share our sufferings.

The precise mechanism of inheritance of epigenetic modifications remains still poorly understood although it seems that the transfer or RNA to germ cells occurs. There are also other hints: it is known that alleles (variants of game gene) can express themselves differently. One allele can also induce other allele to express in the same manner. Some kind of “social pressure” like interaction seems to be involved.

As explained, TGD suggests the notion of magnetic body and cyclotron resonance as this interaction. The DNA of offspring get tuned to the DNA of mother during pregnancy and this gives to epigenetic inheritance. Various epigenetic mechanisms such as methylation and histone modification could affect cyclotron frequencies besides purely geometric modifications of DNA and locking at the level of gene could be accompanied kicking out of tune at the level of magnetic body. In this framework the transfer of RNA to germ cells would be necessary to affect the cyclotron frequencies.

8.2.5 $E_8$ symmetry, harmony, and genetic code

Bee gave in Facebook a link to an article about a connection between icosahedron and $E_8$ root system [BS] (see http://tinyurl.com/zotpm4b). The article (I have seen an article about the same idea earlier but forgotten it!) is very interesting.
The article talks about a connection between icosahedron and $E_8$ root system (see [http://tinyurl.com/y7csb6uh](http://tinyurl.com/y7csb6uh)). Icosahedral group has 120 elements and its double covering $2 \times 120 = 240$ elements. Remarkably, $E_8$ root system has 240 roots. $E_8$ Lie algebra is 248 complex-dimensional contains also the 8 commuting generators of Cartan algebra besides roots: it is essential that the fundamental representation of $E_8$ coincides with its adjoint representation. The double covering group of icosahedral group acts as the Weyl group $E_8$. A further crucial point is that the Clifford algebra in dimension $D = 3$ is 8-D.

One starts from the symmetries of 3-D icosahedron and ends up with 4-D root system $F_4$ assignable to Lie group and also to $E_8$ root system. $E_8$ defines a lattice in 8-D Euclidian space: what is intriguing that dimensions 3,4, 8 fundamental in TGD emerge. To me this looks fascinating - the reasons will be explained below.

1. **What I might have understood**

I try to explain what I have possibly understood.

1. The notion of root system is introduced. The negatives of roots are also roots but not other multiples. Root system is crystallographic if it allows a subset of roots (so called simple roots) such that all roots are expressible as combinations of these simple roots with coefficients having the same sign. Crystallographic root systems are special: they correspond to the fundamental weights of some Lie algebra. In this case the roots can be identified essentially as the quantum numbers of fundamental representations from which all other representations are obtained as tensor products. Root systems allow reflections as symmetries taking root system to itself. This symmetry group is known as Coxeter group and generalizes Weyl group. Both $H_3$ and $H_4$ are Coxeter groups but not Weyl groups.

2. 3-D root systems known as Platonic roots systems ($A_3$, $B_3$, $H_3$) assignable to the symmetries of tetrahedron, octahedron (or cube), and icosahedron (or dodecahedron) are constructed. The root systems consist of 3 suitably chosen unit vectors with square equal to 1 (square of reflection equals to one) and the Clifford algebra elements generated by them by standard Clifford algebra product. The resulting set has a structure of discrete group and is generated by reflections in hyper-planes defined by the roots just as Weyl group does. This group acts also on spinors and one obtains a double covering SU(2) of rotation group SO(3) and its discrete subgroups doubling the number of elements. Platonic symmetries correspond to the Coxeter groups for a "Platonic root system" generated by 3 unit vectors defining the basis of 3-D Clifford algebra. $H_3$ is not associated with any Lie algebra but $A_3$ and $B_3$ are.

Pinors (spinors) correspond to products of arbitrary/even number of Clifford algebra elements. Spinors induced orientation preserving transformations and pinors also orientation reversing ones. They mean something else than usually a bein identified as elements of the Clifford algebra acting and being acted on from left or right by multiplication so that they always behave like spin 1/2 objects since only the left(right)-most spin is counted. The automorphisms involve both right and left multiplication reducing to SO(3) action and see the entire spin of the Clifford algebra element.

3. The 3-D root systems ($A_3$, $B_3$, $H_3$) are shown to allow an extension to 4-D root systems known as ($D_4$, $F_4$, $H_4$) in terms of 3-D spinors. $D_4$ and $F_4$ are root systems of Lie algebras (see [http://tinyurl.com/y97dzqc2](http://tinyurl.com/y97dzqc2)). $F_4$ corresponds to non-simply-laced Lie group related to octonions. $H_4$ is not a root system of any Lie algebra.

4. The observation that the dimension of Clifford algebra of 3-D space is $2^3 = 8$ and thus allows imbedding of at most 8-D root system must have inspired the idea that it might be possible to construct the root system of $E_8$ in 8-D Clifford algebra from 240 pinors of the double covering the 120 icosahedral reflections. Platonic solids would be behind all exceptional symmetry groups since $E_6$ and $E_7$ are subgroups of $E_8$ and the construction should give their root systems also as low-dimensional root systems.

2. **McKay correspondence**

The article explains also McKay correspondence stating that the finite subgroups of rotation group SU(2) correspond to simply laced affine algebras assignable with ADE Lie groups.
1. One considers the irreducible representations of a finite subgroup of the rotation group. Let the number of non-trivial representations be \( m \) so that by counting also the trivial representation one has \( m + 1 \) irreps altogether. In the Dynkin diagram of affine algebra of group with \( m \)-D Cartan algebra the trivial representation corresponds to the added node. One decomposes the tensor product of given irrep with the spin 2 representation into direct sum of irreps and constructs a diagram in which the node associated with the irrep is connected to those nodes for which corresponding representation appears in the direct sum. One can say that going between the connected nodes corresponds to forming a tensor product with the fundamental representation. It would be interesting to know what happens if one constructs analogous diagrams by considering finite subgroups of arbitrary Lie group and forming tensor products with the fundamental representation.

2. The surprising outcome is that the resulting diagram corresponds to a Dynkin diagram of affine (Kac-Moody) algebra of ADE group with Cartan algebra, whose dimension is \( m \). Cartan algebra elements correspond to tensor powers of fundamental representation: can one build any physical picture from this? For \( m = 6, 7, 8 \) one obtains \( E_6, E_7, E_8 \). The result of the article implies that these 3 Lie-groups correspond to basis of 3 3-D unit identified as units of Clifford algebra: could this identification have some concrete meaning as preferred non-orthogonal 3-basis?

3. McKay correspondence emerges also for inclusions of hyper-finite factors of type \( II_1 \) \( [K28] \). The integer \( m \) characterizing the index of inclusion corresponds to the dimensions of Cartan algebra for ADE type Lie group. The inclusions of hyperfinite factors (HFFs) are characterized by integer \( m \geq 3 \) giving the dimension of Cartan algebra of ADE Lie groups (there are also C, F and G type Lie groups). \( m= 6,7,8 \) corresponds to exceptional groups \( E_6, E_7, E_8 \) on one hand and to the discrete symmetry groups of tetrahedron, octahedron, icosahedron on the other hand acting as symmetries of corresponding 3-D non-crystallographic systems and not allowing interpretation as Weyl group of Lie group.

3. Connection with the TGD based model of harmony

These findings become really exciting from TGD point of view when one recalls that the model for bioharmony \([K18], [L3]\) (see [http://tinyurl.com/yad4tqwl]) for 12-note harmonies central in classical music in general relies on icosahedral geometry. Bioharmonies would add something to the information content of the genetic code: DNA codons consisting of 3 letters A,T,C,G would correspond to 3-chords defining given harmony realized as dark photon 3-chords and maybe also in terms of ordinary audible 3-chords. This kind of harmonies would be roughly triplets of 3 basic harmonies and there would be 256 of them (the number depends on counting criteria). The harmonies could serve as correlates for moods and emotional states in very general sense: even biomolecules could have “moods”. This new information should be seen in biology. For instance, different alleles of same gene are known to have different phenotypes: could they correspond to different harmonies? In epigenetics the harmonies could serve as a central notion and allow to realize the conjectured epigenetic code and histone code. Magnetic body and dark matter at them would be of course the essential additional element.

The inspiring observations are that icosahedron has 12 vertices - the number of notes in 12-note harmony and 20 faces- the number of amino-acids and that DNA codons consist of three letters - the notes of 3-chord.

1. Given harmony would be defined by a particular representation of Pythagorean 12-note scale represented as self-non-intersecting path (Hamiltonian cycle) connecting the neighboring vertices of icosahedron and going through all 12 vertices. One assumes that neighboring vertices differ by one quint (frequency scaling by factor 3/2): quint scale indeed gives full octave when one projects to the basic octave. One obtains several realizations (in the sense of not being related by isometry of icosahedron) of 12-note scale. These realizations are characterized by symmetry groups mapping the chords of harmony to chords of the same harmony. These symmetry groups are subgroups of the icosahedral group: \( Z_6, Z_4, \) and two variants of \( Z_3 \) (generated by rotation of \( \pi \) and by reflection) appear. Each Hamiltonian cycle defines a particular notion of harmony with allowed 3-chords identified by the 20 triangles of icosahedron.
2. Pythagoras is trying to whisper me an unpleasant message: the quint cycle does not quite close! This is true. Musicologists have been suffering for two millennia of this problem. One must introduce 13th note differing only slightly from some note in the quint cycle. At geometrical level one must introduce tetrahedron besides icosahedron - only four notes and four chords and gluing along one side to icosahedron gives only one note more. One can keep tetrahedron also as disjoint from icosahedron as it turns out: this would give 4-note harmony with 4 chords something much simpler that 12- note harmony.

3. The really astonishing discovery was that one can understand genetic code in this framework. First one takes three different types of 20-chord harmonies with group $\mathbb{Z}_6$, $\mathbb{Z}_4$, and $\mathbb{Z}_2$ defined by Hamiltonian cycles: this can be done in many different maners (there are 256 of them). One has $20+20+20$ chords and one finds that they correspond nicely to $20+20+20=60$ DNA codons: DNA codons coding for a given amino-acid correspond to the orbit of the triangle assigned with the amino-acid under the symmetry group of harmony in question. The problem is that there are 64 codons, not 60. The introduction of tetrahedron brings however 4 additional codons and gives 64 codons altogether. One can map the resulting 64 chord harmony to icosahedron with 20 triangles (aminoacids) and the degeneracies (number of DNA codons coding for given amino-acid in vertebrate code) come out correctly! Even the two additional troublesome amino-acids Pyl and Sec appearing in Nature and the presence of two variants of genetic code (relating to two kinds of $\mathbb{Z}_2$ subgroups) can be understood.

4. **What could the interpretation of the icosahedral symmetry?**

An open problem is the proper interpretation of the icosahedral symmetry.

1. A reasonable looking guess would be that it quite concretely corresponds to a symmetry of some biomolecule: both icosahedral or dodecahedral geometry give rise to icosahedral symmetry. There are a lot of biomolecules with icosahedral symmetry, such as clathrate molecules at the axonal ends and viruses. Note that dodecahedral scale has 20 notes - this might make sense for Eastern harmonies - and 12 chords and there is only single dodecahedral Hamiltonian path found already by Hamilton and thus only single harmony. Duality between East and West might exist if there is mapping of icosahedral notes and to dodecahedral 5-chords and dodecahedral notes to icosahedral 3-chords and different notions of harmony are mapped to different notions of melody - whatever the latter might mean!).

2. A more abstract approach tries to combine the above described pieces of wisdom together. The dynamical gauge group $E_8$ (or Kac-Moody group) emerging for $m=8$ inclusion of HFFs is closely related to the inclusions for the fractal hierarchy of isomorphic sub-algebras of supersymplectic subalgebra. $h_{eff}/h = n$ could label the sub-algebras: the conformal weights of sub-algebra are be $n$-multiples of those of the entire algebra. The integers $n_i$ resp. $n_f$ for included resp. including super conformal sub-algebra would be naturally related by $n_f = m \times n_i$. $m = 8$ would correspond to icosahedral inclusion and $E_8$ would be the dynamical gauge group characterizing dark gauge degrees of freedom. The inclusion hierarchy would allow to realize all ADE groups as dynamical gauge groups or more plausibly, as Kac-Moody type symmetry groups associated with dark matter and characterizing the degrees of freedom allowed by finite measurement resolution.

3. $E_8$ as dynamical gauge group or Kac-Moody group would result from the super-symplectic group by dividing it with its subgroup representing degrees of freedom below measurement resolution. $E_8$ could be the symmetry group of dark living matter. Bioharmonies as products of three fundamental harmonies could relate directly to the hierarchies of Planck constants and various generalized super-conformal symmetries of TGD! This convergence of totally different theory threads would be really nice!

5. **Experimental indications for dynamical $E_8$ symmetry**

Lubos (see [http://tinyurl.com/htjp55h](http://tinyurl.com/htjp55h)) (thanks to Ulla for the link to the posting of Lubos) has written posting about experimental finding of $E_8$ symmetry emerging near the quantum critical.
point of Ising chain at quantum criticality at zero temperature. Here is the abstract (see [http://tinyurl.com/zulzk9y](http://tinyurl.com/zulzk9y)):

Quantum phase transitions take place between distinct phases of matter at zero temperature. Near the transition point, exotic quantum symmetries can emerge that govern the excitation spectrum of the system. A symmetry described by the $E_8$ Lie group with a spectrum of eight particles was long predicted to appear near the critical point of an Ising chain. We realize this system experimentally by using strong transverse magnetic fields to tune the quasi-one-dimensional Ising ferromagnet $\text{CoNb}_2\text{O}_6$ (cobalt niobate) through its critical point. Spin excitations are observed to change character from pairs of kinks in the ordered phase to spin-flips in the paramagnetic phase. Just below the critical field, the spin dynamics shows a fine structure with two sharp modes at low energies, in a ratio that approaches the golden mean predicted for the first two meson particles of the $E_8$ spectrum. Our results demonstrate the power of symmetry to describe complex quantum behaviors.

Phase transition leads from ferromagnetic to paramagnetic phase and spin excitations as pairs of kinks are replaced with spin flips (shortest possible pair of kinks and loss of the ferromagnetic order). In attempts to interpret the situation in TGD context, one must however remember that dynamical $E_8$ is also predicted by standard physics so that one must be cautious in order to not draw too optimistic conclusions.

In TGD framework $h_{eff}/\hbar \geq 1$ phases or phase transitions between them are associated with quantum criticality and it is encouraging that the system discussed is quantum critical and 1-dimensional.

1. The large value of $h_{eff}$ would be associated with dark magnetic body assignable to the magnetic fields accompanying the $E_8$ “mesons”. Zero temperature is not a prerequisite of quantum criticality in TGD framework.

2. One should clarify what quantum criticality exactly means in TGD framework. In positive energy ontology the notion of state becomes fuzzy at criticality. For instance, it is difficult to assign the above described “mesons” with either ferromagnetic or paramagnetic phase since they are most naturally associated with the phase change. Hence Zero Energy Ontology (ZEO) might show its power in the description of (quantum) critical phase transitions. Quantum criticality could correspond to zero energy states for which the value of $h_{eff}$ differs at the opposite boundaries of causal diamond (CD). Space-time surface between boundaries of CD would describe the transition classically. If so, then $E_8$ “mesons” would be genuinely 4-D objects - “transitons” - allowing proper description only in ZEO. This could apply quite generally to the excitations associated with quantum criticality. Living matter is key example of quantum criticality and here “transitons” could be seen as building bricks of behavioral patterns. Maybe it makes sense to speak even about Bose-Einstein condensates of “transitons”.

The finding suggests that quantum criticality is associated with the transition increasing $n_{eff} = h_{eff}/\hbar$ by factor $m = 8$ or its reversal - maybe the standard value $n_{eff}(i) = 1$. $n_{eff}(f) = 8$ could correspond to the ferromagnetic phase having long range correlations. Could one say that at the side of criticality (say the ”lower” end of CD) the $n_{eff}(f) = 8$ excitations are pure gauge excitations and thus ”below measurement resolution” but become real at the other side of criticality (the ”upper” end of CD)?

3. The 8 “mesons” associated with spin excitations naturally correspond to the generators of the Cartan algebra of $E_8$. If the “mesons” belong to the fundamental (= adjoint) representation of $E_8$, one would expect 120+120 additional particles with non-vanishing $E_8$ charges. Why only Cartan algebra? Is the reasons that Cartan algebra is in preferred role in the representations of Kac-Moody algebras in that charged Kac-Moody generators can be constructed from Cartan algebra generators by standard construction used also in string models. Could this explain why one expects only 8 “mesons”. Are charged “mesons” labelled by the elements of double covering of icosahedral group more difficult to excite?
8.3 Icosahedral Harmonies

In the following the icosahedral harmonies are discussed in detail. This includes overall summary and tables giving the 20 3-chords of the harmonies and illustrations of the Hamiltonian cycles.

8.3.1 About symmetries of the icosahedral harmonies

Some words about the symmetries associated with the icosahedral harmonies and genetic code are in order.

There are 3 different kind of bio-harmonies characterized partially by the symmetry group which can be $Z_6$, $Z_4$, or $Z_2$ which acts either as rotations or reflections.

1. The first variant as $Z_3^{rot} \times Z_2^{refl}$ subgroup of icosahedral group as symmetries and its orbits correspond to 3 6-plets and 1 2-plets for which $Z_3$ leaves the triangle invariant. The counterparts for the orbits are 3 DNA 6-plets and one 2-plet.

2. The second variant has $Z_4$ symmetry generated by two commuting reflection as symmetries as is obvious from figures ??, ??: the reflections act on vertical and horizontal coordinates. The orbits are five 4-plets of chords. Vertical reflection induces half-octave shift and horizontal one permutes the note sequences $B♭CDG♯F♯E$ and $D♯C♯HFGA$.

3. $Z_2^{rot}$ or $Z_2^{refl}$ acts as symmetries of the remaining 3+5 cycles. The covering space of 10 amino-acids involved defined by 20 DNA codons decomposes to 10 2-plets.

The 2-fold rotation symmetry of the Hamiltonian cycles is obvious from the illustration ??: it corresponds to 6-quint rotation and the chord sets must be invariant under this rotation. This rotation corresponds to the 1/2 octave shift realized as rotation. These symmetries are realized as “coordinate transformations” for the cycle - a curve in the “imbedding space” defined by icosahedron but induced from the “imbedding space symmetries” acting as isometries of icosahedron.

DNA codons have also almost exact $Z_2$ symmetry discussed in [K26, K5, K7].

1. For the last codon the reflection A-T, C-G is an almost symmetry broken only for special cases. This approximate symmetry could be understood as following from the fact that the number of DNAs coding given amino-adic is even in most cases. The exceptions are ile, met, trp coded by odd number of DNA codons. By mapping DNAs to binary sequences one can order the situation so that the 6:th binary digit is the almost-symmetry digit.

2. What is trivial is that RNA has chosen the third bi-digit to be the almost symmetry digit with the ordering UCAG of the nucleotides so that a genuine physical symmetry is in question. An interesting question is how this symmetry relates to the model of genetic code based on tetra-icosahedral orbits.

The restriction of DNAs to 60 icosahedral DNAs demonstrates that this symmetry originates from the icosahedral $Z_2$. The tetrahedral extension of the code breaks this symmetry by extending ile and punct multiples by one codon and introducing also 4 singlets met, trp, Pyl, and Sec.

The detailed correspondence between chords of the harmony and DNA codons is also a problem to be solved.

1. The correspondence matters in the proposed scenario since the chords at at the orbits are different and the gluing of tetrahedron breaks the symmetry in $Z_2$ sectors so that quint rule determining harmonic DNA sequences is different.

2. The common face of tetrahedron and icosahedron corresponds to punct so that the quint rule for different representations says something about the pairs of form codon-stop codon that is about the codon preceding the last codon of gene! This codon could allow to recognize what Hamiltonian cycle is in question. If C-major is one of the added chords, stop codons correspond to what was $C6 = CGA$ chord and its $Z_2$ image, which is $X7$ type chord. By the strongest form of the quint rule only the chords having common notes with these chords would correspond to DNA codons of $Z_6$ and $Z_4$ cycles which can precede stopping codon.
8.3 Icosahedral Harmonies

Table 5: Notation of chords inspired by popular music notations.

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>( CEG \equiv C )</td>
<td>( CD_2G \equiv C_m )</td>
<td>( CD_2F^*_3 \equiv C^o )</td>
<td>( CEG_2 \equiv C_{aug} )</td>
</tr>
<tr>
<td>( CFG \equiv C_4 )</td>
<td>( CF_2G \equiv C_{4+} )</td>
<td>( CGG_2 \equiv C_{6-} )</td>
<td>( CGA \equiv C_6 )</td>
</tr>
<tr>
<td>( CGB \equiv C_7 )</td>
<td>( CGB \equiv C_{maj7} )</td>
<td>( CGC_2 \equiv C_{9-} )</td>
<td>( CGD \equiv C_9 )</td>
</tr>
</tbody>
</table>

3. There are some restrictions on the correspondence. \( Z_2^{refl} \) symmetry would correspond to the flipping of the 6th bit for the bit representation defined by nucleotides representing 2-bits in the case of \( Z^3 = Z_3 \times Z_2^{refl} \). \( Z_4 = Z_2^{rot} \times Z_2^{refl} \). For \( Z_2 = Z_2^{rot} \) the role of \( Z_2^{refl} \) must be taken by \( Z_2^{rot} \). One can of course ask whether \( Z_2^{rot} \) cycles are realized at all. For \( Z_4 \) cycles \( Z_2^{rot} \) would correspond to symmetry permuting the AT, CG doublets for the first nucleotide. For \( Z_6 \) subgroup \( Z_3 \) would cyclically permute the 3 doublets with respect to third nucleotide. These constraints do not fix the correspondence completely.

To sum up, there is a connection between genetic code and the groups acting along the Hamiltonian cycle. The simplest option fixes the orbits of the triangles and therefore also the representation of genetic code.

8.3.2 Summary of the basic results

One can find the list of Hamiltonian cycles at [http://tinyurl.com/yacgzm9x](http://tinyurl.com/yacgzm9x). The edge \{1, 2\} is fixed and cycles are oriented so that there are 1024 of them. All of them are relevant from the point of music interpretation and the change of orientation corresponds to major-minor duality, albeit not in the simplest sense. Note that this duality does not affect the characteristics listed above.

The general following general results hold true as one can learn at [http://tinyurl.com/pmgscwd](http://tinyurl.com/pmgscwd). One can classify the cycles using their symmetries which can correspond to isometries of icosahedron leaving them fixed or to a reflection taking the vertex \( n \) at the cycle to vertex \( 12 - n \). This symmetry is not same as change of orientation which is purely internal operation and cannot change the cycle.

One can even find images of the cycles possessing symmetries at [http://tinyurl.com/y8ek7ak8](http://tinyurl.com/y8ek7ak8) and deduce the triplets \( n \) and \( p \) characterizing them by visual inspection. Also one can write explicitly the 3-chords defined by the three kinds of faces. I have deduced the triplets \( n \) and the 3-chords defining the harmony by the inspection of the images. “Bio-harmony” (4, 8, 8) forced by the model of extended genetic code involving also the 21st and 22nd amino-acids is of special interest. The classes of cycles with symmetries 6-fold rotational symmetry and two distinct reflection symmetries realize it.

Before continuing some terminology and notation is in order. Take \( C \) as the major key. Submediant or relative minor corresponds to \( Am \), subdominant (sharp or flat) to \( F \) major (\( F \)) or \( F\)minor (\( Fm \)), dominant to \( G \). The notation for chords is such that quints correspond to subsequent notes in the chord. For 1-chord tuples this means that first two notes define the quint. Table 5 the notation inspired by the popular music notation. The basic different is that the third is in most cases excluded so that the emotional character of the chord is not fixed. Besides these notions it is convenient to introduce additional notations for various dissonant chords appearing as 0-quint chords.

\[
\begin{align*}
CC_2D &\equiv Cex1, & \quad CC_3D &\equiv Cex2, & \quad CDD_2 &\equiv Cex3, & \quad CDE &\equiv Cex4, \\
CD_2E &\equiv Cex5, & \quad CG_3E &\equiv Cex6, & \quad CDF_2 &\equiv Cex7, & \quad CDG_2 &\equiv Cex8.
\end{align*}
\]

Clearly, the sets \{ex1\}, \{ex2, ex3\}, \{ex4, ex5, ex6\}, \{ex7\}, \{ex8\}, corresponds to the span of 2, 3, 4, 6, 8 half notes for the chord. The following summarizes the results. Note that \( Cex7 \) can be seen as part of \( D7 \) chord.

1. There are 6 collections of cycles without any symmetries containing 48 cycles each: these 48 cycle are mutually isometric so that one can say that there 6 different harmonies.
2. There is a collection with 6-fold rotational symmetry, 48/6=8 examples. \( n = (2,12,6) \). The chords of this scale define 6-note scale involving only total steps. \( CDF \) and its 6 translates by integer number of steps define 6 1-quint chords. \( CE♭G \) (\( Cm \)) and its 6 translates (they obviously correspond to the 6-fold rotational symmetry) define also 6 1-quint chords. The reflection transforms these series to those defined by \( GB♭G \) and its translate and by \( FAC \) (\( F \) major) and its translates. Impressionists like Debussy used 6-note scale of this kind. Half-octave shift is an exact symmetry. 1-chords lack the third so that one cannot assign to 3-chords any emotional quality. The extension to 4-chord can however bring either “happy” or “sad” quality. Clearly, these harmonies have “jazzy” character.

0-quint chords are \( Faug \equiv FAC_2^\ast \) and \( Gaug \equiv GHD_2^\ast \) are transformed to each other by both half-octave shift and inversion.

3. There are 2 collections with 2 distinct reflectional symmetries with 12=48/4 representatives in each. Half-octave scaling is a symmetry of both these scales as one might guess.

The first cycle (see Fig. 5) has \( n = (0,16,4) \) so that there are no 0-quint chords which in general are dissonant. Second cycle (see Fig. 6) realizes \( n = (4,8,8) \) bio-harmony and deserves some comments. It will be discussed in detail later.

(a) The 8 2-quint chords consist of \( B♭FG \equiv B9, C9, F9, G9 \) and their half-octave scalings. Clearly, the simple four-note scale appears here.

(b) Using the popular notion introduced earlier 1-quint chords consist of two 4-plets \( Dmaj7, E9, , A7, A6 \) and \( G2maj7, B9, , D7, D6 \) related by half-octave shift. The harmony contains no “simple” major or minor chord and only the extension to tetrahedral harmony can provide them. The same is true for the second bio-harmony.

(c) The 4 0-quint chords are \( Cex3 \equiv CDD_2^\ast \) and \( Eex2 \equiv EFG \) and their half-octave scalings \( F_2^{3}ex3 \equiv F_2^{3}C_2\ast A \) and \( Bex2 \equiv BbC_2\ast G \).

4. There are 3 collections with \( Z_2 \) rotational symmetry with 48/2 = 24 representatives in each. The triplets \( n = (0,16,4) \) (see Fig. 7), \((2,12,6) \) (see Fig. 8), and \((4,8,8) \) (see Fig. 9). All these harmonies are symmetric with respect to half-octave shift (tritonus), which obviously corresponds to the \( Z_2 \) rotation. Tritonus would not have been tolerated by catholic church! This symmetry characterizes all 3 harmonies. Basic 3-chords do not contain pure minor and major chords. The reflection of the scale does not leave the collection of chords invariant but it is not clear whether this corresponds only to a change of scale, probably not.

Consider the \((4,8,8) \) case (see Fig. 9).

(a) The 8 2-quint chords appear as four-plet \( H9, C_9^\ast, D_9^\ast, F9 \) and its half octave shift (tritonus interval) acting as a symmetry of the harmony. 2-quint chords are always of type \( X^9 \) (note that the third is missing) but also 1-quint chord can be of form \( X^9 \) as explicit construction of chords demonstrates: I have denoted these 1-quint chords by symbol \( X4 \) (\( CDG \) is obviously equivalent with \( CDG \)).

(b) Using the popular music notation introduced earlier, the 8 1-quint chords are \( D7, Amaj, A4_+, E7 \) and their half-octave shifts \( G_7^\ast, D_7^\ast, D_4^\ast, B_7^\ast \).

No major and minor chords are included and only the extension to tetra-icosahedral harmony can provide them and also break the symmetry giving rise to well-defined key.

5. The four 0-quint chords appear in two types. \( D_7ex2 \equiv D_7EF_2^\ast \) and its half-octave shift \( Aex2 \equiv AB♭C \) plus \( Hex3 \equiv HC♭G \) and its half-octave shift \( Fex3 \equiv FC_2^\ast \). According to usual thinking these chords involve dissonances. This dissonance character is a rather general phenomenon for the harmonic loners and classical views about harmony would exclude them as asocial cases! In the case of maximally symmetric harmony the loners are diminished chords and thus not so dissonant. In some cases there are no 0-quint chords.

There are 5 collections with \( Z_2 \) reflection symmetry having 24 representatives in each (see Figs. 10, 11, 12, 13, 14). The integer triplets \( n \) are \((2,12,6), (2,12,6), (4,10,6), (2,12,6), (2,12,6) \). Bio-harmony has representative also in this class (see Fig. 12). The half-octave scaling symmetry
Table 6: Table gives various types of 3-chords for harmonies with $Z_6$ rotational symmetry. Note that half-octave shift is an exact symmetry. Note that $G^{	ext{aug}} = \text{CEG}^\sharp_4$, $F^\text{aug}$ act as bridges between the groups related by half octave shift. The chords have been arranged so that they form orbits of $Z_6$. “Amino-acid chords” correspond to preferred chords at the orbits.

<table>
<thead>
<tr>
<th>$(n_0, n_1, n_2)$</th>
<th>0-chords</th>
<th>1-chords</th>
<th>2-chords</th>
</tr>
</thead>
<tbody>
<tr>
<td>(2, 12, 6)</td>
<td>(Faug, Gaug)</td>
<td>(Cm, Dm, Em, F#m, G#m, Bm)</td>
<td>(C9, D9, E9, F#9, G#9, B9)</td>
</tr>
<tr>
<td></td>
<td>(F6, G6, A6, B6, C#6, D#6)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 7: Table gives various types of 3-chords for the two harmonies with $Z_4 = Z_2^{\text{rot}} \times Z_2^{\text{ref}}$ symmetry. 4-plets represent the orbits. First cycle has no harmonic loners. Second cycle gives rise to bio-harmony (4, 8, 8) for which 5-quint chords are dissonant. Both cycles have $Z_4$ rotation symmetry acting as a vertical reflection symmetry in figures and realized also as half-octave shift so that 4-plets contains chords and their half-octave shifts. The genuine reflection symmetry acts as a horizontal reflection symmetry in figures. The cycles correspond to figures ??, ??

<table>
<thead>
<tr>
<th>$(n_0, n_1, n_2)$</th>
<th>0-chords</th>
<th>1-chords</th>
<th>2-chords</th>
</tr>
</thead>
<tbody>
<tr>
<td>(0, 16, 4)</td>
<td>(D7, D6, C#7, C#6)</td>
<td>(B9, B9, E9, F9)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(G#4, A9, C#4, D#9)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(Emaj7, Gmaj7, Bmaj7, C#maj7)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(C#9, A9, F#9, D#9)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>(4, 8, 8)</td>
<td>(Cex3, Exx3, F#x3, B#x3)</td>
<td>(Bmaj7, E9, A7, A6)</td>
<td>(B9, F9, C9, G9)</td>
</tr>
<tr>
<td></td>
<td>(C#maj7, B59, D#7, D#6)</td>
<td>(E9, B9, F#9, C#9)</td>
<td></td>
</tr>
</tbody>
</table>

is broken for these harmonies. I have not found simple characterization for the symmetry which corresponds to reflection in the direction of x-axis since it changes the interval structure of the chords.

Some comments (4, 8, 8) case are in order (see Fig. 12).

1. 2-quint chords appear as reflection related multiplets C9, D9, H#9, D#9 and C#9, H9, F9, B9.
2. 1-quint chords appear as symmetry related multiplets G, D7, Amaj7, E7 and C#m, F#6, H6...E6. Key G major and C# minor would be natural looking keys even without tetrahedral extension. For the mirror image B9 minor and E major would be the natural looking keys. For extension E major would be the key.

To sum up, half octave shift is a symmetry of all harmonies expected those having only $Z_2$ reflection symmetry, and fails thus also for the corresponding bio-harmonies.

8.3.3 Tables of basic 3-chords for the icosahedral harmonies with symmetries

The tables below give list for the three types of 3-chords for the 11 harmonies possessing symmetries. One must remember that the reversal of the orientation for the cycle induces the transformation $C \leftrightarrow C$, $F_2 \leftrightarrow F_2$, $H \leftrightarrow C_2^\sharp$, $F \leftrightarrow G$, $D \leftrightarrow B_9$, $E \leftrightarrow G_9^\sharp$, $A \leftrightarrow D_7^\sharp$ and produces a new scale with minor type chords mapped to major type chords and vice versa. Also one must remember that all 3-chords except those which are simple majors or minors lack the third so that their emotional tone remains uncharacterized. For instance, C6 does could be replaced with Cm6 and G7 with Gm7. The reader can check the chords by direct inspection of the figures. The convention used is that vertex number one corresponds to C note.

8.4 Appendix

8.4.1 Chord tables for some harmonies and their inverses

The formula for inversion of the harmonic keeping note $X$ as fixed can be represented as a product of translation takin X to C, inversion keeping C fixed, and translation taking C back to X. The
Table 8: Table gives various types of 3-chords for harmonies with \(Z_2\) rotation symmetry acting as half-octave shift. The doublets represent 2-chord orbits. The cycles correspond to figures ??, ??, and ??.

<table>
<thead>
<tr>
<th>([n_0, n_1, n_2])</th>
<th>0-chords</th>
<th>1-chords</th>
<th>2-chords</th>
</tr>
</thead>
<tbody>
<tr>
<td>(0, 16, 4)</td>
<td>((Em, Bm), (Cm, F^{#}m))</td>
<td>((D^9, C^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((G^6, C^{#}g), (A^6, D^{#}g))</td>
<td>((E^9, B^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((D^{#}+, G^{#}^{#}+, (B^{#}+, F^3+))</td>
<td></td>
<td></td>
</tr>
<tr>
<td>(2, 12, 6)</td>
<td>((A^{#}4, D^{#}4^{#}2))</td>
<td>((A^{#}m, D^{#}m), (G^9−, C^9−))</td>
<td>((C^9, F^9))</td>
</tr>
<tr>
<td></td>
<td>((C^4, F^4, (E^4+, B^{#}4+))</td>
<td>((A^9, D^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((D^{#}maj, G^{#}maj))</td>
<td>((D^9, C^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((B^{#}maj, F^{#}maj))</td>
<td></td>
<td></td>
</tr>
<tr>
<td>(4, 8, 8)</td>
<td>((A^{#}2, Hex^8, D^{#}2^x2, Hex^8))</td>
<td>((D^7, C^7), (Amaj, D^{#}maj))</td>
<td>((G^9, C^9), (A^9, D^9))</td>
</tr>
<tr>
<td></td>
<td>((A^{#}4+, D^{#}4^{#}2, (E^{#}7, B^7))</td>
<td>((B^9, F^9), (E^9, B^9))</td>
<td></td>
</tr>
</tbody>
</table>

Table 9: Table gives various types of 3-chords for harmonies with single reflection symmetry. The cycles correspond to figures ??, ??, ??, ??, ??.

<table>
<thead>
<tr>
<th>([n_0, n_1, n_2])</th>
<th>0-chords</th>
<th>1-chords</th>
<th>2-chords</th>
</tr>
</thead>
<tbody>
<tr>
<td>(2, 12, 6)</td>
<td>((F^8e^8, Hex^8))</td>
<td>((A^{#}m, D^{#}7), (A^6, D^{#}7))</td>
<td>((C^9, F^9), (B^9, D^9))</td>
</tr>
<tr>
<td></td>
<td>((D^7, B^9), (G^6−, F^{#}maj))</td>
<td>((E^9, C^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((D^{#}+, B^9−)), ((E^9, G^{#}4^{#}+))</td>
<td></td>
<td></td>
</tr>
<tr>
<td>(2, 12, 6)</td>
<td>((Dex^4, Hex^4))</td>
<td>((F, F^m), (C^6−, B^{#}maj))</td>
<td>((C^9, D^9))</td>
</tr>
<tr>
<td></td>
<td>((D^7, G^6), (G^{#}maj, D^{#}6−))</td>
<td>((D^9, C^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((C^{#}4−, A^{#}4+)), ((E^{#}4+, F^3)^{#}6)</td>
<td>((E^9, B^9))</td>
<td></td>
</tr>
<tr>
<td>(4, 8, 8)</td>
<td>((Fex^1, D^{#}ex^3, G^{#}ex^1, Aex^2))</td>
<td>((E^{#}1, E^{#}6), (Amaj, B^9−))</td>
<td>((D^9, B^9), (C^9, C^9))</td>
</tr>
<tr>
<td></td>
<td>((G, C^{#}m), (D^7, F^2)^{#}6)</td>
<td>((F^9, C^{#}9), (D^9, B^9))</td>
<td></td>
</tr>
<tr>
<td>(2, 12, 6)</td>
<td>((Hex^3, Nex^3))</td>
<td>((D^7, G^6), (G, D^3))</td>
<td>((C^9, D^9))</td>
</tr>
<tr>
<td></td>
<td>((F, F^m), (C^6−, B^{#}maj))</td>
<td>((D^9, C^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((A^9−, C^{#}4^{#}+, (E^7, F^2)^{#}6)</td>
<td>((E^9, B^9))</td>
<td></td>
</tr>
<tr>
<td>(2, 12, 6)</td>
<td>((F^{#}ex^2, Fex^3))</td>
<td>((F, B^m), (C^7, G^6))</td>
<td>((B^9, D^9))</td>
</tr>
<tr>
<td></td>
<td>((Amaj, B^9−), (E^{#}6, E^{#}7))</td>
<td>((C^9, C^9))</td>
<td></td>
</tr>
<tr>
<td></td>
<td>((G, C^{#}m), (D^7, B^6))</td>
<td>((D^9, H^9))</td>
<td></td>
</tr>
</tbody>
</table>
8.4 Appendix

Table 10: Inversion of the scale leaving $C$ (and also $F^\#$) invariant.

<table>
<thead>
<tr>
<th>C</th>
<th>G</th>
<th>D</th>
<th>A</th>
<th>E</th>
<th>H</th>
<th>F+</th>
<th>C+</th>
<th>G+</th>
<th>D+</th>
<th>B-</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>F</td>
<td>B♭</td>
<td>D+</td>
<td>G+</td>
<td>C+</td>
<td>F+</td>
<td>H</td>
<td>E</td>
<td>A</td>
<td>D</td>
<td>G</td>
</tr>
</tbody>
</table>

Table 11: Table gives the transformation of inversion leaving $C$ invariant on the basic chords having $C$ as basic note.

\[
\begin{array}{cccccccccccc}
M, 0 & m, 0 & sus4, 0 & aug, 0 & 4, 0 & 9, 0 & 4+, 0 & 9-, 0 & 6-, 0 & maj7, 0 \\
m, 11 & M, 11 & sus, 0 & aug, 0 & 4, 0 & 9, 10 & 9-, 11 & 4+, 11 & maj7, 11 & 6-, 11 \\
6, 0 & 7, 0 & ex1, 0 & ex2, 0 & ex3, 0 & ex4, 0 & ex5, 0 & ex6, 0 & ex7, 0 & ex8, 0 \\
7, 11 & 6, 11 & ex1, 10 & ex3, 3 & ex2, 3 & ex4, 8 & ex6, 8 & ex5, 80 & ex8, 6 & ex7, 6 \\
\end{array}
\]

Inversion maps the chord having $C$ as basic note to its mirror image so that the order of notes can change and basic note can change. For instance, the major chord $CM = CEG$ goes to minor chord $CGF = Fm$ so that $k = 0$ goes to $k \equiv \Delta k_{inv} = 11$. This delicacy must be taken into account. If $X$ remains fixed inversion is just the transformation

\[ k \to k_{inv} = (2 \times k(X) - \Delta k_{inv}) \mod 12. \]

Table 10 gives the inversion of the scale leaving $C$ (and also $F^\#$) invariant:

The inversion for the types of the chords does not depend on the basic note as is clear from the distance preserving character of the inversion. Table 11 gives the inversion of for the types of the chords leaving $C$ fixed. The elements of the rows give the type of the chord and the number of quints $k$ corresponding to it. For chords having $C$ as basic note one has $k = 0$. It is easy to deduce the transformation formula in more general case from the table.

The following tables give the chords and corresponding inverse chords for the 11 icosahedral harmonies.

8.4.2 Calculation of incidence matrices

The most stringent definition of harmonic chord progression is as a chord sequence in which two subsequent chords have at least one common note: the distance between subsequent chords defined as the minimal distance between triangles representing them vanishes. Some general comments are in order.

1. Incidence matrices can be computed by using expressions of chords as sets of three notes (possible in Python) and just counting the number of common notes defining the value of the element of the incidence matrix. The quint distance between the chords vanishes if they have common notes. More general incidence matrices would correspond to a larger quint distance.

2. In the case of genetic code and amino-acids one Hamilton cycle from each class labelled by $Z_n$, $n \in \{6, 4, 2\}$ is involved.

   (a) There are $N = 1 \times 3 \times 8 = 24$ cycle combinations if one does not allow the inverse harmonies. Allowing them gives $N = 8 \times 24$ combinations. If transitions between all representations are possible, there are $M = N^2 20 \times 20$-dimensional incidence matrices to be calculated for the icosahedral restriction of the code. Incidence matrices are symmetric so that only $D(D+1)/2 = 20(20+1)/2 = 210$ independent matrix elements need to be calculated for given $20 \times 20$-D incidence matrix.

   (b) Equivalently, one can calculate the incidence matrix for a space with $N \times 20$ points which is Cartesian product of $N$ amino-acid spaces with 20 points. $N$ has values 24 and $8 \times 24$. Remarkably, the magic number 24 of also stringy mathematics appears.
Table 12: Pairs “X” and “iX” of columns give the chords of the bio-harmonies and their inversions depicted in figures ??, ??, ??, ??.

<table>
<thead>
<tr>
<th>ro6</th>
<th>iro6</th>
<th>ro41</th>
<th>ire41</th>
<th>re42</th>
<th>ire42</th>
<th>ro31</th>
<th>iro31</th>
</tr>
</thead>
<tbody>
<tr>
<td>F.aug</td>
<td>F.aug</td>
<td>D.7</td>
<td>A.6</td>
<td>C.ex3</td>
<td>A.ex2</td>
<td>A.m</td>
<td>F.M</td>
</tr>
<tr>
<td>G.aug</td>
<td>D+.aug</td>
<td>D.6</td>
<td>A.7</td>
<td>E.ex2</td>
<td>F.ex3</td>
<td>B.m</td>
<td>B.M</td>
</tr>
<tr>
<td>C.m</td>
<td>F.M</td>
<td>G+7</td>
<td>D+.6</td>
<td>F+.ex3</td>
<td>D+.ex2</td>
<td>C.m</td>
<td>A.M</td>
</tr>
<tr>
<td>D.m</td>
<td>D+.M</td>
<td>G+.6</td>
<td>D+.7</td>
<td>B-.ex2</td>
<td>B.ex3</td>
<td>F+.M</td>
<td>D+.M</td>
</tr>
<tr>
<td>E.m</td>
<td>C+.M</td>
<td>G.4+</td>
<td>E.9-</td>
<td>D.maj7</td>
<td>B.6-</td>
<td>G.6</td>
<td>D.7</td>
</tr>
<tr>
<td>F+.m</td>
<td>B.M</td>
<td>A.9-</td>
<td>D.4+</td>
<td>E.9-</td>
<td>A.4+</td>
<td>C+.6</td>
<td>G+.7</td>
</tr>
<tr>
<td>G.9-</td>
<td>A.M</td>
<td>G+.4+</td>
<td>B-.9-</td>
<td>A.7</td>
<td>E.6</td>
<td>A.6</td>
<td>C.7</td>
</tr>
<tr>
<td>B.m</td>
<td>G.M</td>
<td>D+.9-</td>
<td>G+.4+</td>
<td>A.6</td>
<td>E.7</td>
<td>D+.6</td>
<td>F+.7</td>
</tr>
<tr>
<td>F.6</td>
<td>C.7</td>
<td>G.maj7</td>
<td>G.6-</td>
<td>G+.maj7</td>
<td>F.6-</td>
<td>D+.4-</td>
<td>G.9-</td>
</tr>
<tr>
<td>G.6</td>
<td>B-.7</td>
<td>G.maj7</td>
<td>E.6-</td>
<td>B-.9-</td>
<td>D+.4+</td>
<td>G+.4+</td>
<td>C+.9-</td>
</tr>
<tr>
<td>A.6</td>
<td>G+.7</td>
<td>B-.maj7</td>
<td>C+.6-</td>
<td>D+.7</td>
<td>B-.6</td>
<td>B+.4-</td>
<td>B-.9-</td>
</tr>
<tr>
<td>B.6</td>
<td>F+.7</td>
<td>C+.maj7</td>
<td>B-.6-</td>
<td>D+.6</td>
<td>B-.7</td>
<td>F+.4-</td>
<td>E.9-</td>
</tr>
<tr>
<td>C+.6</td>
<td>E.7</td>
<td>C.9-</td>
<td>D.4+</td>
<td>F.9</td>
<td>D+.9</td>
<td>C.maj7</td>
<td>A.6-</td>
</tr>
<tr>
<td>D+.6</td>
<td>D.7</td>
<td>A.9-</td>
<td>D.4+</td>
<td>C.9</td>
<td>G+.9</td>
<td>F+.maj7</td>
<td>D+.6-</td>
</tr>
<tr>
<td>F+.9</td>
<td>G.9</td>
<td>F+.9</td>
<td>F+.4+</td>
<td>G.9</td>
<td>D+.9</td>
<td>G+.9</td>
<td>D+.9</td>
</tr>
<tr>
<td>G+.9</td>
<td>E.9</td>
<td>G.9</td>
<td>C+.9</td>
<td>C+.9</td>
<td>G.9</td>
<td>E.9</td>
<td>C.9</td>
</tr>
<tr>
<td>B-.9</td>
<td>D.9</td>
<td>B-.9</td>
<td>G+.9</td>
<td>B-.9</td>
<td>B-.9</td>
<td>B-.9</td>
<td>F+.9</td>
</tr>
</tbody>
</table>

Table 13: Pairs “X” and “iX” of columns give the chords of the bio-harmonies and their inversions depicted in figures ??, ??, ??, ??.

<table>
<thead>
<tr>
<th>ro22</th>
<th>iro22</th>
<th>ro23</th>
<th>iro23</th>
<th>re21</th>
<th>iro21</th>
<th>re22</th>
<th>iro22</th>
</tr>
</thead>
<tbody>
<tr>
<td>A.ex4</td>
<td>G.ex4</td>
<td>A.ex2</td>
<td>B.ex3</td>
<td>B+.ex3</td>
<td>F+.ex3</td>
<td>D+.ex2</td>
<td>D.ex4</td>
</tr>
<tr>
<td>D+.ex2</td>
<td>C.ex3</td>
<td>H.ex8</td>
<td>B+.ex7</td>
<td>H.ex4</td>
<td>B-.ex4</td>
<td>H.ex4</td>
<td>F+.ex4</td>
</tr>
<tr>
<td>A.m</td>
<td>B-.M</td>
<td>D+.ex2</td>
<td>E.ex3</td>
<td>A.m</td>
<td>E.M</td>
<td>E.M</td>
<td>F.M</td>
</tr>
<tr>
<td>D+.m</td>
<td>E.M</td>
<td>F.ex8</td>
<td>F.ex7</td>
<td>D+.M</td>
<td>B.-m</td>
<td>F.m</td>
<td>E.M</td>
</tr>
<tr>
<td>G.9-</td>
<td>C+.4+</td>
<td>D.7</td>
<td>A.6</td>
<td>A.6</td>
<td>E.7</td>
<td>C.6-</td>
<td>A.maj7</td>
</tr>
<tr>
<td>C+.9-</td>
<td>F+.4+</td>
<td>G+.7</td>
<td>D+.6</td>
<td>D+.7</td>
<td>B-.6</td>
<td>B-.maj7</td>
<td>B.6-</td>
</tr>
<tr>
<td>C.4</td>
<td>C.4</td>
<td>A.maj7</td>
<td>D.6-</td>
<td>D.7</td>
<td>B.6</td>
<td>C.9-</td>
<td>A.4+</td>
</tr>
<tr>
<td>F+.4</td>
<td>F+.4</td>
<td>D+.maj7</td>
<td>G+.6-</td>
<td>B-.6</td>
<td>D+.7</td>
<td>D.7</td>
<td>G.6</td>
</tr>
<tr>
<td>E.4+</td>
<td>D+.9-</td>
<td>A+.4+</td>
<td>D.9-</td>
<td>G.6-</td>
<td>F+.maj7</td>
<td>G+.6-</td>
<td>C+.7-</td>
</tr>
<tr>
<td>B+.4+</td>
<td>A-.9-</td>
<td>D+.4+</td>
<td>G+.9-</td>
<td>F.maj7</td>
<td>G+.6-</td>
<td>G.maj7</td>
<td>D.6-</td>
</tr>
<tr>
<td>D.maj7</td>
<td>F.6-</td>
<td>E.7</td>
<td>G.6</td>
<td>D.4+</td>
<td>B.9-</td>
<td>D+.6-</td>
<td>F+.maj7</td>
</tr>
<tr>
<td>G+.maj7</td>
<td>B.6-</td>
<td>B-.7</td>
<td>C+.6</td>
<td>B-.9-</td>
<td>D+.4+</td>
<td>C+.4</td>
<td>C+.4</td>
</tr>
<tr>
<td>B.maj7</td>
<td>G+.6-</td>
<td>B-.9</td>
<td>G+.9</td>
<td>G+.4+</td>
<td>F.9-</td>
<td>A.4+</td>
<td>C.9-</td>
</tr>
<tr>
<td>F.maj7</td>
<td>D.7-</td>
<td>G.9</td>
<td>B.9</td>
<td>E.9-</td>
<td>A.4+</td>
<td>E.4-</td>
<td>F.9-</td>
</tr>
<tr>
<td>C.9</td>
<td>D.9</td>
<td>C+.9</td>
<td>F.9</td>
<td>C.9</td>
<td>G+.9</td>
<td>F+.6</td>
<td>D+.7</td>
</tr>
<tr>
<td>D+.9</td>
<td>G+.9</td>
<td>A.9</td>
<td>A.9</td>
<td>F.9</td>
<td>D+.9</td>
<td>D+.9</td>
<td>C.9</td>
</tr>
<tr>
<td>A.9</td>
<td>F.9</td>
<td>G.9</td>
<td>B.9</td>
<td>A.9</td>
<td>C+.9</td>
<td>D+.9</td>
<td>D.9</td>
</tr>
<tr>
<td>D+.9</td>
<td>B.9</td>
<td>F.9</td>
<td>C+.9</td>
<td>F.9</td>
<td>D.9</td>
<td>E.9</td>
<td>C.9</td>
</tr>
<tr>
<td>D.9</td>
<td>C.9</td>
<td>E.9</td>
<td>D.9</td>
<td>E.9</td>
<td>B.9</td>
<td>F.9</td>
<td>C.9</td>
</tr>
<tr>
<td>G+.9</td>
<td>F+.9</td>
<td>D+.9</td>
<td>D.9</td>
<td>C+.9</td>
<td>G.9</td>
<td>D+.9</td>
<td>C.9</td>
</tr>
</tbody>
</table>
Table 14: Pairs “X” and “iX” of columns give the chords of the bio-harmonies and their inversions depicted in figures ??, ??, ??.

<table>
<thead>
<tr>
<th>re23</th>
<th>ire23</th>
<th>re24</th>
<th>ire24</th>
<th>re25</th>
<th>ire25</th>
</tr>
</thead>
<tbody>
<tr>
<td>F.ex1</td>
<td>F.ex1</td>
<td>H.ex3</td>
<td>G.ex2</td>
<td>F+.ex2</td>
<td>F.ex3</td>
</tr>
<tr>
<td>D+.ex3</td>
<td>G+.ex2</td>
<td>E.ex7</td>
<td>F+.ex8</td>
<td>F.ex3</td>
<td>F+.ex2</td>
</tr>
<tr>
<td>G+.ex1</td>
<td>D.ex1</td>
<td>D.7</td>
<td>A.6</td>
<td>F.M</td>
<td>B..m</td>
</tr>
<tr>
<td>A.ex2</td>
<td>D.ex3</td>
<td>G+.8</td>
<td>D+.7</td>
<td>B..m</td>
<td>F..m</td>
</tr>
<tr>
<td>E.7</td>
<td>B.6</td>
<td>G..M</td>
<td>B.m</td>
<td>C.7</td>
<td>D+.6</td>
</tr>
<tr>
<td>E.6</td>
<td>B.7</td>
<td>D+.m</td>
<td>G+.M</td>
<td>G+.6</td>
<td>G.7</td>
</tr>
<tr>
<td>A.maj7</td>
<td>F+.6-</td>
<td>F.M</td>
<td>F+.m</td>
<td>A.maj7</td>
<td>F+.6-</td>
</tr>
<tr>
<td>B..9-</td>
<td>E.4+</td>
<td>F.m</td>
<td>F+.M</td>
<td>B..9-</td>
<td>E.4+</td>
</tr>
<tr>
<td>G.M</td>
<td>G+.m</td>
<td>C.6-</td>
<td>B.maj7</td>
<td>E.6</td>
<td>B.7</td>
</tr>
<tr>
<td>C+.m</td>
<td>D.M</td>
<td>B-.maj7</td>
<td>C.6-</td>
<td>E.7</td>
<td>B.6</td>
</tr>
<tr>
<td>D.7</td>
<td>C+.6</td>
<td>A.9</td>
<td>D.4+</td>
<td>G.M</td>
<td>G+.m</td>
</tr>
<tr>
<td>F+.6</td>
<td>A.7</td>
<td>C+.4+</td>
<td>B-.9</td>
<td>C+.m</td>
<td>D.M</td>
</tr>
<tr>
<td>B-.9</td>
<td>C.9</td>
<td>E.7</td>
<td>G.6</td>
<td>D.7</td>
<td>C+.6</td>
</tr>
<tr>
<td>D.9</td>
<td>G+.9</td>
<td>F+.6</td>
<td>F.7</td>
<td>B.6</td>
<td>E.7</td>
</tr>
<tr>
<td>B.9</td>
<td>B.9</td>
<td>C.9</td>
<td>F+.9</td>
<td>D+.9</td>
<td>G.9</td>
</tr>
<tr>
<td>C.9</td>
<td>B.9</td>
<td>D+.9</td>
<td>D+.9</td>
<td>C.9</td>
<td>B.9</td>
</tr>
<tr>
<td>F.9</td>
<td>F.9</td>
<td>D.9</td>
<td>E.9</td>
<td>C+.9</td>
<td>A.9</td>
</tr>
<tr>
<td>G+.9</td>
<td>D.9</td>
<td>C+.9</td>
<td>F.9</td>
<td>B-.9</td>
<td>C.9</td>
</tr>
<tr>
<td>D+.9</td>
<td>G.9</td>
<td>E.9</td>
<td>D.9</td>
<td>B.9</td>
<td>G+.9</td>
</tr>
<tr>
<td>C+.9</td>
<td>A.9</td>
<td>B.9</td>
<td>G.9</td>
<td>H.9</td>
<td>B-.9</td>
</tr>
</tbody>
</table>

(c) If the transitions can be restricted to single triplet of cycles, one must calculate 6 × 20-dimensional incidence matrices. This situation could be realistic for portions of the genetic code if the transitions between different cycle triplets are analogous to phase transitions. The number of incidence matrices (one can also use single 60 × 60 incidence matrix) is still reasonably small and can be documented in written form. In a model for random chord sequences one must specify the probabilities for the transitions between chords with different \( n \) for \( Z_n \). Simplest starting point assumption is that the probabilities are identical.

3. For the extended genetic code the most natural assumption is that the extension of the code to icosahedral code takes place only in \( Z_2 \) sector meaning the extension of amino-acid space by 4 amino-acids and the increase of the number of DNA codons from 60 to 64. There are two kinds of transitions between icosahedral and tetrahedral codons. Tetrahedral codon can correspond to a codon, which is outside the icosahedron having at least one common vertex with the icosahedral codon: this allows 3+3 transitions. Tetrahedral codon can correspond also to punct. Unless the codon/amino-acid contains at least one of these notes, it cannot precede stopping codon. These chords extend the harmony by the counterparts of \( CM \) and \( Am \) and punct corresponds to \( C6 = CGA \).

4. Also the situation in which tetrahedral and icosahedral codes are disjoint must be considered. In this case there are no transitions between tetrahedral and icosahedral sectors. In tetrahedral sector the distances between faces always vanish so that the calculation of this part of the incidence matrix is trivial. Icosahedral part of the incidence matrix can be readily written. The difficult part of the calculation of incidence matrices reduces to that for the icosahedral case such that the common face corresponds to either punct or Sec/Pyl. This gives selection rules telling which codons/amino-acids can precede stopping codon/punct in given bio-harmony.

8.4.3 Simulation of harmonic DNA sequence

The following sequence represents a random harmonic sequence based on zero quint distance between neighboring chords (at least one common note). The harmony if combination 3 harmonies ??, ??, and ?? extended by adding chords \( B_9 \), \( Gm \) and \( G7 \) and associated \( B96 \) representing stopping codon and punct in tetra- icosahedral codeandSec or Pyl in their unfused variants. These three
8.4 Appendix

harmonies correspond to groups of 20, 20, and 24 DNA codons at orbits of $Z_6$, $Z_4$, and $Z_2$ which is now taken to be $Z_2^{<r/4}$'. To deduce DNA sequence one must assume detailed correspondence between the codons at the orbits and corresponding chords.

It is assumed that all transitions between neighboring DNAs occurs with the same probability and induce the transitions between amino-acids.

Faug, A6, Dm, G6, G6, G6, Em, G6, Cm, G6, F6, Faug, F+m, Dm, G6, G6, Gaug, G+m, Cm, F6, Dm, Dm, F+m, Dm, F6, F6, F6, B-m, C+6, B-m, F6, Dm, G6, G6, Gaug, G+m, Cm, Gaug, G6, Dm, B-m, F6, Faug, A6, G6, Gaug, G+m, Cm, F6, Faug, F6, Cm, F6, Gaug, Em, A6, Gaug, B-m, B-m, Gaug, F6, G6, Gaug, Em, A6, Gaug, B+m, Dm, G6, Em, A6, F+m, B+m, F6, Cm, Gaug, G6, Gaug, Em, A6, Faug, B+m, B-m, Faug, F6, G6, G6, Faug, F6, Dm, G6, F6, Dm, F+m, Dm, F+m, A6, Faug, F6, Faug, Dm, Dm, B-m, B-m, C+6, C+6, G+m, B6, A6, F+m, Faug, B-m, Dm, B-m, C+6, B-m, F+m, B6, Gaug, Cm, G+m, Cm, F6, F6, B-m, Dm, F6, F6, G6, Dm, G6, G6, Em, A6, G6, Cm, Cm, G+m, B6, G+m, C+6, C+6, C+6, Faug, B-m, Dm, Dm, G6, Cm, Gaug, Cm, F6, Cm, G6, Gaug, G6, F6, Dm, F6, Faug, Faug, Faug, A6, Em, Em, G6, Dm, Faug, F6, B-m, F6, Cm, F6, B-m, F+m, Dm, G6, F6, F6, Cm, Cm, Em, G+m, Em, A6, Em, A6, F+m, B-m, B-m, B-m, F+m, B6, A6, Em, G+m, B6, B6, Em, G6, Dm, B-m, Dm, Dm, B-m, Dm, Faug, Faug, F6, Cm, G6, Gaug, B6, G+m, Em, G6, G6, Dm, Faug, Faug, F6, Cm, Gaug, G+m, Gaug, B6, F+m, A6, G6, Em, Cm, F6, Dm, Dm, Dm, G6, Em, Em, A6, Em, Gaug, Em, Cm, Cm, Gaug, G6, G6, Cm, F6, Dm, Faug, A6, Faug, A6, Faug, F+m, F+m, B-m, C+6, G+m, Em, Gaug, G6, Gaug, G6, G6, Dm, G6, Dm, Dm, F6, B-m, F6, G6, Cm, G+m, Em, G+m, B6, G+m, Cm, Cm, F6, Faug, Faug, F6, Dm, G6, Dm, F+m, Faug, Faug, B-m, C+6, G+m, C+6, Faug, F+m, B-m, Faug, Faug, A6, G6, Em, Cm, F6, G6, Cm.

8.4.4 Illustrations of icosahedral Hamiltonian cycles with symmetries

The figures below illustrate the Hamiltonian cycles involved. Quite generally, the $Z_n$ symmetry acts by a shift by $12/n$ quints along the cycle and the orbits of chords consist of at most $n$ chords of same type as the reader is encouraged to verify.

Figure 4: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 6-fold rotation symmetry acting shifts generated by a shift of 2 quints.

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 manners just like bits can be represented in very many manners. 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
9.1 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 [K8] and [L1, K10]). One can argue that genetic code is realized in several manners just like bits can be represented in very many manners.

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.

Figure 7: \((n_0, n_1, n_2) = (0, 16, 4)\) Hamiltonian cycle with 2-fold rotational symmetry realized as 6-quint shift along the cycle.

Figure 8: \((n_0, n_1, n_2) = (2, 12, 6)\) Hamiltonian cycle with 2-fold rotation symmetry.

summarized and also its connection with the model of harmony is discussed.
9.1 Background

Figure 9: \((n_0, n_1, n_2) = (4, 8, 8)\) Hamiltonian cycle with 2-fold rotation symmetry.

Figure 10: \((n_0, n_1, n_2) = (2, 12, 6)\) Hamiltonian cycle with 2-fold reflection symmetry realized as horizontal reflection.

9.1.1 Genetic code and Combinatorial Hierarchy

The first proposal [K9] was purely mathematics inspired and in terms of so called Combinatorial Hierarchy consisting of certain Merseene 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 Merseene 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.
9.1 Background

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 \[L6\] 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

\[ n_0, n_1, n_2 = (2, 12, 6) \] Hamiltonian cycle with 2-fold reflection symmetry.

\[ n_0, n_1, n_2 = (4, 8, 8) \] Hamiltonian cycle with 2-fold reflection symmetry.

9.1.2 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 \[L6\] 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 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

**Figure 13:** $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

**Figure 14:** $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.
frequencies with emotions.

9.1.3 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 \( \bar{u} \) and \( \bar{d} \). 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 parallel flux tubes [K16 K17]. 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 [O1 L11] leads to the idea that Pollack's EZs [L5] are accompanied by dark nuclear strings consisting of dark protons connected by color flux tubes analogous to mesons [L7 L11]. 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 [L12 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 [L12] 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 occurrence of cold fusion in living matter gives support for the role of dark nuclear strings [K35 L11].

One 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 [I17]. TGD based model [L9] 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 \( \rho \) and \( \omega \) 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 \( u \bar{u}, d \bar{d}, u \bar{u}, d \bar{d} \) with the ordering of \( q \) and \( \bar{q} \) 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 \( \bar{d}u, \bar{u}d, \bar{d}d \) or \( \bar{u}d, \bar{u}d, \bar{u}d \).

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.

9.1.4 Codon-wise representations of genetic code realized in terms of dark nuclear 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 [L9] 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.

9.2 Models of genetic code based on dark nuclear 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 [K10, K24], [I22]. 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.

9.2.1 Mapping DNA and amino-acids to dark nucleon states

The dark model emerged from the attempts to understand water memory [K10]. The outcome was a totally unexpected finding [L1, K10]: 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, 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. 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 \( \eta \).

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 mapping 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 [L11] 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 \( \Delta \) 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 \( 1/h_{\text{eff}} \) as indeed assumed in the model of dark nuclear strings [L7, L11].

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 \( \rho \) 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 would 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 [L12].

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 \( 4 \times 5 \) 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 \( 4 \times 5 \) 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 \( D_b \in \{1, 2, 2, 1\} \): \( D = D_B \times D_b \). Only the observed degeneracies
9.2 Models of genetic code based on dark nuclear strings

$D = 1, 2, 3, 4, 6$ 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 $(2, 9, 1, 5, 3)$!

It is difficult to exaggerate the importance of this simple observation suggesting that genetic code is 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.

9.2.2 Objections based on group theory and statistics

The model and its generalization replacing $u, d$ with nucleon states $p, n$ works amazingly 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 $(4 \oplus 2_1 \oplus 2_2) \otimes (4 \oplus 2_1 \oplus 2_2)$ 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 $\Delta$ 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 $\bar{10}$ and color entanglement cold guarantee color singletness for the codon pairs. This would however require anti-quarks for the conjugate strand.

3 10s associated with 3 codons contains in their tensor product a singlet (see [http://tinyurl.com/zjxxqhj](http://tinyurl.com/zjxxqhj)). Minimal color singlet dark DNA sequence would require 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 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.

9.2.3 It is also possible to map DNA and amino-acids to dark 3-nucleon states

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 [L9] 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.

Amazingly, 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 bonds 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.

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 $\Delta$ 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.

9.2.4 Ordinary or braid statistics?

There are four options to consider: ordinary/braid statistics (1/2) and dark nucleon/dark nucleon triplet as representation of DNA codon (a/b). One has options 1a,1b,2a,2b.

1. Option 1a. For the ordinary statistics amino-acid like dark nucleons are color singlets. Part of DNA codons 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. Option 1b requires in ordinary statistics for antisymmetric doublet an 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 altogether.

5. Option 2b. The 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.

9.2.5 Objections Against the Identification of Codons as Dark Nucleon States

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

1. The realization of the model requires the dark scaled variants of spin 3/2 baryons known as $\Delta$ resonance and the analogs (and only the analogs) of spin 1 mesons known as $\rho$ 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 could be scaled up.

2. Both the absolute and relative mass differences between $\Delta$ and $N$, resp. $\rho$ and $\pi$ are large in ordinary hadron physics and this makes the decays of $\Delta$ and $\rho$ 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 $\alpha_s$ 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 $E_c \propto h g B/m$, where $m$ is mass parameter which is of the order of baryon mass. Magnetic flux scales as $h$ by flux quantization and if flux tube thickness scales as $h^2$, one has $B \propto 1/h$. Mass splittings would not depend on $h$, which does not make sense. Mass splitting becomes small for large $h$ if the area of flux quantum scales as $h^{2+n}$, $n > 0$ so that color magnetic hyper-fine splitting scales as $1/h^n$ from flux conservation. The magnetic energy for a flux tube of length $L$ scaling as $h$ and thickness $S \propto h^{2+n}$ has order of magnitude $g^2 B^2 LS$ and does not depend on $h$ 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 $h/h_{bar0} = 2^{38}$. The proton-$\Delta$ 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 $h$ 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.

9.3 The model mapping codons to dark 3-nucleon states

The model based on dark 3-nucleon states is discussed seems more realistic and will be discussed in more detail in the sequel.

9.3.1 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 \textit{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 neutralization 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 \times 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 would 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\(_2\) \(\rightarrow\) NH\(^+=\) 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\(^+=\) 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 attachment 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 3 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 (deoxyribose 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 \(\rightarrow\) I and U \(\rightarrow\) 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 \(\rightarrow\) I could correspond to these 3 situations whereas for U \(\rightarrow\) I the correspondence would not depend on the ordering. Also for RNA one would have pnn,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 \(\rightarrow\) 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 pnn (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.

### 9.3.2 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 codons and their 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 $h_{\text{eff}}$ 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: $3 10:3$ give singlet. One can of course ask whether dark DNA RNA sequences exist rather than being built during replication and transcription.

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

I got a link to a very interesting article [28] 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 temporary 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 does 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).
9.3 The model mapping codons to dark 3-nucleon states

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 induce 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 \( h_{\text{eff}} \) 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](http://tinyurl.com/gpmxcmk)) relates to this general picture.

1. There are strong conditions on the predecessor 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/y9mex4v](http://tinyurl.com/y9mex4v) 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 predecessor of DNA since the evolution would occur at the level of dark nucleon strings and DNA as the dark proton string is the simplest 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.

9.3.4 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](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 \( h_{\text{eff}} \) 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](http://tinyurl.com/kp3sdlm) This is just what the proposal predicts!
9.3 The model mapping codons to dark 3-nucleon states

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/jlxag](http://tinyurl.com/jlxag) 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 [L9] assumes that the predecessor 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 wead to the idea that flux tubes being at $O=\text{-bonds}$ [K5].

9.3.5 Comparing TGD view about quantum biology with McFadden’s views

McFadden [I25] 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 [K7]. 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 [25] 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.

9.3.6 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 recon-

nections 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 ↔ state of dark nucleon or codon ↔ 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 [L2]. This option does not favor the idea about separate 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
9.3 The model mapping codons to dark 3-nucleon states

amino-acid correspond to the orbit of the triangle of icosahedron corresponding to the amino-acid. The decomposition \( 60 \rightarrow 20 + 20 + 20 \) suggests strongly decomposition of \( I \) to \( 20 \mathbb{Z}_3 \) 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 \( \mathbb{Z}_3 \) 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 \( I/\mathbb{Z}_3 \) these maps correspond to coset projections. Could the decomposition \( (4 \oplus 2_2 \oplus 2_2) \otimes (5 \oplus 3) \) 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/ho4onba). 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 \([L10]\) 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 icosahedron 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 \((m_p - m_n)/m_p \simeq 0.0014\) making itself possible visible in cyclotron frequency scale? The idea does not seem plausible: \(\left(\frac{3}{2}\right)^{12} - 2^7 \simeq 0.014\) is 10 times larger than \((m_p - m_n)/m_p \simeq 0.0014\).

The conclusion is that genetic code can be understood 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.

## 10 Flux Tube Realization Of The Divisor Code

Divisor code discovered by Khrennikov and Nilsson [K27] allows a flux tube realization and a close connection with dark baryon code seems to be possible.

### 10.1 Divisor Code

The idea of divisor code discussed in [A9] is inspired by the following observations.

1. Consider the number \(N(n)\) of integer divisors for integers \(n\) in the range \([1, 21]\) corresponding to amino-acids with stopping sign counted as amino-acid.

2. Denote the number of integers \(n \leq 21\) for which the number of divisors is \(k\) by \(B(k)\). Also stopping sign is counted as an amino-acid and \(n = 0\) corresponds to amino-acid also. This number \(N(k)\) varies in the range \([1, 6]\). \(B(k)\) has the values \((1, 8, 2, 5, 1, 3)\) where \(k\) runs from 1 to 6.

3. Denote by \(A(k)\) the number of amino-acids coded by \(k\) DNA codons. \(A(k)\) has the values \(2, 9, 2, 5, 0, 3\).

The spectrum of \(A(k)\) is very similar to that of \(B(k)\) and this raises the question whether one could understand genetic code as a divisor code in the sense that the degeneracy of amino-acid would be dictated by the number of the integers \(1 \leq n \leq 21\) coding it. One might also ask whether the amino-acids which are abundant and thus important are coded by integers with a large number of divisors. Also one can ask whether the divisor structure possibly correlates with the structure of the amino-acid.

Divisor code in this form would be only approximate and one can wonder could try to imagine some simple symmetry breaking mechanism. In this respect the crucial observations might be following.

1. The number of DNAs needed to realize divisor code would be 70 instead of 64. One must drop 6 codons and by choosing them suitably one might hope of getting correct degeneracies.

2. The most natural manner to break the symmetry is to drop the 4 codons from the codons coding for 5-plet which would thus become 1-plet. 5-plet corresponds to integer \(n = 16\) and its product decompositions \((16, 1), (1, 16), (2, 8), (8, 2), (4, 4)\) correspond to the DNAs coding for it. \((4, 4)\) would naturally correspond to singlet.

3. By dropping 2 codons from some 4-plet one obtains 2-plet and correct degeneracies. One candidate for 4-plet corresponds to \(n = 8\) and its product decompositions \((1, 8), (8, 1), (2, 4), (4, 2)\). By dropping two of these one obtains correct degeneracies. It might that power of 2 property of \(n = 8\) and \(n = 16\) somehow relates to 2-adicity and to the special role of these amino-acids.

4. A possible interpretation is in terms of symmetry based on cyclic group \(Z(n)\) serving as a symmetry of DNA codons coding for amino-acid labeled \(n\). \(Z_n\) allows decompositions \(Z_n = Z_{n_1} \times Z_{n_2}, n = n_1 \times n_2\) and if the representations are invariant under \(Z_{n_2}\) and thus
10.2 Topological Interpretation Of The Divisor Code In TGD Framework

The most concrete physical interpretation of the divisor code found in TGD framework is topological and based on TGD inspired vision about the role of dark matter in biology [K27].

1. The generalized 8-D imbedding space has a book like structure with pages glued together along back which is 4-D surface of $H = M^4 \times CP_2$ [K9, K15]. Particles at different pages are dark relative to each other since they cannot have local interactions (appear in the same vertex of Feynman diagram). The pages are partially characterized by the value of Planck constant which can be arbitrary large. This explains the macroscopic quantum coherence of living matter. Matter can leak between different pages meaning a phase transition changing Planck constant.

2. The notion of magnetic body with flux tubes carrying dark matter and connecting different bio-molecules central for the TGD inspired model of living matter [K5]. Magnetic bodies of bio-molecules can be also connected by magnetic flux tubes, even those in different pages of the book. For instance, the phase transition reducing $\hbar$ reduces the distance between two bio-molecules connected in this manner and forces them near to each other. This explains the extreme selectivity of bio-catalysis and the miraculous ability of two bio-molecules to find each other in the dense soup of bio-molecules. In particular, DNA and its conjugate codons, mRNA codons, and tRNA would be connected by this kind of flux tubes. Also amino-acids would be connected to tRNA codons in this manner since tRNA molecules catch the amino-acids and bring them to the mRNA-amino-acid translation site. Genetic code could reduce to the selection rules for the flux tube connections connecting in general situation magnetic bodies belonging to different pages of the book.

3. The pages of book are almost copies of $M^4 \times CP_2$. This means that $M^4$ is replaced with $n_a$-fold singular covering and $CP_2$ with $n_b$-fold singular covering. The coverings have cyclic groups $Z_{n_a}$ and $Z_{n_b}$ act as discrete symmetries for the wave functions of particles in the covering. A given page is thus labeled by two pager numbers $(n_a, n_b)$. Two pages contain common points and thus a direct tunnelling of 3-surfaces between these pages is possible only if the number $n_{a1}$ of the sheets of covering divides $n_{a2}$ or vice versa. Same holds true for $n_{b1}$ and $n_{b2}$. This rule is just the basic rule about how symmetries of system can change in phase transition. This number theoretic rule could be behind genetic code and the extreme selectivity of bio-catalysis.

4. Suppose that both bio-molecules correspond to ordinary matter with $n_a = n_b = 1$ but that the magnetic body of a given amino-acid corresponds to $(n_a(A), n_b(A))$ and DNA, RNA, and tRNA codon to $(r_a(DNA), r_b(DNA))$. Since the flux tube from tRNA codon to the amino-acid page is essential for the process in which amino-acid is attached to tRNA, only tRNA for with $r_a(tRNA)$ divides $n_a(A)$ can catch an amino-acid labeled by $n_a$. Same applies to $r_b$ and $n_b$.

5. Without the presence of the integer $n_b$ the code would fail since DNA codon labeled by $r_a$ would code for all amino-acids for which $n_a$ has $r_a$ as a factor. $n_b$ can indeed save the situation. Suppose that one has $r_b(tRNA) = n_b(A)$ if DNA codes for an amino-acid. Assume also that $n_b(A)$ is prime: $n_b(A) = p_b(A)$, and different for each amino-acid. This prime does not correspond to p-adic prime, which is expected to be very large in the length scales of atomic physics (electron corresponds to $M_{127} = 2^{127} - 1$). Note that the assumption that amino-acids are labeled by small primes was made in both TGD inspired number theoretical models of the genetic code.
6. The assumptions mean that tRNA and amino-acid can be connected by a magnetic flux tube only if one has

\[ p_b(tRNA) = p_b(A) \]

and \( r_a(tRNA) \) divides \( n_a(A) \). If the pages numbers \( n_a \) vary in the range \([1, 21]\) the divisor code follows from the argument of the previous section. Taking the previous argument seriously, one should also understand why there is no amino-acid labeled by \( n_a = 4 \) and why corresponding DNAs correspond to prime characterizing \( n_a = 4 \), why the number of DNA codons labeled by the factors of \( n_a = 8 \) is two, and why the number of codons associated with \( n_a = 16 \) only one.

Figure 15: Illustration of the book-like structure of the generalized embedding space.

Figure 16: Illustration of the selection rules for magnetic flux tubes connecting magnetic bodies of tRNA and amino-acid.

Some further comments are in order.

1. The realization of the genetic code is not unique since the integers \( r_a \) and \( n_a \) could be replaced with \( Nn_a \), where \( N \) is a product of primes larger than \( p = 19 \). It is also enough that the integers characterizing amino-acids are relative primes (have not common factors). The simplest assumption would be that the primes \( p(A) \) satisfy \( p(A) > 19 \) so that \( p(A) \) does not divide \( n(A) \) for any \( A \). If \( p(A) \) is as small as possible the value spectrum of \( p(A) \) is


If one assumes that the two additional amino-acids coded in some cases by non-vertebrate genetic code correspond to primes also the primes 113, 127 are included.
What is interesting is that Mersenne prime $M_7 = 2^7 - 1 = 127$ appears in the model of genetic code based on the notion of Combinatorial Hierarchy [K9]. This model assumes that DNA codons correspond to 64 integers in the range 1, . . . , 127. This realization of the genetic code cannot however be consistent with the divisor code realized in the proposed manner since it would require that the integers $n(A)p(A)$ belong to the range 1, . . . , 127. The prime factors of these integers can however belong to this range.

2. The quantum states of dark baryons realize vertebrate genetic code with very general assumptions group theoretically [L1, K10, K24, L1]. Since dark matter is involved in both cases, one might wonder whether these codes could be related somehow. A one-one correspondence between the quantum states of dark nucleons representing codon and the integers $r_0, p_0$ is required in order to have this connection. The simplest possibility is that energy minimization implies that given dark nucleon resides with high probability at aflux tube labeled by unique value of $r_a$. Same applies to amino-acids.

3. The model in principle allows an infinite number of analogous codes and an interesting question is whether the bio-catalysis involves this kind of codes. The quantum antenna model for remote replication discussed in [K10] allows a dynamical interpretation for the flux tube realization of the genetic code as a divisor code in terms of quantum antenna hypothesis [K14], and predicts that sequences of DNA codons serve as names for polar molecules quite generally so that genetic code would define a universal language in living matter. This leads to an identification of the basic mechanism responsible for the functioning and evolution of the immune system.

10.3 About Detailed Correspondence Between DNA Codons, Dark Baryon Codons, And Their Divisor Code Counterparts

One can make some conclusions also about the detailed correspondence between DNA codons and dark baryon codons as well as their divisor code counterparts. $L_z = -1$ requires that there is a rotating kink in flux tube representing nuclear string. One can ask whether also the corresponding DNA codons could be somehow special.

1. Maximal spin projections for both quarks ($J_z^q = 3/2$) and flux tube $J_z^f = \pm 2$ correspond to amino-acids met and trp coded by single codon. For the proposed interpretation of the divisor code these codons would correspond to $n = 1$ and $n = 16$.

2. Amino-acids coded by two codons correspond to ($J_z^q = 3/2, J_z^f \in \{1, 0, -1\}$) and ($J_z^q \in \{1/2, -1/2\}, J_z^f \in \{2, -2\}$). For the divisor code these amino-acids correspond to 8 primes plus lacking 9: th doublet results when one drops two codons from one 4-plet ($n = 8$ 4-plet is a good candidate).

3. For the baryonic realization 2 3-plets $J_z^q = -3/2, J_z^f \in \{2, -2\}$ contain one member corresponding to rotating kink. The first corresponds to ile and the DNA coding for met if T-C symmetry of the third nucleotide were exact. Second corresponds to stop codon coding for trp if T-C symmetry were exact. In divisor code triplets corresponds to $n = 4$ (stop codon?) and $n = 9$.

4. Three 6-plets correspond to ($J_z^q = -3/2, J_z \in \{1, 0, -1\}$) contain one anomalous member each and the corresponding codon would naturally belong to the doublet part of 6-plet in the code table. In divisor code 6-plets correspond to $n \in \{12, 18, 20\}$.

5. Three of the six 4-plets ($J_z^q = 1/2, -3/2, J_z \in \{1, 0, -1\}$) contain 2 anomalous members. From one 4-plet 2 codes for nothing or formally stop codon so that it becomes 2-plet: naturally these codons correspond to $L_z = -1$ and a rotating kink in the helix model of the nuclear string. From second 3-plet one $L_z = -1$ codon would codes for nothing becoming formally stop codon and one obtains second 2-plet.

6. The only regularity which comes in mind is that the 3 anomalous 4-plets and 2 anomalous doublets could populate the lowest row of the code table. The 16 oddballs would
reside at the boundaries of the code table. In divisor code these would correspond to \( n \in \{6, 8, 10, 14, 15, 21\} \). Dropping from \( n = 8 \) 4-plet codons one would obtain 5 4-plets and 9 2-plets as required. Besides this one must drop 4 codons from \( n = 16 \) 5-plet to get singlet. As already noticed, 2-adicity suggests that \( n = 2^k \) represents something special.

11 A Model For Protein Folding And Catalytic Action

It would be fascinating if the vision about the role of flux tube connections would generalize to interactions of all molecules in living matter. The mere selection rules would mean hidden simplicity behind extremely complex looking interactions in living matter. The model for protein folding and catalytic action discussed in [K1] is the first attempt in this direction. In the following this model is briefly summarized and the improvement of the model inspired by recent considerations is suggested.

11.1 Earlier Model For The Folding Code

The model for the evolution of the genetic code led [K7] to the idea that the folding of proteins obeys a code inherited from the genetic code. One can imagine several variants of this code. One of the is that amino-acid behaves like the conjugate \( Y_c \) of the middle nucleotide of the codon \( XYZ \) coding for it. Conjugation for amino-acids would correspond to the hydrophilic-hydrophobic dichotomy. Also catalyst action could reduce to effective base pairing in this picture chemically and at the level of quarks associated with the flux tube to matter antimatter conjugation. The guess that amino-acid and its conjugate form pairs turned out to be wrong however and after various twists and turns I ended up with the hypothesis that the amino-acid in protein behaves like \( Y_cZ \), where \( Z \) corresponds to third nucleotide for some codon coding for the amino-acid.

It however turned that the model as such is probably too restrictive and not fully consistent in the particular cases studied. In the following this model is discussed briefly and later an improved model for protein folding is proposed.

11.1.1 Flux tubes as correlates of directed attention at molecular level

After some trials one ends up with a general conceptualization of the situation with the identification of ("wormhole") magnetic flux tubes as correlates for attention at molecular level so that a direct connection with TGD inspired theory of consciousness emerges at quantitative level. Whether wormhole flux tubes or ordinary flux tubes are needed is not a completely settled question yet and the attribute “wormhole” will not be used in the sequel. This allows a far reaching generalization of the DNA as topological quantum computer paradigm and makes it much more detailed. The final outcome is very simple quantitative model for both protein folding and catalyst action based on minimization of energy, which seems to be consistent with basic experimental facts as well as general ideas.

11.1.2 What kind of atoms can be connected by flux tubes?

1. Hydrogen bonds play a key role in bio-catalysis but are not understood completely satisfactorily in the standard chemistry. Hence the basic question is whether hydrogen bonds can be regarded as or are accompanied by short (wormhole) magnetic flux tubes: note that the subject-object asymmetry of directed attention would correspond to donor-acceptor asymmetry of they hydrogen bond. If this is the case, the identification of the magnetic flux tube connection as a prerequisite for a hydrogen bond or as hydrogen bond becomes natural. At least the atoms able to form hydrogen bonds could form flux tube contacts so that the model would be very predictive and would conform with the known important role of hydrogen bonds in bio-catalysis.

2. The fact that hydrogen bonds connect base pairs suggests a generalization of the notion of base pairing stating that under some conditions amino-acids coded by \( XYZ \) and \( UY,V \) can behave like base pairs. These amino-acid pairs correspond to pairs of amino-acid residues which are hydrophilic \( \text{resp.} \) hydrophobic and hydrophobic residue do not form hydrogen
bonds in general. These flux tubes would thus be more general and in general long. The model for DNA as topological quantum computer requires this kind of flux tubes and they would in general connect atoms or molecules which act as acceptors in hydrogen bonding: \( \Omega \) = atom in amino-acid and aromatic ring are basic examples.

3. If one assumes that both \( N - H \) and \( O = \) associated with the constant part of the amino-acid can act as flux tube terminals and represent \( Z \) and \( Y \) nucleotides of the codon \( XYZ \) coding for the amino-acid, one obtains \( Y = Z \) pairing of \( O = -\Omega = \) flux tubes are allowed and \( Y = Z_c \) pairing if only hydrogen bond like pairings are allowed.

### 11.1.3 Color inheritance by a reconnection of flux tubes

1. There should exist some mechanism allowing amino-acids to inherit the base pairing property from the tRNA associated with them so that one can identify amino-acid with the middle nucleotide of the codon coding it. If tRNA middle nucleotide is connected to \( O = \) of the amino-acid, this becomes possible since the reconnection of flux tubes preserves the “color” of the flux tubes coded by \( (A, T, G, C) \) that is by the quark or anti-quark coding for the nucleotide. The temporary formation of a hydrogen bond between \( N - H \) and \( O = \) of two amino-acids as in the case of alpha helix would allow \( N - H \) to inherit the conjugate of the color associated with \( O \) =. Alternative interpretation is that this hydrogen bond is possible only if the predetermined color of \( N - H \) is consistent with the inherited one. The inheritance of flux tube color would be a completely general mechanism and even the donor atoms in the residues of amino-acids could inherit the color of \( O = \) in this manner.

2. A possible interpretation for the fixing of the flux tube color is in terms of quantum measurement selecting one color from quantum superposition in the reconnection process. This would mean that the unitary process can bring superposition back and reconnection process can change the inherited color. The hydrogen bonds between water molecules could correspond to quantum superpositions of different colors. This superposition property might relate to the wobble base pairing phenomenon for the third nucleotide in tRNA.

### 11.1.4 Folding code

The identification of \( N - H \) as a representation for the conjugate of the third nucleotide \( Z \) means that amino-acids would remember which codon coded them. If only hydrogen bond like flux tubes are allowed, flux tubes can connect only amino-acids satisfying \( Y = Z_c \). If \( O = \) is flux tubes are allowed \( Y = Z \) rule favored by the model of DNA as topological quantum computer follows. The isospin symmetry of the third nucleotide implies that both rules are quite flexible. If one identifies hydrogen bond with flux tube \( (Y(n) = Z(n + k)) \) the model works badly for both options. If one assumes only that the presence of a flux tube connecting amino-acids in either direction \( (Y(n) = Z(n + k) \text{ or } Z(n) = Y(n + k)) \) is a prerequisite for the formation of hydrogen bond, the model works. \( Y = Z \) rule is favored by the study of five enzymes: the possible average length of alpha helix is considerably longer than the average length of alpha helix if gene is the unique gene allowing to satisfy \( Y = Z \) rule. The explicit study of alpha helices and beta sheets for these enzymes demonstrates that the failure to satisfy the condition for the existence of hydrogen bond fails rarely and at most for two amino-acids (for 2 amino-acids in single case only).

\( Y = Z \) rule could mean a solution of the basic problem of proteomics: Do genes determine the folding of proteins and how this would take place? The interpretation would be that the information loss suggested by the many-to-one character of the genetic code is only apparent. The apparently lost information which corresponds to the \( A - G \) and \( T - C \) symmetries of the third nucleotide codes for the hydrogen bonding and hence for the folding of the protein. The model in its most stringent form is easy to kill since in the case of alpha helices and beta sheets the hydrogen bonding fixes completely the DNA sequence coding for the protein. A weaker variant of the model based on quantum variant of wobble base pairing: in this case there are no conditions on DNA sequence. It turns out that only this variant works. Hence hydrogen bonded amino-acid behave as if they were coded by the unique codon consistent with \( Y = Z \) rule.
11.1.5 Quantitative model

The quantitative model relies on the assumption that the contribution of a flux tube connecting two amino-acids to the potential energy depends only on the distance between the molecules in question. The extremals of the total interaction energy are same for any choice of the potential and only the absolute minimum of the interaction energy depends on the choice of the potential. The simplest potential corresponds to harmonic oscillator potential and would explain formation of alpha helices and beta sheets and with the fact that hydrophilic and hydrophobic residues tend to have a large distance and only few flux tube contacts. For large Planck constant also long flux tubes could correspond to attractive harmonic oscillator potential. Also the contribution of other interactions between neighboring amino-acids are expected to be present but are neglected in the simplest model. The model predicts alpha helices and beta sheets, and more generally, periodic structures, as solutions to energy minimization equations.

The model fails to catch completely the basic rules of protein folding, and the predictions are not fully consistent with empirical facts in the cases studied. A model in which the hydrophilic and hydrophobic interactions are mediated by flux tubes between magnetic bodies of the molecule and water molecule and in this manner induce long range interactions between amino-acids - somewhat like the attractive interactions of electrons with ions induce attractive interaction between the members of a Cooper pair - looks more attractive. This model is however computationally much heavier and is not discussed in [K1]. In the sequel a formulation of this model is discussed.

11.2 Hydrophily And Hydrophoby Number Theoretically

Amino-acids can be classified to hydrophilic and hydrophobic ones whereas all DNA codons are hydrophilic. Hydrophily and hydrophoby are believed to relate to the standard chemistry alone and this might be the case. One can however just for fun ask whether hydrophily and hydrophoby could have a connection with divisor code, formation of flux tubes connecting the molecule to water molecules, and phase transitions changing the value of Planck constant and changing the length of flux tube. I have discussed this idea already in the model of protein folding [K1].

To simplify the model assume that only single dark page is associated with water molecule and labeled by \((n_W^a, n_W^b)\). Of course, several levels characterized by different integers are also possible and this would bring in additional flexibility. Both hydrophoby and hydrophily would mean interaction mediated by the flux tubes to the magnetic body of water with the sign of the force differing for hydrophilic and hydrophobic amino-acids. There is no need to assume that quarks and anti-quarks generate the interaction. Gly for which the residue is just hydrogen atom does not allow classification as a hydrophilic or hydrophobic which would suggest that it does not have any flux tube connections with the magnetic body of the water. The interaction mediated by flux tubes between amino-acids and water molecules would be analogous to the interaction induced by the interaction between electrons and ions inducing attractive interaction between the members of Cooper pair. It would induce attractive interaction between hydrophilic amino-acids and repulsive interaction between hydrophilic and hydrophobic amino-acids favoring the formation of hydrophilic outer surfaces and hydrophobic inner surfaces.

One could understand hydrophily/hydrophoby dichotomy number theoretically for both options. The discussion of the first option makes clear that also second option is possible to realize.

1. Assume that \(n_W^a\) is divisible by all integers \(n_{DNA}^a\) associated with DNA codons and thus involves suitable powers of primes \(p \leq 19\). It could contain also an integer factor which is product of primes larger than \(p = 19\). This is necessary for achieving hydrophily of DNA codons.

2. Hydrophily of DNA codons also requires \(n_W^b\) must be proportional to the product of coprime integers \(n_{DNA}^b\) (primes for the simplest option) assignable to DNA codons. \(n_W^b\) could involve also a factor proportional to second integer expressible as product of primes \(p > 19\). The simplest option is that this integer equals to 1.

3. For hydrophobic amino-acids integers \(n_b^a\) must be of form \(mn_b^a = n_{DNA}^b m_b\) such that \(m_a\) does not divide \(n_W^b\) and \(n_W^a\). This is enough to guarantee that magnetic flux tubes in either direction are impossible so that hydrophoby is guaranteed in the proposed sense. This
definition extends also to other molecules and can be expressed in terms of the integers \((n_a, n_b)\) labeling the magnetic body of the molecule.

4. Second option is obtained by assigning the integer \(m_b\) only to Gly which is neither hydrophilic nor hydrophobic.

### 11.3 Could There Be New Physics Behind Hydrophily And Hydrophoby

One could accept just as a fact that magnetic flux tubes to the magnetic body of water mediate an interaction which is attractive or repulsive between water molecules and amino-acids and attractive between DNA molecules and water. Accepting that this induces interaction between amino-acids one could proceed to model building without any mention about TGD.

One could also try to dig deeper and ask what might be the origin of this interaction.

1. **Option I**: Could one understand the interaction in terms of phase transitions changing the Planck constant of the magnetic flux tube. The interaction would be repulsive (attractive) would result if the interaction energy increases (decreases) when Planck constant is reduced. Magnetic interaction energy is certainly the best candidate and could also imply the equivalence of the divisor code and dark baryon code.

2. **Option II**: Could hydrophily and hydrophoby be described in terms of em interactions of quarks representing nucleotides in the model of DNA as TQC. For instance, could amino-acids and water molecules be characterized by charges which are of opposite sign for water molecules and hydrophilic molecules and of same sign for water molecules and hydrophobic molecules.

For **Option I**, which represents completely new physics (using the standards of TGD!), the situation looks promising. The magnetic interaction energy assignable to the flux tube is a function of the integers \((n_a, n_b)\) -in particular of the Planck constant of the flux tube- and the minimization is performed by keeping the charges of the quarks possibly at its ends fixed. This new physics fits also nicely with the idea that magnetic body controls the living matter by utilizing phase transitions changing Planck constant.

What comes in mind in the case of **Option II** is that the ends of the flux tube carry opposite charges correlating with the codon coding for the amino-acid and giving rise to ordinary gauge interactions. Unfortunately this scenario does not seem to work.

1. In [K1] it was found that (denoting codons by \(XYZ\)) only \(Y = A, G\) type amino-acid residue can form hydrogen bonds and is hydrophilic and thus interacts strongly with water and DNA and RNA. If water end of flux tube corresponds to anti-quarks the attractive interaction between quark and anti-quark at the ends of flux tube could relate to hydrophily. For hydrophobic amino-acids one would have interaction between identical quarks and already Fermi statistics would cause repulsion. In DNA as TQC model based on the coding of A, G and T, C in terms of quarks u, d and their anti-quarks hydrophily-hydrophoby dichotomy corresponds to matter-antimatter dichotomy for quark assigned to the ends of the flux tube. Quarks and anti-quark have opposite charges. Hence the flux tube ends of hydrophilic amino-acids could correspond to quarks and water and hydrophobic ends of flux tubes to anti-quarks. Therefore the DNA as TQC model would predict the needed behavior of the forces. In the case of Gly containing only hydrogen as residue the flux tube might be simply absent.

2. DNA codons A, T, C, G are bases and thus polar and hydrophilic. In the case of DNA charge conjugation for quarks corresponds to the puridine-pyrimidine complementarity corresponding to conjugation of nucleotides. The rule applying in the case of amino-acids would predict T, C to be hydrophobic nucleotides which does not make sense. Therefore it seems that hydrophily and hydrophoby cannot reduce to the interactions of dark quarks and that they only represent conjugation of nucleotides symbolically.
11.4 An Improved Model For Protein Folding

To begin with let us summarize some basic facts about protein folding.

1. Hydrophily and hydrophoby play a key role in protein folding and dictate to a high degree the resulting folding patterns. This suggests that one cannot neglect the role of water in the process.

2. Protein folding proceeds from short to long length scales starting with the formation of secondary structures such as alpha helices, beta sheets, and random coil portions and is followed by the formation of tertiary and higher structures.

3. The formation of hydrogen bonds is in a decisive role in the formation of secondary structures. The mechanism leading to their formation might be contraction of magnetic flux tube by a phase transition changing Planck constant.

4. The folding patterns do not depend strongly on the precise primary structure, that is precise amino-acid decomposition which suggests that instead of the detailed chemistry the forces between quarks and anti-quarks mediated by flux tubes is what matter so that hydrophily and hydrophoby would become the basic characterizers of the interaction. The phase transitions changing Planck constant would indeed represent this kind of universal interactions independent of the chemistry.

5. In the first approximation amino-acids could be labeled by a variable telling whether it is hydrophobic, hydrophilic, or neither or these (Gly). This approximation would be broken by special amino-acids which appear in edges if beta sheets (Pro) and Cys which often appear as S-S boded pair in junctions. By bringing in forces depending on the angles between tangent vectors of successive amino-acids and on amino-adics themselves this tendency could be modeled.

The earlier approach to protein folding inspired by DNA as TQC idea did not start from this picture but assumed that direct flux tube connections between amino-acids rather than the interactions induced by flux tube connections with the magnetic bodies of water molecules were responsible for the folding. The model did not lead to any spectacular results and the proposed rules were not fully consistent in the cases studied.

11.5 The Model For Which The Magnetic Body Of Water Is Involved

The improved approach to protein folding starts from the general vision about magnetic body containing dark matter as a controller of visible matter in living system. The protein and its magnetic body would be regarded as a living system in itself.

1. Magnetic body must have large number of flux tube contacts to the visible matter. An excellent candidate for the magnetic body is that assignable with water and having flux tube connections to DNA and both hydrophilic and hydrophobic amino-acids. The magnetic body could control and at least fasten the self-organization process leading to the folding pattern which - by applying standard argument - would otherwise take astronomical time otherwise. The two-step attractive connections between all hydrophilic amino-acids would be possible via the magnetic body of water. The non-hydrophilic amino-acids not in direct contact with water are known to be more like passive structural stuff responsible for a fixed structure but not so relevant for the functioning of the bio-molecule. Hydrophilly and hydrophoby would reflect the dependence of interaction energy on the value of Planck constant associated with the flux tube mediating the interaction.

2. This picture implies a straightforward modification of the earlier model. The simplest model would minimize a potential function $V$ expressible as a sum $V = V_1 + V_2 + V_3$ of three terms. $V_1$ would be sum of the values of a universal two-particle potential function $V_{\phi,\phi}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophilic amino-acid pairs and giving rise to an attractive force. $V_2$ would be a sum of a universal two-particle potential function $V_{\phi,\phi}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophobic amino-acid pairs. $V_3$ would be
be sum of the values of a universal potential function \( V_{\text{phi,pho}}(r) \) for arguments \( r_{ij} = |r_i - r_j| \) varying over all pairs of hydrophilic and hydrophobic amino-acids. This potential function would induce a repulsive force. Besides this a constraint force due to the fact that amino-acids form a sequence would be present.

3. The resultant of the forces along lines connecting amino-acids would be parallel to the amino-acid sequence in the mechanical equilibrium. Hydrogen bonds and other bonds are indeed formed between neighboring hydrophilic amino-acids and the contraction of the flux tubes connecting the amino-acids in question to the magnetic body of water could be the mechanism. The model seems to be consistent with the basic qualitative facts about folding. The quantitative testing of the model would require determination of the conformations minimizing the potential function subject to the constraint provided by amino-acid sequence. Here of course the freedom to choose the three functions provides a considerable flexibility and symmetry arguments might allow to pose conditions on the form of these functions.

4. One could also include to the potential function describing a direct interaction with water molecules depending on parameters like pH affecting the folding pattern. The resultant for a given amino-acid would be sum of forces directed from a hydrophilic amino-acids to neighboring water molecules. It is not clear whether the normal component of this force could be compensated by the induced forces between amino-acids in a typical equilibrium configuration and the formation of hydrogen bonds involving the contraction of the flux tube could be the manner to achieve this.

11.5.1 Could one regard amino-acids and DNAs of given type as analog of species?

An interesting idea raised by the work with the model for protein folding is that the magnetic bodies amino-acids or DNA codon of a given type could behave like single phase on their respective page of the book so that the mutual interactions of their magnetic bodies could affect considerably the behavior of this phase to first order although amino-acids themselves are at different positions and one might expect only small correlations between their motions. Whether the dynamics of amino-acids of given type in protein folding are strongly correlated could be tested.

In certain sense one could speak of single species formed by amino-acids of given type and folding as long range interaction could be seen as an outcome of self-organizing interaction between members of various species and between species themselves plus short range constraints due to the fact that amino-acids form a sequence. The question applies to DNA and RNA codons and also to larger units such as genes formed to which one could assign their own page of the book. Water would represent the page to which all DNAs can send flux tubes. Even the notion of biological species could involve common dark space-time sheet(s) where the magnetic bodies of the members of species are and interact making the members of species to behave like single coherent unit.

12 Appendix: Generalization Of The Notion Of Imbedding Space

This section summarizes the attempt to understand how the hierarchy of Planck constants is realized at the level of imbedding space and what quantum criticality for phase transitions changing Planck constant means.

12.1 Hierarchy Of Planck Constants And The Generalization Of The Notion Of Imbedding Space

In the following the recent view about structure of imbedding space forced by the quantization of Planck constant is summarized. The question is whether it might be possible in some sense to replace \( H \) or its Cartesian factors by their necessarily singular multiple coverings and factor spaces. One can consider two options: either \( M^4 \) or the causal diamond CD. The latter one is the more plausible option from the point of view of WCW geometry.
12.1.1 The evolution of physical ideas about hierarchy of Planck constants

The evolution of the physical ideas related to the hierarchy of Planck constants and dark matter as a hierarchy of phases of matter with non-standard value of Planck constants was much faster than the evolution of mathematical ideas and quite a number of applications have been developed during last five years.

1. The starting point was the proposal of Nottale [E1] that the orbits of inner planets correspond to Bohr orbits with Planck constant \( \hbar_{gr} = GMm/v_0 \) and outer planets with Planck constant \( \hbar_{gr} = 5GMm/v_0, v_0/c \approx 2^{-11} \). The basic proposal [K20] was that ordinary matter condenses around dark matter which is a phase of matter characterized by a non-standard value of Planck constant whose value is gigantic for the space-time sheets mediating gravitational interaction. The interpretation of these space-time sheets could be as magnetic flux quanta or as massless extremals assignable to gravitons.

2. Ordinary particles possibly residing at these space-time sheet have enormous value of Compton length meaning that the density of matter at these space-time sheets must be very slowly varying. The string tension of string like objects implies effective negative pressure characterizing dark energy so that the interpretation in terms of dark energy might make sense [K21].

3. The quantization of Planck constant does not make sense unless one modifies the view about standard space-time is. Particles with different Planck constant must belong to different worlds in the sense local interactions of particles with different values of \( \hbar \) are not possible. This inspires the idea about the book like structure of the imbedding space obtained by gluing almost copies of \( H \) together along common “back” and partially labeled by different values of Planck constant.

4. Darkness is a relative notion in this framework and due to the fact that particles at different pages of the book like structure cannot appear in the same vertex of the generalized Feynman diagram. The phase transitions in which partonic 2-surface \( X^2 \) during its travel along \( X^3 \) leaks to another page of book are however possible and change Planck constant. Particle (say photon-) exchanges of this kind allow particles at different pages to interact. The interactions are strongly constrained by charge fractionization and are essentially phase transitions involving many particles. Classical interactions are also possible. It might be that we are actually observing dark matter via classical fields all the time and perhaps have even photographed it [K24].

5. The realization that non-standard values of Planck constant give rise to charge and spin fractionization and anyonization led to the precise identification of the prerequisites of anyonic phase [K15]. If the partonic 2-surface, which can have even astrophysical size, surrounds the tip of CD, the matter at the surface is anyonic and particles are confined at this surface. Dark matter could be confined inside this kind of light-like 3-surfaces around which ordinary matter condenses. If the radii of the basic pieces of these nearly spherical anyonic surfaces - glued to a connected structure by flux tubes mediating gravitational interaction - are given by Bohr rules, the findings of Nottale [E1] can be understood. Dark matter would resemble to a high degree matter in black holes replaced in TGD framework by light-like partonic 2-surfaces with a minimum size of order Schwartschild radius \( r_S \) of order scaled up Planck length \( l_{Pl} = \sqrt{\hbar_{gr}G} = GM \). Black hole entropy is inversely proportional to \( \hbar \) and predicted to be of order unity so that dramatic modification of the picture about black holes is implied.

6. Perhaps the most fascinating applications are in biology. The anomalous behavior ionic currents through cell membrane (low dissipation, quantal character, no change when the membrane is replaced with artificial one) has a natural explanation in terms of dark supra currents. This leads to a vision about how dark matter and phase transitions changing the value of Planck constant could relate to the basic functions of cell, functioning of DNA and amino-acids, and to the mysteries of bio-catalysis. This leads also a model for EEG interpreted as a communication and control tool of magnetic body containing dark matter.
and using biological body as motor instrument and sensory receptor. One especially amazing outcome is the emergence of genetic code of vertebrates from the model of dark nuclei as nuclear strings [L1, K24, L1].

12.1.2 The most general option for the generalized imbedding space

Simple physical arguments pose constraints on the choice of the most general form of the imbedding space.

1. The fundamental group of the space for which one constructs a non-singular covering space or factor space should be non-trivial. This is certainly not possible for $M^4$, CD, $CP_2$, or $H$. One can however construct singular covering spaces. The fixing of the quantization axes implies a selection of the sub-space $H_4 = M^2 \times S^2 \subset M^4 \times CP_2$, where $S^2$ is geodesic sphere of $CP_2$. $M^4 = M^4 \setminus M^2$ and $CP_2 = CP_2 \setminus S^2$ have fundamental group $Z$ since the codimension of the excluded sub-manifold is equal to two and homotopically the situation is like that for a punctured plane. The exclusion of these sub-manifolds defined by the choice of quantization axes could naturally give rise to the desired situation.

2. $CP_2$ allows two geodesic spheres which left invariant by $U(2 \text{ resp. } SO(3))$. The first one is homologically non-trivial. For homologically non-trivial geodesic sphere $H_4 = M^2 \times S^2$ represents a straight cosmic string which is non-vacuum extremal of Kähler action (not necessarily preferred extremal). One can argue that the many-valuedness of $\hbar$ is un-acceptable for non-vacuum extremals so that only homologically trivial geodesic $S^2$ would be acceptable. One could go even further. If the extremals in $M^2 \times CP_2$ can be preferred non-vacuum extremals, the singular coverings of $M^4$ are not possible. Therefore only the singular coverings and factor spaces of $CP_2$ over the homologically trivial geodesic sphere $S^2$ would be possible. This however looks a non-physical outcome.

(a) The situation changes if the extremals of type $M^2 \times Y^2$, $Y^2$ a holomorphic surface of $CP_3$, fail to be hyperquaternionic. The tangent space $M^2$ represents hypercomplex subspace and the product of the Kähler-Dirac gamma matrices associated with the tangent spaces of $Y^2$ should belong to $M^2$ algebra. This need not be the case in general.

(b) The situation changes also if one reinterprets the gluing procedure by introducing scaled up coordinates for $M^4$ so that metric is continuous at $M^2 \times CP_2$ but CDs with different size have different sizes differing by the ratio of Planck constants and would thus have only piece of lower or upper boundary in common.

3. For the more general option one would have four different options corresponding to the Cartesian products of singular coverings and factor spaces. These options can be denoted by $C - C$, $C - F$, $F - C$, and $F - F$, where $C$ ($F$) signifies for covering (factor space) and first (second) letter signifies for $CD$ ($CP_2$) and correspond to the spaces $(CD \times G_a) \times (CP_2 \times G_b)$, $(CD \times G_a) \times CP_2/G_b$, $CD/G_a \times (CP_2 \times G_b)$, and $CD/G_a \times CP_2/G_b$.

4. The groups $G_i$ could correspond to cyclic groups $Z_n$. One can also consider an extension by replacing $M^2$ and $S^2$ with its orbit under more general group $G$ (say tetrahedral, octahedral, or icosahedral group). One expects that the discrete subgroups of $SU(2)$ emerge naturally in this framework if one allows the action of these groups on the singular sub-manifolds $M^2$ or $S^2$. This would replace the singular manifold with a set of its rotated copies in the case that the subgroups have genuinely 3-dimensional action (the subgroups which corresponds to exceptional groups in the ADE correspondence). For instance, in the case of $M^2$ the quantization axes for angular momentum would be replaced by the set of quantization axes going through the vertices of tetrahedron, octahedron, or icosahedron. This would bring non-commutative homotopy groups into the picture in a natural manner.

12.1.3 About the phase transitions changing Planck constant

There are several non-trivial questions related to the details of the gluing procedure and phase transition as motion of partonic 2-surface from one sector of the imbedding space to another one.
1. How the gluing of copies of imbedding space at \( M^2 \times CP^2 \) takes place? It would seem that the covariant metric of CD factor proportional to \( \hbar^2 \) must be discontinuous at the singular manifold since only in this manner the idea about different scaling factor of CD metric can make sense. On the other hand, one can always scale the \( M^4 \) coordinates so that the metric is continuous but the sizes of CDs with different Planck constants differ by the ratio of the Planck constants.

2. One might worry whether the phase transition changing Planck constant means an instantaneous change of the size of partonic 2-surface in \( M^4 \) degrees of freedom. This is not the case. Light-likeness in \( M^2 \times S^2 \) makes sense only for surfaces \( X^1 \times D^2 \subset M^2 \times S^2 \), where \( X^1 \) is light-like geodesic. The requirement that the partonic 2-surface \( X^2 \) moving from one sector of \( H \) to another one is light-like at \( M^2 \times S^2 \) irrespective of the value of Planck constant requires that \( X^2 \) has single point of \( M^2 \) as \( M^2 \) projection. Hence no sudden change of the size \( X^2 \) occurs.

3. A natural question is whether the phase transition changing the value of Planck constant can occur purely classically or whether it is analogous to quantum tunnelling. Classical non-vacuum extremals of Chern-Simons action have two-dimensional \( CP^2 \) projection to homologically non-trivial geodesic sphere \( S^4_1 \). The deformation of the entire \( S^4_1 \) to homologically trivial geodesic sphere \( S^4_0 \) is not possible so that only combinations of partonic 2-surfaces with vanishing total homology charge (Kähler magnetic charge) can in principle move from sector to another one, and this process involves fusion of these 2-surfaces such that \( CP^2 \) projection becomes single homologically trivial 2-surface. A piece of a non-trivial geodesic sphere \( S^4_1 \) of \( CP^2 \) can be deformed to that of \( S^4_0 \) using 2-dimensional homotopy flattening the piece of \( S^4 \) to curve. If this homotopy cannot be chosen to be light-like, the phase transitions changing Planck constant take place only via quantum tunnelling. Obviously the notions of light-like homotopies (cobordisms) are very relevant for the understanding of phase transitions changing Planck constant.

12.1.4 How one could fix the spectrum of Planck constants?

The question how the observed Planck constant relates to the integers \( n_a \) and \( n_b \) defining the covering and factors spaces, is far from trivial and I have considered several options. The basic physical inputs are the condition that scaling of Planck constant must correspond to the scaling of the metric of CD (that is Compton lengths) on one hand and the scaling of the gauge coupling strength \( g^2/4\pi\hbar \) on the other hand.

1. One can assign to Planck constant to both CD and \( CP^2 \) by assuming that it appears in the commutation relations of corresponding symmetry algebras. Algebraist would argue that Planck constants \( h(CD) \) and \( h(CP^2) \) must define a homomorphism respecting multiplication and division (when possible) by \( G_i \). This requires \( r(X) = h(X)/h_0 = n \) for covering and \( r(X) = 1/n \) for factor space or vice versa.

2. If one assumes that \( h^2(X), X = M^4 \), \( CP^2 \) corresponds to the scaling of the covariant metric tensor \( g_{ij} \) and performs an over-all scaling of \( H \)-metric allowed by the Weyl invariance of Kähler action by dividing metric with \( h^2(CP^2) \), one obtains the scaling of \( M^4 \) covariant metric by \( r^2 \equiv h^2/h_0^2 = h^2(M^4)/h^2(CP^2) \) whereas \( CP^2 \) metric is not scaled at all.

3. The condition that \( h \) scales as \( n_a \) is guaranteed if one has \( h(CD) = n_a h_0 \). This does not fix the dependence of \( h(CP^2) \) on \( n_b \) and one could have \( h(CP^2) = n_b h_0 \) or \( h(CP^2) = h_0/n_b \). The intuitive picture is that \( n_b \)-fold covering gives in good approximation rise to \( n_a n_b \) sheets and multiplies YM action by \( n_a n_b \) which is equivalent with the \( h = n_a n_b h_0 \) if one effectively compresses the covering to \( CD \times CP^2 \). One would have \( h(CP^2) = h_0/n_b \) and \( h = n_a n_b h_0 \). Note that the descriptions using ordinary Planck constant and coverings and scaled Planck constant but contracting the covering would be alternative descriptions.

This gives the following formulas \( r \equiv h/h_0 = r(M^4)/r(CP^2) \) in various cases.

<table>
<thead>
<tr>
<th>( C - C )</th>
<th>( F - C )</th>
<th>( C - F )</th>
<th>( F - F )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( n_a n_b )</td>
<td>( n_a )</td>
<td>( n_b )</td>
<td>( 1/n_a n_b )</td>
</tr>
</tbody>
</table>
12.2 Updated View About The Hierarchy Of Planck Constants

12.1.5 Preferred values of Planck constants

Number theoretic considerations favor the hypothesis that the integers corresponding to Fermat
polygons constructible using only ruler and compass and given as products \( n_F = 2^k \prod F_n \), where
\( F_n = 2^{2^n} + 1 \) are distinct Fermat primes, are favored. The reason would be that quantum phase
\( q = \exp(i \pi / n) \) is in this case expressible using only iterated square root operation by starting from
rationals. The known Fermat primes correspond to \( s = 2, 3, 4 \) so that the hypothesis is very
strong and predicts that p-adic length scales have satellite length scales given as multiples of \( n_F \)
of fundamental p-adic length scale. \( n_F = 2^{11} \) corresponds in TGD framework to a fundamental
constant expressible as a combination of Kähler coupling strength, \( CP_2 \) radius and Planck length
appearing in the expression for the tension of cosmic strings, and the powers of \( 2^{11} \) was proposed
to define favored as values of \( n_a \) in living matter [K4].

The hypothesis that Mersenne primes \( M_k = 2^k - 1, k \in \{89, 107, 127\} \), and Gaussian Mersennes
\( M_{G,k} = (1 + i)k - 1, k \in \{113, 151, 157, 163, 167, 239, 241\} \) (the number theoretical miracle is that
all the four scaled up electron Compton lengths \( L_e(k) = \sqrt{5}L(k) \) with \( k \in \{151, 157, 163, 167\} \)
are in the biologically highly interesting range 10 nm-2.5 \( \mu \)m) define scaled up copies of electro-
weak and QCD type physics with ordinary value of \( h \) and that these physics are induced by
dark variants of corresponding lower level physics leads to a prediction for the preferred values of
\( r = 2^{k_4}, k_d = k_1 - k_4 \), and the resulting picture finds support from the ensuing models for biological
evolution and for EEG [K4]. This hypothesis - to be referred to as Mersenne hypothesis - replaces
the rather ad hoc proposal \( r = h/h_0 = 2^{11k} \) for the preferred values of Planck constant.

12.1.6 How Planck constants are visible in Kähler action?

\( h(M^4) \) and \( h(CP_2) \) appear in the commutation and anti-commutation relations of various super-
conformal algebras. Only the ratio of \( M^4 \) and \( CP_2 \) Planck constants appears in Kähler action
and is due to the fact that the \( M^4 \) and \( CP_2 \) metrics of the imbedding space sector with given
values of Planck constants are proportional to the corresponding Planck. This implies that Kähler
function codes for radiative corrections to the classical action, which makes possible to consider the
possibility that higher order radiative corrections to functional integral vanish as one might expect
at quantum criticality. For a given p-adic length scale space-time sheets with all allowed values of
Planck constants are possible. Hence the spectrum of quantum critical fluctuations could in the
ideal case correspond to the spectrum of \( h \) coding for the scaled up values of Compton lengths
and other quantal lengths and times. If so, large \( h \) phases could be crucial for understanding of
quantum critical superconductors, in particular high \( T_c \) superconductors.

12.2 Updated View About The Hierarchy Of Planck Constants

The original hypothesis was that the hierarchy of Planck constants is real. In this formulation
the imbedding space was replaced with its covering space assumed to decompose to a Cartesian
product of singular finite-sheeted coverings of \( M^4 \) and \( CP_2 \).

Few years ago came the realization that it could be only effective but have some practical impli-
cations. The basic observation was that the effective hierarchy need not be postulated separately
but follows as a prediction from the vacuum degeneracy of Kähler action. In this formulation
Planck constant at fundamental level has its standard value and its effective values come as its
integer multiples so that one should write \( h_{eff} = nh \) rather than \( h = nh_0 \) as I have done. For
most practical purposes the states in question would behave as if Planck constant were an integer
multiple of the ordinary one. In this formulation the singular covering of the imbedding space
became only a convenient auxiliary tool. It is no more necessary to assume that the covering
reduces to a Cartesian product of singular coverings of \( M^4 \) and \( CP_2 \) but for some reason I kept
this assumption.

The formulation based on multi-furcations of space-time surfaces to \( N \) branches. For some
reason I assumed that they are simultaneously present. This is too restrictive an assumption. The
\( N \) branches are very much analogous to single particle states and second quantization allowing all
0 < \( n \leq N \)-particle states for given \( N \) rather than only \( N \)-particle states looks very natural. As
a matter fact, this interpretation was the original one, and led to the very speculative and fuzzy
notion of \( N \)-atom, which I later more or less gave up. Quantum multi-furcation could be the root
concept implying the effective hierarchy of Planck constants, anyons and fractional charges, and related notions- even the notions of N-nuclei, N-atoms, and N-molecules.

12.2.1 Basic physical ideas

The basic phenomenological rules are simple and there is no need to modify them.

1. The phases with non-standard values of effective Planck constant are identified as dark matter. The motivation comes from the natural assumption that only the particles with the same value of effective Planck can appear in the same vertex. One can illustrate the situation in terms of the book metaphor. Imbedding spaces with different values of Planck constant form a book like structure and matter can be transferred between different pages only through the back of the book where the pages are glued together. One important implication is that light exotic charged particles lighter than weak bosons are possible if they have non-standard value of Planck constant. The standard argument excluding them is based on decay widths of weak bosons and has led to a neglect of large number of particle physics anomalies [K25].

2. Large effective or real value of Planck constant scales up Compton length - or at least de Broglie wave length - and its geometric correlate at space-time level identified as size scale of the space-time sheet assignable to the particle. This could correspond to the Kähler magnetic flux tube for the particle forming consisting of two flux tubes at parallel space-time sheets and short flux tubes at ends with length of order $CP_2$ size.

This rule has far reaching implications in quantum biology and neuroscience since macroscopic quantum phases become possible as the basic criterion stating that macroscopic quantum phase becomes possible if the density of particles is so high that particles as Compton length sized objects overlap. Dark matter therefore forms macroscopic quantum phases. One implication is the explanation of mysterious looking quantal effects of ELF radiation in EEG frequency range on vertebrate brain: $E = hf$ implies that the energies for the ordinary value of Planck constant are much below the thermal threshold but large value of Planck constant changes the situation. Also the phase transitions modifying the value of Planck constant and changing the lengths of flux tubes (by quantum classical correspondence) are crucial as also reconnections of the flux tubes.

The hierarchy of Planck constants suggests also a new interpretation for FQHE (see http://tinyurl.com/y89xp4bu) (fractional quantum Hall effect) in terms of anyonic phases with non-standard value of effective Planck constant realized in terms of the effective multi-sheeted covering of imbedding space: multi-sheeted space-time is to be distinguished from many-sheeted space-time.

3. In astrophysics and cosmology the implications are even more dramatic if one believes that also $\hbar_{gr}$ corresponds to effective Planck constant interpreted as number of sheets of multifurcation. It was Nottale (see http://tinyurl.com/ya6f3e4l) who first introduced the notion of gravitational Planck constant as $h_{gr} = GMm/v_0$, $v_0 < 1$ has interpretation as velocity light parameter in units $c = 1$. This would be true for $GMm/v_0 \geq 1$. The interpretation of $h_{gr}$ in TGD framework is as an effective Planck constant associated with space-time sheets mediating gravitational interaction between masses $M$ and $m$. The huge value of $h_{gr}$ means that the integer $h_{gr}/h_0$ interpreted as the number of sheets of covering is gigantic and that Universe possesses gravitational quantum coherence in super-astronomical scales for masses which are large. This would suggest that gravitational radiation is emitted as dark gravitons which decay to pulses of ordinary gravitons replacing continuous flow of gravitational radiation.

It must be however emphasized that the interpretation of $h_{gr}$ could be different, and it will be found that one can develop an argument demonstrating how $h_{gr}$ with a correct order of magnitude emerges from the effective space-time metric defined by the anti-commutators appearing in the Kähler-Dirac equation. Why Nature would like to have large effective value of Planck constant? A possible answer relies on the observation that in perturbation theory the expansion takes in powers of gauge couplings strengths $\alpha = g^2/4\pi\hbar$. If the effective value of $\hbar$ replaces its real value as one might expect to happen for multi-sheeted particles
behaving like single particle, $\alpha$ is scaled down and perturbative expansion converges for
the new particles. One could say that Mother Nature loves theoreticians and comes in rescue in
their attempts to calculate. In quantum gravitation the problem is especially acute since the
dimensionless parameter $GMm/h$ has gigantic value. Replacing $h$ with $h_{\text{pr}} = GMm/v_0$ the
coupling strength becomes $v_0 < 1$.

12.2.2 Space-time correlates for the hierarchy of Planck constants

The hierarchy of Planck constants was introduced to TGD originally as an additional postulate
and formulated as the existence of a hierarchy of imbedding spaces defined as Cartesian products
of singular coverings of $M^4$ and $CP_2$ with numbers of sheets given by integers $n_a$ and $n_b$ and
$h = nh_0$, $n = n_a n_b$.

With the advent of zero energy ontology, it became clear that the notion of singular covering
space of the imbedding space could be only a convenient auxiliary notion. Singular means that the
sheets fuse together at the boundary of multi-sheeted region. The effective covering space
emerges naturally from the vacuum degeneracy of Kähler action meaning that all deformations
of canonically imbedded $M^4$ in $M^4 \times CP_2$ have vanishing action up to fourth order in small
perturbation. This is clear from the fact that the induced Kähler form is quadratic in the gradients
of $CP_2$ coordinates and Kähler action is essentially Maxwell action for the induced Kähler form.
The vacuum degeneracy implies that the correspondence between canonical momentum currents
$\partial L_K/\partial (\partial_\alpha h^k)$ defining the Kähler-Dirac gamma matrices \[K29\] and gradients $\partial_\beta h^k$ is not one-to-
one. Some canonical momentum current corresponds to several values of gradients of imbedding
space coordinates. At the partonic 2-surfaces at the light-like boundaries of CD carrying the
elementary particle quantum numbers this implies that the two normal derivatives of $h^k$ are many-
valued functions of canonical momentum currents in normal directions.

Multi-furcation is in question and multi-furcations are indeed generic in highly non-linear sys-
tems and Kähler action is an extreme example about non-linear system. What multi-furcation
means in quantum theory? The branches of multi-furcation are obviously analogous to single par-
ticle states. In quantum theory second quantization means that one constructs not only single
particle states but also the many particle states formed from them. At space-time level single
particle states would correspond to $N$ branches $b_i$ of multi-furcation carrying fermion number.
Two-particle states would correspond to 2-fold covering consisting of 2 branches $b_i$ and $b_j$ of multi-
furcation. $N$-particle state would correspond to $N$-sheeted covering with all branches present and
carrying elementary particle quantum numbers. The branches co-incide at the partonic 2-surface
but since their normal space data are different they correspond to different tensor product factors
of state space. Also now the factorization $N = n_a n_b$ occurs but now $n_a$ and $n_b$ would relate to
branching in the direction of space-like 3-surface and light-like 3-surface rather than $M^4$ and $CP_2$
as in the original hypothesis.

In light of this the working hypothesis adopted during last years has been too limited: for some
reason I ended up to propose that only $N$-sheeted covering corresponding to a situation in which
all $N$ branches are present is possible. Before that I quite correctly considered more general option
based on intuition that one has many-particle states in the multi-sheeted space. The erratic form
of the working hypothesis has not been used in applications.

Multi-furcations relate closely to the quantum criticality of Kähler action. Feigenbaum bifurca-
tions (see \[http://tinyurl.com/2swb2p\]) represent a toy example of a system which via successive
bifurcations approaches chaos. Now more general multi-furcations in which each branch of given
multi-furcation can multi-furcate further, are possible unless on poses any additional conditions.
This allows to identify additional aspect of the geometric arrow of time. Either the positive or
negative energy part of the zero energy state is “prepared” meaning that single $n$-sub-furcations
of $N$-furcation is selected. The most general state of this kind involves superposition of various
$n$-sub-furcations.

12.2.3 Basic phenomenological rules of thumb in the new framework

It is important to check whether or not the refreshed view about dark matter is consistent with
existent rules of thumb.
1. The interpretation of quantized multi-furcations as WCW anyons explains also why the effective hierarchy of Planck constants defines a hierarchy of phases which are dark relative to each other. This is trivially true since the phases with different number of branches in multi-furcation correspond to disjoint regions of WCW so that the particles with different effective value of Planck constant cannot appear in the same vertex.

2. The phase transitions changing the value of Planck constant are just the multi-furcations and can be induced by changing the values of the external parameters controlling the properties of preferred extremals. Situation is very much the same as in any non-linear system.

3. In the case of massless particles the scaling of wavelength in the effective scaling of $\hbar$ can be understood if dark $n$-photons consist of $n$ photons with energy $E/n$ and wavelength $n\lambda$.

4. For massive particle it has been assumed that masses for particles and their dark counterparts are same and Compton wavelength is scaled up. In the new picture this need not be true. Rather, it would seem that wave length are same as for ordinary electron.

On the other hand, p-adic thermodynamics predicts that massive elementary particles are massless most of the time. ZEO predicts that even virtual wormhole throats are massless. Could this mean that the $n$-electron has same mass as electron, the mass for dark single electron state would be scaled down by $1/n$. This does not look sensible unless the p-adic length defined by prime is scaled down by this fact in good approximation.

This suggests that for fermions the basic scaling rule does not hold true for Compton length $\lambda_c = \hbar m$. Could it however hold for de-Broglie lengths $\lambda = \hbar/p$ defined in terms of 3-momentum? The basic overlap rule for the formation of macroscopic quantum states is indeed formulated for de Broglie wave length. One could argue that an $1/N$-fold reduction of density that takes place in the de-localization of the single particle states to the $N$ branches of the cover, implies that the volume per particle increases by a factor $N$ and single particle wave function is de-localized in a larger region of 3-space. If the particles reside at effectively one-dimensional 3-surfaces - say magnetic flux tubes - this would increase their de Broglie wave length in the direction of the flux tube and also the length of the flux tube. This seems to be enough for various applications.

One important notion in TGD inspired quantum biology is dark cyclotron state.

1. The scaling $\hbar \rightarrow k\hbar$ in the formula $E_n = (n + 1/2)\hbar eB/m$ implies that cyclotron energies are scaled up for dark cyclotron states. What this means microscopically has not been obvious but the recent picture gives a rather clearcut answer. One would have $k$-particle state formed from cyclotron states in $N$-fold branched cover of space-time surface. Each branch would carry magnetic field $B$ and ion or electron. This would give a total cyclotron energy equal to $kE_n$. These cyclotron states would be excited by $k$-photons with total energy $E = khf$ and for large enough value of $k$ the energies involved would be above thermal threshold. In the case of Ca$^{++}$ one has $f = 15$ Hz in the field $B_{end} = .2$ Gauss. This means that the value of $\hbar$ is at least the ratio of thermal energy at room temperature to $E = hf$. The thermal frequency is of order $10^{12}$ Hz so that one would have $k \approx 10^{11}$. The number branches would be therefore rather high.

2. It seems that this kinds of states which I have called cyclotron Bose-Einstein condensates could make sense also for fermions. The dark photons involved would be Bose-Einstein condensates of $k$ photons and wall of them would be simultaneously absorbed. The biological meaning of this would be that a simultaneous excitation of large number of atoms or molecules can take place if they are localized at the branches of N-furcation. This would make possible coherent macroscopic changes. Note that also Cooper pairs of electrons could be $n = 2$-particle states associated with $N$-furcation.

There are experimental findings suggesting that photosynthesis involves de-localized excitations of electrons and it is interesting so see whether this could be understood in this framework.
1. The TGD based model relies on the assumption that cyclotron states are involved and that dark photons with the energy of visible photons but with much longer wavelength are involved. Single electron excitations (or single particle excitations of Cooper pairs) would generate negentropic entanglement automatically.

2. If cyclotron excitations are the primary ones, it would seem that they could be induced by dark $n$-photons exciting all $n$ electrons simultaneously. $n$-photon should have energy of a visible photon. The number of cyclotron excited electrons should be rather large if the total excitation energy is to be above thermal threshold. In this case one could not speak about cyclotron excitation however. This would require that solar photons are transformed to $n$-photons in $N$-furcation in biosphere.

3. Second - more realistic looking - possibility is that the incoming photons have energy of visible photon and are therefore $n = 1$ dark photons de-localized to the branches of the $N$-furcation. They would induce de-localized single electron excitation in WCW rather than 3-space.

12.2.4 Charge fractionalization and anyons

It is easy to see how the effective value of Planck constant as an integer multiple of its standard value emerges for multi-sheeted states in second quantization. At the level of Kähler action one can assume that in the first approximation the value of Kähler action for each branch is same so that the total Kähler action is multiplied by $n$. This corresponds effectively to the scaling $\alpha_K \rightarrow \alpha_K/n$ induced by the scaling $\hbar_0 \rightarrow n\hbar_0$.

Also effective charge fractionalization and anyons emerge naturally in this framework.

1. In the ordinary charge fractionalization (see http://tinyurl.com/26tmhoe) the wave function decomposes into sharply localized pieces around different points of 3-space carrying fractional charges summing up to integer charge. Now the same happens at at the level of WCW (“world of classical worlds” ) rather than 3-space meaning that wave functions in $E^3$ are replaced with wave functions in the space-time of 3-surfaces (4-surfaces by holography implied by General Coordinate Invariance) replacing point-like particles. Single particle wave function in WCW is a sum of $N$ sharply localized contributions: localization takes place around one particular branch of the multi-sheeted space time surface. Each branch carries a fractional charge $q/N$ for teh analogs of plane waves.

Therefore all quantum numbers are additive and fractionalization is only effective and observable in a localization of wave function to single branch occurring with probability $p = 1/N$ from which one can deduce that charge is $q/N$.

2. The is consistent with the proposed interpretation of dark photons/gravitons since they could carry large spin and this kind of situation could decay to bunches of ordinary photons/gravitons. It is also consistent with electromagnetic charge fractionalization and fractionalization of spin.

3. The original - and it seems wrong - argument suggested what might be interpreted as a genuine fractionalization for orbital angular momentum and also of color quantum numbers, which are analogous to orbital angular momentum in TGD framework. The observation was that a rotation through $2\pi$ at space-time level moving the point along space-time surface leads to a new branch of multi-furcation and $N + 1$: th branch corresponds to the original one. This suggests that angular momentum fractionalization should take place for $M^4$ angle coordinate $\phi$ because for it $2\pi$ rotation could lead to a different sheet of the effective covering.

The orbital angular momentum eigenstates would correspond to waves $\exp(i m/\hbar)$, $m = 0, 2, ..., N - 1$ and the maximum orbital angular momentum would correspond the sum $\sum_{m=0}^{N-1} m/N = (N - 1)/2$. The sum of spin and orbital angular momentum be therefore fractional.

The different prediction is due to the fact that rotations are now interpreted as flows rotating the points of 3-surface along 3-surface rather than rotations of the entire partonic surface
in imbedding space. In the latter interpretation the rotation by $2\pi$ does nothing for the 3-surface. Hence fractionalization for the total charge of the single particle states does not take place unless one adopts the flow interpretation. This view about fractionalization however leads to problems with fractionalization of electromagnetic charge and spin for which there is evidence from fractional quantum Hall effect.

12.2.5 What about the relationship of gravitational Planck constant to ordinary Planck constant?

Gravitational Planck constant is given by the expression $\hbar_{gr} = G M m / v_0$, where $v_0 < 1$ has interpretation as velocity parameter in the units $c = 1$. Can one interpret also $\hbar_{gr}$ as effective value of Planck constant so that its values would correspond to multi-furcation with a gigantic number of sheets. This does not look reasonable.

Could one imagine any other interpretation for $\hbar_{gr}$? Could the two Planck constants correspond to inertial and gravitational dichotomy for four-momenta making sense also for angular momentum identified as a four-vector? Could gravitational angular momentum and the momentum associated with the flux tubes mediating gravitational interaction be quantized in units of $\hbar_{gr}$ naturally?

1. Gravitational four-momentum can be defined as a projection of the $M^4$-four-momentum to space-time surface. It’s length can be naturally defined by the effective metric $g_{\alpha\beta}^{eff}$ defined by the anti-commutators of the modified gamma matrices. Gravitational four-momentum appears as a measurement interaction term in the Kähler-Dirac action and can be restricted to the space-like boundaries of the space-time surface at the ends of CD and to the light-like orbits of the wormhole throats and which induced 4-metric is effectively 3-dimensional.

2. At the string world sheets and partonic 2-surfaces the effective metric degenerates to 2-D one. At the ends of braid strands representing their intersection, the metric is effectively 4-D. Just for definiteness assume that the effective metric is proportional to the $M^4$ metric or rather - to its $M^2$ projection: $g_{eff}^{kl} = K^2 m^{kl}$.

One can express the length squared for momentum at the flux tubes mediating the gravitational interaction between massive objects with masses $M$ and $m$ as

$$g_{eff}^{\alpha\beta} p_{\alpha} p_{\beta} = g_{eff}^{\alpha\beta} \partial_{\alpha} k^{\gamma} \partial_{\gamma} h_{k^l} p_{k} p_{l} \equiv g_{eff}^{kl} p_{k} p_{l} = n^2 \hbar^2 L^2 .$$

Here $L$ would correspond to the length of the flux tube mediating gravitational interaction and $p_k$ would be the momentum flowing in that flux tube. $g_{eff}^{kl} = K^2 m^{kl}$ would give

$$p^2 = n^2 \hbar^2 K^2 L^2 .$$

$h_{gr}$ could be identified in this simplified situation as $h_{gr} = \hbar / K$.

3. Nottale’s proposal requires $K = G M m / v_0$ for the space-time sheets mediating gravitational interacting between massive objects with masses $M$ and $m$. This gives the estimate

$$p_{gr} = \frac{G M m}{v_0 L} .$$

For $v_0 = 1$ this is of the same order of magnitude as the exchanged momentum if gravitational potential gives estimate for its magnitude. $v_0$ is of same order of magnitude as the rotation velocity of planet around Sun so that the reduction of $v_0$ to $v_0 \approx 2^{-11}$ in the case of inner planets does not mean that the propagation velocity of gravitons is reduced.

4. Nottale’s formula requires that the order of magnitude for the components of the energy momentum tensor at the ends of braid strands at partonic 2-surface should have value $G M m / v_0$. 

For $v_0 = 1$ this is of the same order of magnitude as the exchanged momentum if gravitational potential gives estimate for its magnitude. $v_0$ is of same order of magnitude as the rotation velocity of planet around Sun so that the reduction of $v_0$ to $v_0 \approx 2^{-11}$ in the case of inner planets does not mean that the propagation velocity of gravitons is reduced.
Einstein’s equations $T = \kappa G + \Lambda g$ give a further constraint. For the vacuum solutions of Einstein’s equations with a vanishing cosmological constant the value of $h_{gr}$ approaches infinity. At the flux tubes mediating gravitational interaction one expects $T$ to be proportional to the factor $GMm$ simply because they mediate the gravitational interaction.

5. One can consider similar equation for gravitational angular momentum:

$$g_{eff}^{\alpha\beta} L_\alpha L_\beta = g_{ijkl} L_i L_j = l(l+1)\hbar^2 .$$  \hspace{1cm} (12.3)

This would give under the same simplifying assumptions

$$L^2 = l(l+1)\frac{\hbar^2}{K^2} .$$  \hspace{1cm} (12.4)

This would justify the Bohr quantization rule for the angular momentum used in the Bohr quantization of planetary orbits.

Maybe the proposed connection might make sense in some more refined formulation. In particular the proportionality between $m_{eff}^{kl} = Km^{kl}$ could make sense as a quantum average. Also the fact, that the constant $v_0$ varies, could be understood from the dynamical character of $m_{eff}^{kl}$.

### 12.2.6 Could $h_{gr} = h_{eff}$ hold true?

The obvious question is whether the gravitational Planck constant deduced from the Nottale’s considerations and the effective Planck constant $h_{eff} = nh$ deduced from ELF effects on vertebrate brain and explained in terms of non-determinism of Kähler action could be identical. At first this seems to be non-sensical idea since $\hbar_{gr} = GMm/v_0$ has gigantic value.

It is however essential to realize that by Equivalence Principle one describe gravitational interaction by reducing it to elementary particle level. For instance, gravitational Compton lengths do not depend at all on the masses of particles. Also the radii of the planetary orbits are independent of the mass of particle mass in accordance with Equivalence Principle. For elementary particles the values of $h_{gr}$ are in the same range as in quantum biological applications. Typically 10 Hz ELF radiation should correspond to energy $E = h_{eff} f$ of UV photon if one assumes that dark ELF photons have energies of biophotons and transform to them. The order of magnitude for $n$ would be therefore $n \approx 10^{14}$.

The experiments of M. Tajmar et al [E2, E3] discussed in [K33] provide a support for this picture. The value of gravimagnetic field needed to explain the findings is 28 orders of magnitude higher than theoretical value if one extrapolates the model of Meissner effect to gravimagnetic context. The amazing finding is that if one replaces Planck constant in the formula of gravimagnetic field with $h_{gr}$ associated with Earth-Cooper pair system and assumes that the velocity parameter $v_0$ appearing in it corresponds to the Earth’s rotation velocity around its axis, one obtains correct order of magnitude for the effect requiring $r \approx 3.6 \times 10^{14}$.

The most important implications are in quantum biology and Penrose’s vision about importance of quantum gravitation in biology might be correct.

1. This result allows by Equivalence Principle the identification $h_{gr} = h_{eff}$ at elementary particle level at least so that the two views about hierarchy of Planck constants would be equivalent. If the identification holds true for larger units it requires that space-time sheet identifiable as quantum correlates for physical systems are macroscopically quantum coherent and gravitation causes this. If the values of Planck constant are really additive, the number of parallel space-time sheets corresponding to non-determinism evolution for the flux tube connecting systems with masses $M$ and $m$ is proportional to the masses $M$ and $m$ using Planck mass as unit. Information theoretic interpretation is suggestive since hierarchy of Planck constants is assumed to relate to negentropic entanglement very closely in turn providing physical correlate for the notions of rule and concept.
2. That gravity would be fundamental for macroscopic quantum coherence would not be surprising since by EP all particles experience same acceleration in constant gravitational field, which therefore has tendency to create coherence unlike other basic interactions. This in principle allows to consider hierarchy in which the integers $h_{gr,i}$ are additive but give rise to the same universal dark Compton length.

3. The model for quantum biology relying on the notions of magnetic body and dark matter as hierarchy of phases with $h_{eff} = n \times h$, and biophotons [K32, K31] identified as decay produces of dark photons. The assumption $h_{gr} \propto m$ becomes highly predictable since cyclotron frequencies would be independent of the mass of the ion.

   (a) If dark photons with cyclotron frequencies decay to biophotons, one can conclude that biophoton spectrum reflects the spectrum of endogenous magnetic field strengths. In the model of EEG [K4] it has been indeed assumed that this kind spectrum is there: the inspiration came from music metaphors suggesting that musical scales are realized in terms of values of magnetic field strength. The new quantum physics associated with gravitation would also become key part of quantum biophysics in TGD Universe.

   (b) For the proposed value of $h_{gr}$ 1 Hz cyclotron frequency associated to DNA sequences would correspond to ordinary photon frequency $f = 3.6 \times 10^{14}$ Hz and energy 1.2 eV just at the lower limit of visible frequencies. For 10 Hz alpha band the energy would be 12 eV in UV. This plus the fact that molecular energies are in eV range suggests very simple realization of biochemical control by magnetic body. Each ion has its own cyclotron frequency but same energy for the corresponding biophoton.

   (c) Biophoton with a given energy would activate transitions in specific bio-molecules or atoms: ionization energies for atoms except hydrogen have lower bound about 5 eV [http://tinyurl.com/233vcad]. The energies of molecular bonds are in the range 2-10 eV [http://tinyurl.com/bfsy4ft]. If one replaces $v_0$ with $2v_0$ in the estimate, DNA corresponds to 62 eV photon with energy of order metabolic energy currency and alpha band corresponds to 6 eV energy in the molecular region and also in the region of ionization energies. Each ion at its specific magnetic flux tubes with characteristic palette of magnetic field strengths would resonantly excite some set of biomolecules. This conforms with the earlier vision about dark photon frequencies as passwords. It could be also that biologically important ions take care of their ionization self. This would be achieved if the magnetic field strength associated with their flux tubes is such that dark cyclotron energy equals to ionization energy. EEG bands labelled by magnetic field strengths could reflect ionization energies for these ions.

   (d) The hypothesis means that the scale of energy spectrum of biophotons depends on the ratio $M/v_0$ of the planet and on the strength of the endogenous magnetic field, which is 2 Gauss for Earth (2/5 of the nominal value of the Earth’s magnetic field). Therefore the astrophysical characteristics of planets should be tuned for molecular life. Taking $v_0$ to be rotational velocity one obtains for the ratio $M(planet)/v_0(planet)$ using the ratio for Earth as unit the following numbers for the planets (Mercury, Venus, Earth, Mars, Jupiter, Saturnus, Uranus, Neptune): $M/v_0 = (8.5, 209.1, 214223, 1613, 6149, 9359)$. If the energy scale of biophotons is required to be the same, the scale of endogenous magnetic field should be divided by this ratio in order to obtain the same situation as in Earth. For instance, in Mars the magnetic field should be roughly 5 times stronger: in reality the magnetic field of Mars is much weaker. Just for fun one can notice that for Sun the ratio is $1.4 \times 10^6$ so that magnetic field should be by the inverse of this factor weaker.

4. An interesting question is how large systems can behave as coherent units with $h_{gr} = GMm/v_0$. In living matter one might consider the possibility that entire organism might be this kind of system. Interestingly, for larger masses the gravitational quantum coherence would be easier. For particle with mass $m$ $h_{gr}/h > 1$ requires larger mass to satisfy $M > M_\pi^2/m_c$. The first guess that life has evolved from long to shorter scales and reached
elementary particle last. Planck mass is the critical mass corresponds to the mass of water blog with volume of size scale of $10^{-4}$ m (big neuron) is the limit.

5. The Universal gravitational Compton wave length of $GM/v_0 \simeq 864$ meters gives an idea about largest possible living matter system if Earth is the second body. Of course, also other large bodies are possible.In the case of solar system this length is $3 \times 10^3$ km. The radius of Earth is $6.37 \times 10^3$ km - roughly twice the Compton length. The radii of Mercury, Venus, Earth, Mars, Jupiter, Saturnus, Uranus, Neptunus are (.38, .99, .533, 1, 10.6, 8.6, 4.0, 3.9) using Earth radius as unit the value of $h_{gr}$ is by factor 5 larger than for three inner planets so that the values are reasonably near to gravitational Compton length or twice it. Does this mean that dark matter associated with Earth and maybe also other planets is in macroscopic quantum state at some level of the hierarchy of space-time sheets? Does this mean that Mother Gaia as conscious entity might make sense. One can of course make same question in the case of Sun. The universal gravitational Compton length in Sun would be 18 per cent of the radius of Sun if $v_0$ is taken to be the rotational velocity at the surface of Sun. The radius of solar core, where fusion takes place, is 20-25 per cent of solar radius.

6. There are further interesting numerical co-incidences. One can for a moment forget the standard hostility of scientist towards horoscopes and ask whether Sun and Moon could have somehow affect our life via astroscopic quantum coherence. The gravitational Compton length for particle-Moon or particle-Sun system multiplied by the natural value of magnetic field is the relevant parameter. For Sun the parameters in question are mass of Sun, and rotational velocity of Earth with respect to Sun, plus magnetic fields of Sun at flux tubes associated with solar magnetic field measured to be about 5 nT at the position of Earth and 100 times stronger than expected from dipole field behavior. This gives that the range of biophoton energies is scaled down with factor of 1/4 in good approximation so that Father Sun might affect terrestrial biology! If one uses for the rotational velocity of particle at surface of Moon as parameter $v_0$ (particle would be at Moon), biophoton energy scaled scaled up by factor 1.2.

The general proposal discussed above is testable. In particular, a detailed study of molecular energies with those associated with resonances of EEG could be highly rewarding and reveal the speculated spectroscopy of consciousness.

12.2.7 Summary

The hierarchy of Planck constants reduces to second quantization of multi-furcations in TGD framework and the hierarchy is only effective. Anyonic physics and effective charge fractionalization are consequences of second quantized multi-furcations. This framework also provides quantum version for the transition to chaos via quantum multi-furcations and living matter represents the basic application. The key element of dynamics of TGD is vacuum degeneracy of Kähler action making possible quantum criticality having the hierarchy of multi-furcations as basic aspect. The potential problems relate to the question whether the effective scaling of Planck constant involves scaling of ordinary wavelength or not. For particles confined inside linear structures such as magnetic flux tubes this seems to be the case.

There is also an intriguing connection with the vision about physics as generalized number theory. The conjecture that the preferred extremals of Kähler action consist of quaternionic or co-quaternionic regions led to a construction of them using iteration and also led to the hierarchy of multi-furcations [K20]. Therefore it seems that the dynamics of preferred extremals might indeed reduce to associativity/co-associativity condition at space-time level, to commutativity/co-commutativity condition at the level of string world sheets and partonic 2-surfaces, and to reality at the level of stringy curves (conformal invariance makes [K23] so that conformal dynamics represents conformal evolution) [K22].
REFERENCES

Mathematics


[A3] Why are there 1024 Hamiltonian cycles on an icosahedron? Available at: http://tinyurl.com/pmghcwd


Theoretical Physics


Particle and Nuclear Physics


Condensed Matter Physics


Cosmology and Astro-Physics


Biology


[I13] tRNA. Available at: http://en.wikipedia.org/wiki/tRNA


Books related to TGD


Articles about TGD


