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

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Abstract

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

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

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

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

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

Contents

1   Introduction

During last years kind of brain storming period has occurred in the model of bio-harmony [L2]. A lot of ideas, some of them doomed to be short lived, have emerged, and it seems that now it its time for a thorough cleanup and integration with the general ideas of TGD inspired quantum biology.

TGD leads to 3 basic realizations of genetic code: this is now relatively well established part of TGD inspired quantum biology. One can also consider 3 realization also for bio-harmony. The question is which of them is the realistic one or whether several options can be considered.

1.1   3 basic realizations of the genetic code

In TGD Universe there are at least 3 realizations of the genetic code.

Besides biochemical realization one has a realization in terms of dark nuclei realized as dark proton sequences and possibly in terms of more general sequences involving effective dark neutrons. The states of 3 dark protons defining the dark codon have multiplet decomposition 64 + 64+ 40 + 20 corresponding to dark variants of DNA, RNA, tRNA, and amino-acids (AA). I will denote these dark variants by DDNA, DRNA, DtRNA, and DAA.

If one allows also dark analogs of neutrons by allowing negatively charged color bonds between protons, the number of code letters doubles: this could relate to the recently constructed Hachimoji DNA [I8] (see `http://tinyurl.com/y2mcjb4r`) discussed from TGD viewpoint in [L24].

Dark photon 3-chords assignable to the realization of bio-harmony with the note scale identified as Hamilton cycle on a polytope with triangular faces gives a third realization coupling dark and ordinary representations together. I have proposed 3 realizations in terms of icosahedral and tetrahedral [L2], icosahedral and toric [L16], and icosahedral and dodecahedral [L24] geometries (for the latter 5-chords would effectively reduce to 3-chords).

If there is DDNA-DNA, DRNA-RNA, DAA-AA pairing, the negative charges of DNA, RNA, and tRNA nucleotides finds explanation in terms of positive charge of dark proton sequence. For AAs the situation is not clear since the charge per unit length for amino-acids varies and depends on pH. DAA-AA pairing would require that dark analogs of neutrons are present in the dark proton sequence.

1.2   3 models of bioharmony

There are now 3 models of bioharmony [L2, L16, L24] making very similar pedictions. Harmony for given graph is defined as a Hamiltonian cycle connecting neighboring points and going through all points of the graph without self-intersections. Scale is identified by assigning notes to the vertices and faces correspond to the chords of the harmony obtained in this way. Bio-harmonies are fusions of 3 or 4 sub-harmonies.

1. The original proposal - icosa-tetrahedral bio-harmony - is based on the fusion of 3 icosahedral harmonies with symmetry groups Z_6, Z_4 and Z_2 permuting the triangles of given orbit of Z_n. Given icosahedral harmony corresponds to an imbedding of 12-note scale as a Hamilton cycle at icosahedron. The 12 vertices of icosahedron are identified as the notes of 12-note scale and 20 triangular faces define the 3-chords of the harmony.

The distance between nearest vertices is assumed to correspond to quint that is scaling of the frequency by 3/2. Each cycle defines a collection of 20 3-chords defining an icosahedral harmony. Octave equivalence is used to map the 12 frequencies obtained to single octave. There is however a slight inconsistency since 12 quints corresponds to slightly more than 7 octaves as already Pythagoras realized. The addition of tetrahedron to icosahedral harmony is interpreted as an addition of one vertex adding one note which should be very near to one of the 12 notes.

Icosahedral harmonies are characterized by a symmetry group Z_n, $n = 6, 4, 2, 1$, $n = 1$ corresponds to chaotic cycles, which might serve as correlate for dis-harmony and might relate to the correlates of emotions: at the level of genetic code is AA would be coded by single DNA codon.

Icosahedron decomposes to orbits of Z_n consisting of triangles or equivalently chords. The chords can be classified further by the frequency ratios correlating with the emotional effect. One has the orbits $3 \times 6 + 2 = 20$ for Z_6, $5 \times 4 = 20$ for Z_4 and 10×2 for Z_2. Z_6 harmony is unique but there are 3 Z_4 and even more Z_2 harmonies for which Z_2 can correspond to rotation by π or reflection. This can be understood as breaking of symmetry splitting the Z_6 orbits to pieces. This gives $60 = 2 + 20 + 20$ 3-chords. The numbers of chords at give orbit rather neatly correspond the numbers of DNA codons coding for given AA.

4 chords and DNAs and AAs are however missing. Tetrahedral harmony would add $3 + 1 = 4$ chords: Z_3 would the symmetry group instead of Z_4. This would be due to the symmetry breaking due to gluing of one-tetrahedral face with icosahedral face, which is however counted as separate face and corresponds to 1-triangle orbit under Z_3 permuting its vertices. This gives 64 3-chords corresponding to codons of genetic code.

$3 + 1$ decomposition would naturally correspond to (ile, ile, ile, met) 4-plet coded by codons AUX. The numbers of codons coding given AA identified as orbit of Z_n come out almost correctly. The only exception is trp-stop doublet for which doublet decomposes to stop and singlet. One must understand the reason for this symmetry breaking - it might just the need to have stop codon and this could be arranged if there is no tRNA coupling to this codon. Note that for some code variants stop codon UAG corresponds to Pyl and UGA to Sec.

Since music generates and expresses emotions, the interpretation would be in terms of moods. Even molecules would have moods.

2. Also icosa-dodecahedral and icosahedral-toric harmonies contain the Z_6 and Z_4 icosahedral harmonies (20_1 and 20_2) so that one must only add the missing 10 doublets and 3+1 codons assigned to tetrahedron in icosa-tetrahedral case.

   The dodecahedral harmony with 6 chords arranged in doublets is unique from the uniqueness of the Hamiltonian cycle [L24]. The icosa-dodecahedral harmony would give $20_1 + 20_2 + 12_1 + 12_2 = 64$. 12 decomposes into 6 Z_2 doublets so that one has 12 doublets. The realization of scale for dodecahedral harmony would in 20 powers of rational scaling x such that x^{20} is as near to a power of two as possible [L24]. $x = 2^{1/20}$ would correspond to the Eastern variant of well-tempered scale.

   There are objections against icosa-dodecahedral harmony. Chords are 5-chords rather than 3-chords. The 5-chords of dodecahedral harmony however turn out to be equivalent to 3-chords as far as information content is considered [L24]. The number of vertices for dodecahedron is 20, not 12, but one could argue that dodecahedron corresponds to Eastern harmony having micro-intervals. Two copies of the dodecahedral harmony are needed. What could distinguish between these copies will be discussed later. Also 3+1 is missing.

3. The icosahedral-toric harmony [L16] decomposes as $20_1 + 20_2 + 24 = 64$ involving torus with 24 triangles and 12 vertices. Toric harmony has Z_{24} as isometries and gives 12 doublets. One could argue that the fusion of icosahedral and toric harmonies is geometrically un-natural. One must be however cautious if the geometric realization is in extension of rationals. Also now 3+1 is missing.

The considerations in the sequel suggests that the icosa-tetrahedral option is the most realistic if not unique.

1.3   About the geometric interpretation of icosahedral and other symmetries

The geometric interpretation of icosahedral and possible other geometries is a challenge. The 60-element group A_5 of rotations - alternating group of 5-letters - acts as orientation preserving isometries of icosahedron.

1. Since Galois group is central in adelic physics, and all finite groups can appear as Galois groups, one can ask whether icosahedral group and tetrahedral groups could act as Galois group for some extension of rationals relevant for biology. Going to web gives an affirmative answer [A12] (see `http://tinyurl.com/y4qsea6h`)! Icosahedral symmetry appears as Galois group of the general quintic equation! The lowest order polynomial equation not allowing closed expressions for the roots.

   Galois theory (see `http://tinyurl.com/y6e955ke`) allows to understand the situation in terms of the discriminant defined as product $D = \prod_{i<j}(r_i - r_j)^2$, where r_i are the roots of the irreducible polynomial considered. S_n is the symmetry group in the generic case and odd permutations of S_n change the sign of D. If D is square of rational number in the field K considered (which can be also extension of rationals now), Galois group reduces to alternating group A_5.

   Remark: For octahedron and its dual cube the group is S_4 and can be realized as Galois group of 4th order polynomials. For tetrahedron the group is A_4 and can be also realized as Galois group of 4th order polynomials for which discriminant is square in K.

2. Icosahedral and dodecahedral geometries having the same isometry group are common in biology, and one can wonder whether there could be a gometric realization - perhaps at the level of magnetic body. This might somehow relate also to the frequent appearance of Golden mean involving $\sqrt{5}$ in biology and Golden angle rated to the fifth root of unity.

3. $M^8 - H$ duality provides besides the usual formulation of TGD also a formulation in complexified M^8 identified as complexified octonions [L10]. The associativity of the tangent or normal space of space-time surface is assumed as a dynamical principle and implies quaternionicity. Quaternions have $SO(3)$ as automorphism group analogous to Galois group and have the finite isometry groups of Platonic solids as finite subgroups.

   Could quaternionicity give a connection with the geometric picture? In adelic physics discretizations of space-time points as points with coordinates in the extension of rationals are in central role. Could discretizations contain orbits of the Platonic isometries as quaternionic Galois groups? This could also give to the geometric picture although icosahedral symmetries are not obvious in the geometry of say DNA.

4. Is the genetic code really unique as its dark nucleus realization and the fact that the isometry groups of Platonic solids are finite subgroups of quaternionic isomorphisms suggests? Could any Galois group give rise to an analog of bioharmony and of genetic code? Could the recent genetic code correspond to a first step in the process going beyond the solvable polynomial equations?

   What about toric code? The group of toric isometries is Z_{24} and 24 is one of the magic number of mathematics, and dimension 24 is crucial in bosonic string model. Could Z_{24} correspond to the Galois group for 24:th roots of unity defining 24-D algebraic extension of rationals. We cannot sensorily imagine higher dimensions but can do this cognitively. I have proposed that the ability to imagine higher dimensions could be due to the possibility of higher-dimensional extensions of rationals and p-adics.

   Could one realize the icosahedron and 24-torus as imagined object in the algebraic extension of rationals? Could the n-dimensional discrete geometric objects assignable to n-dimensional extensions of rationals have quite generally this kind of representations as a generalized Platonic solid in algebraic extension. Could they define cognitive harmonies as Hamiltonian cycles? Could one imagine also cognitive variant of genetic code whereas as sensory/biological variant of genetic code would be forced by dark proton physics?

1.4   Mistracks

In the attempts to understand the connection with standard realization of the genetic code I have also considered the possibility that the frequencies of 3-chord might be mapped to their sum in the interactions. This possibility was considered in the model of homonymy [L20]. In the light of afterwisdom this proposal looks ad hoc.

Also a proposal for how 12-note scale could quite concretely correspond DNA codons was discussed [L21]. The idea was to assign notes with individual letters of the codon such that the note depends on the position of the letter whereas the model of harmony assignment the chord to the entire codon represented as entangled state of 3 dark protons. It is now clear this proposal very probably cannot realize all possible harmonies and is in conflict with the general model which as such fixes the correspondence between chords and codons without any additional assumptions.

2   Interactions between various levels

One challenge is to understand how the various realizations of the genetic code interact with each other. There are DX-DY interactions, DX-Y interactions and X-Y interactions and in living matter they should occur in long length scales so that they should be mediated by dark photons.

1. How dark photon triplets assumed to be generated by dark nucleon sequences interact with ordinary DNA? Here one can bring in rather stable ideas of TGD inspired view about quantum biology. Dark matter in TGD sense represents long length scale quantum coherence and bio-chemistry short scale coherence. The interaction is therefore between long and short scales.

2. There are two ways to interact: frequency resonance and energy resonance. Frequency resonance mediates long length scale interactions and if DX-X pairing exists, the exchange of dark photon triplets - 3-chords - allows long range DX-DY interactions. DX-X interaction by energy resonance is short range interaction so that X-(DX-DY)-Y interaction would give rise to long range interaction between X-Y as interaction induced by dark level (MB).

3. DX-X interaction involves energy resonance and transformation of dark photons to ordinary photons with the same energy. Bio-photons would be an outcome of the transition $h_{eff} \to h$. Also the reversal of this transition and more general transitions $h_{eff,1} \to h_{eff,2}$ are of course possible.

   Bio-photons have a universal energy spectrum corresponding to molecular and atomic transition energies. This is possible if they result from dark cyclotron photons if the condition $h_{eff} = h_{gr} = GMm/v_0$ introduced originally by Nottale and implying that the cyclotron energy does not depend on the mass of the charged particle producing the dark cyclotron photons.

2.1   The independence of the interaction energy on frequency

Dark matter as a hierarchy phases labelled by $h_{eff}/h_0 = n$ identifiable as a dimension of extension of rationals implies evolutionary hierarchy: n serves as a kind of IQ. This strongly suggests that ordinary matter is controlled by dark matter at MB and mimics its behavior.

Evolution would not proceed by change and necessity but would be a process controlled and guided by MB. MB would be an active intentional agent guiding the evolution. Situation in biology would be much like that in modern technological society where intentional technical progress leads to more and more refined products. How could this be realized at the level of basic bio-molecules? One should also understand how genetic code evolves gradually to a more refined form.

1. The selection of basic bio-molecules having energy resonance with their dark variants mediated by dark photon 3-chords by change would be extremely in-effective process. MB should have mechanisms of tuning the energies of dark photons to achieve energy resonance.

   This is achieved if the value of h_{eff} at the flux tubes mediating the interaction can be controlled. Since the length of flux tube is proportional to the h_{eff} by Uncertainty Principle,

the variation of h_{eff} would mean variation of the length L of the flux tube: a kind of motor action of MB. Cyclotron frequencies are proportional to the value of monopole magnetic field B at flux tube and by flux quantization one has $B \propto 1/S$, S the area of flux tube cross section (which for monopole flux tubes is closed 2-surface). The variation of the thickness/area of the flux tube, second motor action of MB, would allow to vary cyclotron frequencies.

2. The ideal situation concerning the coupling to ordinary matter would be that same chemical transition with fixed energy for given molecule could couple to several frequencies. This would be achieved if the cyclotron energy is constant.

   The condition that the cyclotron energies in a coupling to a given molecule do not depend on the frequency requires that $h_{eff,i}$ at flux tube i compensates this dependence. MB can vary the value of B to vary frequencies and the value of $h_{eff,i}$ to keep energy unaffected. The areas S and length L of flux tubes are varied so that the volume remains unaffected. $B \propto 1/S$ and $L \propto h_{eff}$ by Uncertainty Principle. $E_c \propto \hbar_{eff} B = constant$ implies that L/S is constant. S increases like $S \to x^2 S$ and $L \to x^2 L$ in the scaling changing $f_c \to f_c/x^2$. The magnetic energy $E_{magn} = B^2 SL \propto L/S$ of the flux tube is not changed. Kind of energy criticality would be in question - one would have a large number of flux tube configurations with the same energy and volume ideal for control purposes. Quantum criticality is actually basic dynamical principle of quantum TGD allowing to predict the spectrum of various coupling parameters.

3. Besides cyclotron frequences Josephson energies are central in TGD based model of nerve pulse and EEG. Josephson energy $E_J = ZeV$ and cyclotron frequency $f_c = ZeB/m$ do not depend on h_{eff}. An attractive possibility is that cyclotron photons couple to Josephson junctions meaning that they become Josephson photons and then transform to ordinary photons inducing molecular transitions.

4. In the case of bio-harmony the frequencies would be rational multiples of basic frequency and by separating common numerator they are certain integer multiples $f_i = n_i f_0$ of a basic frequency f_0. The integers n_i have decomposition to products of powers of certain primes: $n_i = \prod p_i^{k_i}$ and each of p_i appears as some maximal power $k_{i,max}$. If one has $n = \prod_i p^{k_{i,max}} n_0$ one can obtain $h_{eff,i} = h_{eff}/n_i$. In this manner one would obtain the desired independence of $E_{c,i}$ on f_i. For Pythagorean scale only primes $p = 2$ and $p = 3$ would be involved.

All codons coding for given AA could have same coupling energy. Unless the values of Planck constants and frequencies associated with flux tubes coupling to given codon are fixed, one could have same transition energy for all letters but this is an unrealistic condition. Transition energies are naturally different and can code for letters if not even codons. For this option only the correct combination of frequencies and values of $h_{eff,i}$ allows resonant coupling.

The 3-chords associated with different harmonies would naturally correspond to the same energy. The physics of emotions would not be directly visible at the level of chemistry: chemist would certainly agree with this. The values of Planck constants would characterize the frequencies: I have indeed speculated that nucleotides could be labelled by values of h_{eff}. Number theory would be essential for the understanding life at the level of genes: Galois groups would characterize the nucleotides. Galois groups code for complexity at the level of dark matter so that the behavior guided by the MB of molecule would depend on the $IQ = n = h_{eff}/h_0$ of MB.

2.2   The independence of cyclotron energy on frequency and Nottale hypothesis

Is the independence of interaction energy on frequencies consistent with $h_{gr} = GMm/v_0$ hypothesis [E1] [K7, K6, K4]? Here one might encounter difficulties. The division by n_i should change one of the parameters appearing in the formula. The interpretation has been m corresponds to the dark proton mass at the end of the flux tube connecting it to large mass M. If so m cannot be varied.

Could M be varied?

1. The parameter $v_0 \simeq 2^{-11}$ can be varied by powers of two, which do not affect the notes identified by octave equivalence.

2. Could M correspond to atomic or molecular mass in good approximation equal to sum of atomic numbers A of atoms involved? The divisors of the total atomic number A_{tot} would define the allowed integers n_i characterizing the frequencies of Pythagorean scale in the model of bio-harmony. One must have $h_{gr}/h > 1$ with requires $M > \hbar/Gm = 1.3 \times 10^{19} m_p v_0$. For $v_0 = 2^{-11}$ this corresponds to $M > \hbar/Gm = 6 \times 10^{15} m_p$. The scale of a water blob with $A = 20$ containing this number of protons is about 70 μ, which is of order cell size. One can wonder how A_{tot} could be kept as divisible by n_i characterizing the frequencies of the Pythagorean scale. The problem is that an addition of one proton spoils the divisibility conditions completely.

3. The solution of the problem could be based on a more precise view about h_{eff} [L23]. The understanding of the variation of Newton's constant - too large to be due to experimental errors - led to the realization of the meaning of the fact that space-time surfaces can be regarded simultaneously coverings of n_2-fold M^4 and n_1 fold CP_2 and that one has $n = n_1 n_2$ in $h_{eff}/h_0 = n$ and n_1 would have interpretation as the number of flux tubes which are parallel in M^4 and can be even disjoint. This would give $h_{gr} \propto n_1$ and the factors of n_1 should correspond to the integers characterizing the notes of the 12-note scale. One could perhaps say that effectively single proton is replaced with n_1 protons located at different flux tubes so that also proton mass becomes $n_1 m$. One would have effectively a Bose-Einstein condensate like state of n_1 protons (at different flux tubes).

4. In the Pythagorean representation of octave the notes correspond to powers $(3/2)^k$, $k = 0, 1, ..., 11$, if $3/2)^{12} \simeq 2^7$ is not included. The corresponding integers are $3^k 2^{11-k}$. Only powers of primes $p = 2$ and $p = 3$ are involved and one just have $n_1 \propto 3^{11} 2^{11}$. If one increases the number of octaves involved to 14 to get a representation for chords needed to avoid the mapping of two dark codons to same 3-chords, one must have $n \propto 3^{23} 2^{23} = 6^{23}$. One can consider also simpler representations using integers expressible in terms of powers of primes $p = 2, 3, 5$ but one must give up exact quint cycle in this case. Interestingly, a good guess for the standard value h of h_{eff} is as $h = 6 h_0$ [L8, L18].

5. Small p-adic primes $p = 2$, $p = 3$ and perhaps also $p = 5$ (Golden Mean) are expected to be of special importance in TGD inspired biology [K3]. $p = 2$ seems to appear everywhere and there is also support for $p = 3$ in biology [I11, I12] (see `http://tinyurl.com/ycesc5mq`): great evolutionary leaps seem to correspond to time scales coming in powers of 3.

6. The branching of the flux tube bundle to n_i sub-bundles $N_i = n/n_i$ could correspond to the reduction $h_{eff} \to h_{eff}/n_i$. This could be seen as reduction of h_{eff}. One can also consider phase transitions reducing n to n/n_i.

3 Homonymy of the genetic code

In the following I will discuss briefly the basic facts about genetic code at Wikipedia level with emphasis on the poorly understood aspects of the code. There are two interesting phenomena: synonymy and homonymy. Synonymy means several names for AA or tRNA codon so that several RNAs are mapped to the sama AA or tRNA codon: the understanding of the genetic code is the understanding of synonymy.

Homonymy means that the same RNA codon can correspond to several tRNAs or even AAs. A general TGD based view about homonymy differing from that discussed in [L20] based on the recent understanding of the interaction between various representations of the genetic code is described below.

3.1 Variations of the genetic code

There exists also as many as 31 genetic codes (see `http://tinyurl.com/ydeeyhjl`) and an interesting question is whether this relates to the context dependence. Mitochondrial codes differs from the nuclear code and there are several of them. The codes for viruses, prokaryotes, mitochondria and chloroplasts deviate from the standard code. As a rule, the non-standard

codes break U-C or A-G symmetries for the third code letter. Some examples are in order (see `http://tinyurl.com/puw82x8`).

1. UUU can code Leu instead of Phe and CUG can code Ser rather than Leu. In bacteria the GUG and UUG coding for Val and Leu normally can serve as Start codons.

2. UGA can code to Trp rather than Stop: in this case the broken symmetry is restored since also UGG codes for Trp.

3. There is variation even in human mitochondrial code (see `http://tinyurl.com/puw82x8`). In 2016, researchers studying the translation of malate dehydrogenase found that in about 4 per cent of the mRNAs encoding this enzyme the UAG Stop codon is naturally used to encode the AAs Trp and Arg. This phenomenon is known as Stop codon readthrough (see `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5133446/`).

4. There is also a variant of genetic code in which there are 21st and 22nd AAs Sec and Pyl coded by Stop codons. UGA can code for Sec and Stop in the same organism. UAG can code for Pyl instead of Stop and introduces additional breaking of A-G symmetry for the third letter (UAA to Stop and UAG to Pyl).

3.2   Wobble base pairing

Wobble base pairing (see `http://tinyurl.com/y73se8vs`) emerges from the observation that the number of tRNAs pairing with mRNAs is smaller than 45 and considerably smaller than that of mRNAs. The needed minimum number of tRNAs is 32. Therefore the RNA-tRNA pairing cannot be 1-1 and some mRNA codons must correspond to several tRNA codons.

 Remark: One could ask whether mRNAs code for tRNAs just like DNAs code for AAs. Homonymy for mRNA-tRNA pairing implies that the pairing can be many-to-1 only in given context.

1. According to the standard code, the first two bases of mRNA codon corresponds to two last bases of tRNA anti-codon and obey standard code. Wobble base pairing hypothesis applies to the pairing of the 3rd mRNA base to the 1st base in tRNA anticodon. At the level of chemistry the hypothesis is that the position of the first tRNA anticodon base pairing with the third mRNA base is variable and allows it to pair with several bases appearing as 3rd base in mRNA. This homonymy would be due to "wobbling" of the position of the first tRNA anticodon.

2. In the original model for wobble base pairing tRNA bases contain besides standard A, C, G, U also inosine I as a modification of G obtained by dropping NH_2 from the 6-cycle of G. It has turned out that there are actually variants of C and 5 variants of U (see `http://tinyurl.com/y73se8vs`). The large amount of homonymy for tRNAs forces to ask whether chemistry alone really dictates the genetic code.

3. The first tRNA letter is assumed to be spatially wobbling so that the association of tRNA with RNA is not unique and mRNA-tRNA pairing involves both synonymy and homonymy as the two tables for the pairing of the 1st 5' anticodon base of tRNA and 3rd 3' codon base of mRNA show. In the second column bold letters for mRN bases allow to read the standard pairing with tRNA codons in the first column and non-bold letters allow to deduce the non-standard behavior.

4. The first table (see `http://tinyurl.com/y73se8vs`) represents the original Watson-Crick proposal.

    (a) The pairings of the 3rd letter of mRNA codon to the 1st letter of tRNA anti-codon are following.
        - U → G.
        - G → U
        - {A, C or U} → I.

The 2nd and 3rd tRNA letters A and C are paired with the 1st and 2nd mRNA letters in the canonical manner. There are only 3 tRNA letters, which implies that the number of tRNAs is smaller than maximal.

(b) There is single 1-to-many pairing: U→ {G, I} giving rise to 2-fold homonymy.

5. Revised pairing rules (see `http://tinyurl.com/y73se8vs`) are more complex since the number of tRNA bases is larger (U has 5 variants and C has 2 variants). All mRNA letters have 1-to-many pairing. Even if one counts the variants of U as single U there is 4-fold homonymy for U and homonymies for other codons. For A one has 9-fold homonymy.

These variations do not induce variation in DNA → AA pairing if the AA associated with the homonyms of tRNA are identical. This seems to be the case almost always since the variation of the genetic code is surprisingly small. This raises the question whether there is some mechanism eliminating to high degree the expected effects of homonymy in mRNA→ tRNA pairing.

4 TGD view about homonymies

One should understand the homonymies of the genetic code [L20]. One can imagine homonymies at the level of DDNA-3-chord and DRNA-3-chord correspondences and between RNA-AA and RNA-tRNA correspondences.

4.1 Homonymies for DRNA-3-chord correspondence

It is possible that homonymies are present already at the dark photon level in the sense that the sub-harmonies have common chords.

1. Are the icosahedral orbits for different symmetry groups Z_6, Z_4, Z_2 disjoint? If they contain common triangles, the outcome is homonymy for dark codons unless one can scale the 12-note scales with respect to each other (different keys) to avoid common chords.

   This question finds an answer from the tables of [L2] representing the chords. If the two scales considered contain 3-chords with the same frequency ratios this can happen. Z_6 harmony contains chords of same type with whole note intervals: $C_x, D_x, E_x, ..., x = m, 6, 9$ coding the frequency ratios as is done in popular music. If second harmony contains several types such that they are not separated by a multiple of whole note interval, at least one common chord is unavoidable also for shifted harmonies.

2. From the tables 2 and 3 of Appendix one finds that for Z_6 and 2 Z_4 harmonies this is indeed the case and they have 2-chords involving 2 quints in common: 6-orbit and 4-orbit containing $x = 9$ 3-chords have 2 common chords. One has homonymy at dark level. If entire orbits are mapped to the same AA there would be 8 AAs in the same multiplet. Some DDNA and DRNA codons are mapped to the same 3-chord of dark photons. This problem is shared by all 3 models of bio-harmony.

3. For the unique Z_6 harmony and 3 $Z_{2,rot}$ (table 4 of Appendix) of harmonies common chords can be avoided by shifting the latter harmonies by a half-note. The reason is that the chords of same type are now separated by a multiple of whole note interval. For $Z_{2,refl}$ harmonics (table 5 of Appendix) the chords of same type are separated by odd number of half-notes so that common chords are unavoidable since 3-chords of the same type appear. There are also common chords with Z_4 harmony.

4. Z_6 and $Z_{2,rot}$ harmonies possess no common chords by a shift by odd number of half notes. Z_4 and $Z_{2,rot}$ and Z_4 and Z_6 possess at least 2 common chords. $Z_{2,refl}$ possesses more common chords with Z_4 and Z_6.

   The fusion of Z_6, Z_4, and $Z_{2,rot}$ harmonies with 2 common chords between in $Z_6 \cap Z_4$ $Z_4 \cap Z_{r,rot}$ seems seems to be best that one can achieve. This would give $1 \times 2 \times 3 = 6$ harmonies altogether unless one obtains new harmonies by by relative shifts of the key.

   How to solve the problem?

1. The above described homonymies involving 6-plets involve either 6-plet or 2-plet as second multiplet so that these deviations cannot be due to homonymy at the level of DRNA-3-chord correspondence.

2. Should one take seriously the puzzle that teased Pythagoras and led him to seriously consider that the structure of the Universe based on rationals has serious flaw in it. 12 quints give slightly more than 7 octaves: one has $(3/2)^{12} = 129.746337890625$ rather than $(3/2)^{12} = 128$ so that one obtains slightly more than octave under octave equivalence.

   Why not represent notes as powers of algebraic number $2^{1/12}$ and this is indeed done in practice (in rational approximation of course) but very musical people notice the difference and dislike this representation. There should be something deep in the representation of the scsale in terms of rationals as TGD indeed predicts. Note that a strict resonance is not required, it represents only the optimal situation.

3. Repeating the quint cycle gives slightly displaced chords: one can of course do this several times [L24]. Could these slightly displaced chords represent DDNA and RNA codons as 3-chords otherwise mapped to the same chords? This would also mean that the corresponding DNAs and RNAs correspond to 3-chords with at least one note differing only slightly. This kind of notes is shared by 5 chords in icosa-tetrahedral harmony. The addition of second quite cycle means that the integers $n_i = 2^k 3^{23-k}$ characterize the notes of the 3-chords and $2^k 3^{23-k}$ and $2^{k+12} 3^{11-k}$ represent the nearby notes.

4. The minimal modification would replace only minimum number of notes in the problematic chords with new ones. A stronger modification would replace the problematic chords with displaced variants with notes in the second quint cycle. One could also do the same for all chords and say that the number of codons for non-problematic dark codons is doubled.

   One could also consider the doubling of each letter of the codon so that each chord would be replaced with 8 almost copies except in the case of homonymic AAs. A non-homonymic AA coded by n RNAs would be coded by $8n$ 3-chords. If the frequency differences are small enough this is not seen at the level of transition energies of AAs: this must be the case for non-homomymous AAs. For homonymous RNAs the energy differences must be seen and remove the homonymy. This DRNA-3-chord homonymy would be analogous to the RNA-tRNA homonymy.

5. One can consider the problem from a different perspective. For Hachimoji DNA [I8] (see http://tinyurl.com/y2mcjb4r) the number of DNA letters seem to double so that codon is replaced with 8 codons. An explanation based on the Pythagorean dilemma was discussed in [L24]. In the model it was however assumed that the doubling of dark DNA and DNA is real being due to the possibility of having also negatively charged color bonds between dark protons so that dark proton is effectively dark neutron (this might happen even in ordinary nuclear physics in nuclear string model [K5]). The Pythagorean double covering of 3-chords could describe the doubling of codons. The doubling would not occur for the codons for which one has the homonymy - a prediction, which could be perhaps tested.

4.2   The map DRNA-DtRNA by 3-chords

The map $64 \to 40$ for DRNA-DtRNA inducing the corresponding map for $RNA - tRNA$ is not unique since there are many ways to reduces 64 to 40. Could this relate to tRNA-RNA homonomy? Consider icosa-tetrahedral code $20 + 20 + 20 + 4 = (3 \times 6 + 2) + (5 \times 4) + (10 \times 2) + (3 + 1)$ as example.

1. Suppose Z_2 is the divisor group (also Z_4 and $Z_3 \subset Z_6$ can be considered) so that the orbit can split to two and two tRNAs are associated with given amino-acid coded by n codons. At the first step one can take $20_1 + 20_2 + 20_3 + 4 \to 20_1 + 10_2 + 10_3 + 4 = 44$. Also $10_1 + 20_2 + 10_3 + 4$ and $10_1 + 10_2 + 20_2 + 4$ can be considered. Since Z_n has Z_2 as subgroup, the simplest manner to achieve $20_k = 10_k$ is to divide all orbits to 2 Z_2 cosets. This can be carried out in 3 ways.

2. One must get rid of 4 tRNAs. This can be achieved in several ways. In $20_1 = 3 \times 6 + 2$ one could have $6 + 2 \rightarrow 3 + 1$: there are 3 alternatives. In $20_2 = 5 \times 4$ one could have $5 \times 4 \rightarrow 3 \times 4 + 2 + 2$ (10 ways). In $20_3 = 10 \times 2$ one can take two 2:s to 1 (45) ways.

3. Could all these maps be realized and could they correspond to different maps at the level of dark codons? If the independence of resonances energies on frequencies is true with an appropriate choice of $h_{eff,i}$, it would seem that in all these cases same chemical tRNA is possible.

4.3   Homonymies for RNA-AA correspondence

There are two basic types of homonymies involving bio-molecules.

1. RNA-AA correspondence can vary somewhat and there are 31 variants of genetic code. RNA-tRNA homonymies are common and wobble phenomenon could be regarded as as such homonomy. This homony is poorly understood.

   I made the first attempt to understand homonymies in [L20] but failed to realize one absolutely essential feature. Despite RNA-tRNA homononmies there are practically no RNA-AA homonymies. They might be completely absent for given genetic code. There must be a simple explanation for this.

2. In TGD framework the genetic code is replaced with 3 codes. There is DRANA-DtRNA code mapping 64 DRNA codons to 40 DtRNA codons and $DtRNA - DAA$ code mapping 40 DtRNA codons to 20 DAAs. The composition of these codes gives DRNA-DAA code inducing the RNA-AA code.

   The highly non-trivial fact is that one has what mathematician would call commuting triangle: RNA-tRNA-AA = RNA-AA for given code. All the homonymies of RNA-tRNA code are possibly completely compensated for given $RNA - AA$ code. This must have simple explanation and once one has made this question, one also knows its answer in TGD framework.

3. For Hamiltonian cycles the $n(A)$ codons coding for given AA corresponds to orbit of a fixed codon at the orbit having symmetry group $Z_{n(A)}$. Genetic code maps the codons at the orbit to the AA corresponding to the orbit and replaces the symmetry group Z_n with trivial group $Z_n/Z_n = Z_1$.

   Remark: There are 6 chaotic icosahedral Hamiltonian cycles with symmetry group Z_1 so that therefore 20 amino-acids each coded by single codon. Could one interpret the 20 amino-acids with the chaotic representation of chaotic icosahedral Hamiltonian cycle?

   For RNA-tRNA correspondence similar process is possible. Now one replaces Z_n/Z_k where k is factor of n.

   Consider icosa-tetrahedral code as an example. $k = 2$ is simplest choice since it divides $n = 6, 4, 2$ for icosahedral codes but not for tetrahedral code for which one has $n = 3$: (ile, ile, ile, met) would naturally correspond to the 2 orbits under tetrahedral Z_3. This symmetry appears only for icosa-tetrahedral option. For other options one can explain it as an outcome of symmetry breaking for doublets and (ile,ile) and symmetry broken (ile,met) would have ile in common. This looks un-natural.

   One can indeed construct $64 \rightarrow 40$ map for DRNA and DtRNA codons by replacing some orbits with their Z_2 cosets but this map is not completely unique. This is possible for all code candidates, which all contain Z_6 and Z_4 symmetric icosahedral harmonies giving rise to amino-acids corresponding to 3 6-orbits and one 2-orbit for Z_6 symmetry and 5 4-orbits with Z_4 symmetry. The remaining orbits are 3-orbit and 1-orbit for tetrahedral symmetry broken to Z_3 and 2-plets for Z_2 orbits.

There are are however codes for which RNA-AA correspondence is non-standard. As explained above, the simultaneous replacement UUC-Leu $\rightarrow$ UUC-Phe and UUG-Leu $\rightarrow$ UUG-Ser can take place. Also AUG-met $\rightarrow$ CUG-met and GUG-met $\rightarrow$ GUG-met can occur.

A general explanation could be as follows. If the two homonymous amino-acids - Phe and Leu and Leu and Ser in the first example and met and Leu and Val in the second example- have very nearly same transition energy, and if the 3-chords correspond transition energies of AA irrespective of frequencies, homonymy becomes possible.

This problem can be avoided if the tRNA pairing second AA with the RNA codon is not present. Both options might be realized in the same organism. It could also happen that second AA is so far from energy resonance that it is only rarely translated.

4.4   Homonymies for RNA-tRNA correspondence

Could the possibility of several harmonies/moods with different chords increase the number of tRNA codons from the minimal value 40? Are these homonymies forced by necessity or do their reflect freedom of MB to choose? Do dialects emerge already at the molecular level and do they have some practical advantage?

1. Could the possibility of several moods demand more than the minimal number of tRNAs. Harmonies correspond to different collections of triplets (n_1, n_2, n_3) characterizing the chord.

   It was however already noticed that the variation of the Planck constants $h_{eff} \to h_{eff}/n_i$ associated with the flux tubes can modify the cyclotron energies. This would mean that the emotions are not directly seen at the level of molecular transitions as bio-chemist would certainly argue. If energy resonance couples dark photons to ordinary matter it could be possible to guarantee the coupling energy does not depend on the values of frequencies of the 3-chord at flux tubes. This would suggest that there is no motivation to increase the number of tRNAs for the lack of required resonance energies.

2. Could a large number of tRNAs as mediators of RNA-AA pairing be something chosen intentionally by MB rather than being forced by chemical limitations. Could surplus of different tRNAs be a safer option when some tRNAs are not produced. In natural languages there is large number of dialects and new are born all the time.

   No hard-wired correspondence would exist at chemical level. MB would be to some degree creative and able to build tRNAs from the stuff that it happens to find from the lab! Biology could be creative already at RNA-tRNA level and this flexibility could emerge from the intelligence coded by $h_{eff} = n$: the larger the number of factors of n the higher the intelligence of the system would be.

   This flexibility might also explain the homonymy at RNA-AA level and different genetic codes as a formation of dialects.

5   About the details of the genetic code based on bio-harmony

TGD suggests several realizations of music harmonies in terms of Hamiltonian cycles representing the notes of music scale, most naturally 12-note scale represented as vertices of the graph used. The most plausible realization of the harmony is as icosahedral harmony [L2] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/yyjpm25r`).

1. Icosahedron (see `http://tinyurl.com/l5sphzz`) has 12 vertices and Hamiltonian cycle as a representation of 12-note scale would go through all vertices such that two nearest vertices along the cycle would differ by quint (frequency scaling by factor 3/2 modulo octave equivalene). Icosahedron allows a large number of inequivalent Hamiltonian cycles and thus harmonies characterized by the subgroup of icosahedral group leaving the cycle invariant. This group can be Z_6, Z_4, or Z_2 which acts either as reflection group or corresponds to a rotation by π.

2. The fusion of 3 icosahedral harmonies with symmetry groups Z_6, Z_4 and Z_2 gives 20+20+20=60 3-chords and 3+1 + 5 + 10 =19 orbits of these under symmetry group and almost vertebrate genetic code when 3-chords are identified as analogs of DNA codons and their orbits as amino-acids. One obtains counterparts of 60 DNA codons and 3+1 + 5 + 10 =19 amino-acids so that 4 DNA codons and 1 amino-acid are missing.

3. The problem disappears if one adds tetrahedral harmony with 4 codons as faces of tetrahedron and 1 amino-acid as the orbit of the face of tetrahedron. One obtains 64 analogs of DNA codons and 20 analogs of amino-acids. I call this harmony bio-harmony. The predicted number of DNA codons coding for given amino-acid is the number of triangles at the orbit of given triangle and the numbers are those for genetic code.

4. How to realize the fusion of harmonies? Perhaps the simplest realization that I have found hitherto is based on union of tetrahedron of 3 icosahedrons obtained by gluing tetrahedron to icosahedron along its face which is triangle. The precise geometric interpretation of this realization has been however missing and I have considered several variants. I have proposed that the model could explain the two additional amino-acids Pyl and Sec appearing in Nature.

There is also a slight breaking of symmetries: ile 4-plet breaks into ile triplet and met singlet and trp double breaks into stop and trp also leu 4-plet can break in leu triplet and ser singlet (see http://tinyurl.com/puw82x8). This symmetry breaking should be understood.

5.1   Why 3 icosahedral harmonies and 1 tetrahedral harmony?

The following argument suggests a more detailed solution of these problems than proposed earlier.

1. The copies of icosahedron would differ by a rotation by multiples of $2\pi/3$ (Z_3) around axis through the common triangular face. This face unlike the other faces remains un-affected. Also tetrahedron remains un-affected so that it is counted only once.

   If the 3 copies of the icosahedral common face are counted as separate (this is important!), one obtains 20+20+20 faces from icosahedron. If also tetrahedral shared faces is counted as separate, tetrahedron gives 4 faces: 64 codons altogether as required. One obtains 19 orbits from the 3 icosahedra and 1 orbit from tetrahedron: 20 orbits as counterparts of amino-acids altogether.

2. But can one really counter the 4 common faces as separate? One must do so. Could these faces be interpreted as somehow special codons? Maybe as stop codons or start codons for the vertebrate genetic code which also corresponds to the realization of DNA, RNA ,tRNA, and amino-acids as dark proton triplets so that DNA sequences would correspond to dark proton sequences. Could the shared codons be assigned with various modifications of the vertebrate code involving also exotic amino-acids Pyl and Sec.

3. Consider first the tetrahedral face. If the common face is removed from the 4-face orbit of tetrahedron, the orbit has only 3 faces and correspond to an amino-acid coded by 3 DNA codons. ile is the only such amino-acid and the interpretation could be that one ile corresponds to the 3 tetrahedral faces and met acting as start codon to the fourth shared face.

4. Also 3 icosahedral amino-acids corresponding to orbits containing the shared face can lose 1 codon each. To nake this more concrete, one can look for the deviations from the vertebrate code.

   (a) There are 10 doublets if the doublet UAA, UAG acting as stop codons is counted as doublet coding for stop regarded formally as amino-acid.

   (b) The second member in the doublet UGA, UGG coding for tyr in code table could correspond to a common face and act as a stop codon.

   (c) For the modifications of genetic code UAG coding for stop can code for Pyl and UGA coding for stop can also code for Sec. UGA can also code for trp so that there would not be any symmetry breaking in this case. Could UAG and UGA correspond to common faces for two icosahedra?

   (d) There is also third icosahedral shared face. CUG coding for leu can also code for ser. Could this correspond to the third exceptional codon associated with the icosahedral part of the code?

5. If the answers to the questions are affirmative, all basic deviations from the vertebrate code can be understood. The translation of the codons associated with shared face would be unstable for some reason.

   (a) 3-chord representation is more fundamental than the chemical one. This could mean that the chords associated with the shared faces are very near to each other so that the correspondence between 3-chord representation and chemical representation of codons becomes unstable if based on triple resonance.

   (b) The proposal has indeed been that the 13th vertex implied by tetrahedron corresponds to a note very near to one of the notes of 12-note scale - this note is necessary since the 12-note scale defined by quints gives 12th note slightly more than octave under octave equivalence as discovered already by Pythagoras.

   If this picture is correct, the symmetry breaking of the genetic code would be due to the presence of the face common to icosahedron and tetrahedron and reflect the problem discovered already by Pythagoras. The rational number based Pythagorean scale defined by quints is special: people with absolute pitch prefer it over the well-tempered scale involving powers of irrational number $2^{1/12}$ requiring extension of rationals.

5.2   Could stop codons correspond to dissonant 3-chords?

One can approach the situation also from the point of view of harmony - or rather, dis-harmony: could dissonance 3-chords act as stop codons. The 3-chords of icosahedral harmonies can be classified to three groups depending on whether the triangle representing the chord contains 0, 1, or 2 sides [L2]: in in other words, whether the chord contains 0 , 1, or 2 quints. The harmonies can be labelled by the triplet (n_0, n_1, n_2) telling the numbers of chords with 0, 1, and 2 quints.

1. The unique Z_6 harmony necessarily present in the bio-harmony has $(2, 12, 6)$. It has two augmented chords (transposes of $C_{aug} = CDG\sharp$) containing two major thirds and defining the 3-chord of a harmony assignable to triangle). This beautiful chord to which finnish tangos so often end, cannot be regarded as dissonance.

2. The 2 Z_4 harmonies have $(n_0, n_1, n_2) = (0, 16, 4)$ and $(4, 8, 8)$. For the latter harmony one has genuine dissonances since the highest and lowest note of 3-chord are separated by major or minor third. The chords with 0 quints labelled by script "ex1","ex2",...,"ex6" (for the notation see [L2]) are dissonances in this sense. "ex7" and "ex8" ($CDF\sharp$ and $CDG\sharp$) cannot be regarded as dissonances in this sense.

3. The 3 $Z_{2,rot}$ harmonies have $(0, 16, 4)$, $(2, 12, 6)$, and $(4, 8, 8)$. Both 2-plets and 4-plets contain 2 dissonances.

4. There are 3 $Z_{2,refl}$ harmonies with $(2, 12, 6)$ and 1 with $(4, 8, 8)$. These harmonies have genuine dissonances. Interestingly, $(2, 12, 6)$ corresponds to a doublet for which only the second member corresponds to dissonance.

5. For tetrahedral harmony single step should correspond to 1/4:th of octave (using suitable power of 3/2 as a rational approximation) so that the notes at the vertices of tetrahedron should correspond to $CE\flat F\sharp$ defining C_{dim}. This does not appear in the icosahedral code table as 0-quint chord. Although the triangles of tetrahedron and icosahedron would be shared in some sense, the chords cannot be same. This support the idea that ile triplet and met are coded by tetrahedral faces.

The chords containing 0 quints appearing in Z_4 and Z_2 harmonics can be regarded as dissonant. The minimization of dissonance would give a fusion of the unique Z_6 harmony $(2, 12, 6)$, unique Z_4 harmony $(0, 16, 4)$ and unique $Z_{2,rot}$ harmony $(0, 16, 4)$. Bio-harmony would be unique and contain no dissonances. Recall however that the proposal is that bio-harmonies serve as correlates for moods realized even at the level of basic bio-molecules.

For other options one would have dissonant chords. $Z_{2,refl}$ harmony $(2, 12, 6)$ has only single dissonant chord. Since stop codons would naturally correspond to dissonances, this observation raises some questions.

1. Could the dissonant chord of $Z_{2,refl}$ harmony $(2, 12, 6)$ correspond to the triangle shared by tetrahedron and icosahedron? Could this correspond to (stop,trp) pair with stop coded by dissonant chord "ex"7 ($CDF\sharp$ defining part of D7 chord). This would fix the code to contain Z_6 harmony $(2, 12, 6)$, unique Z_4 harmony $(0, 16, 4)$ and unique $Z_{2,refl}$ harmony $(2, 12, 6)$. There would be single dissonance coding for stop in stop,trp doublet.

2. The doublet coding for stop should formally code for amino-acid. One cannot realize this doublet as a doublet of dissonances with "ex"n, with $n \in \{1, .., 6\}$ for single bio-harmony. The second member of this doublet could however correspond to the shared triangle.

This tentative picture should be of course checked. There are also cycles without any symmetries. Could these chaotic cycles be interpreted as disharmonies.

5.3 How could the representations of genetic code as dark 3-chords and nucleotide triplets relate?

One of the poorly understood aspects of the model is how the various representations of the code relate.

5.3.1 Frequency coding of nucleotides is not possible

Frequency coding of nucleotides would look natural but it is easy to see that it is in conflict with bio-harmony.

1. The representations as dark proton triplets and dark photon triplets do not involve decomposition to ordered triplet of letters as the ordinary chemical representation does. Dark protons are entangled and one cannot order them and there is no obvious ordering of the frequencies of dark photons.

   This is not a problem for the correspondence between dark proton triplets and dark photon triplets and one can even imagine assignment of dark cyclotron photons with 3 parallel flux tubes acting as wave guides. This could mediate the interaction between dark variants of basic biomolecules with same value of h_{eff} as frequency resonance.

2. The interaction between ordinary DNA/RNA/tRNA and its dark variant should involve the transformation of dark photon triplet associated with flux tube triplet emanating from dark bio-molecule to ordinary photons (possibly bio-photons) and energy resonance would be involved. Is the energy resonance involved with the formation of the dark-ordinary pairs or with the sustainment of these pairings? The example of benzene suggests sustainment.

3. The assumption that energy resonance is involved with dark-ordinary pairing indeed leads to problems. The first guess would be that ordinary photon triplet somehow carries information about the position of nucleotide in the codon. The 4 nucleotides would correspond to 4 frequencies with frequency scale depending on the position inside the codon. There are indeed 12 frequencies in the 12-note scale so that 3 frequency scales with 4 frequencies associated with each of them would give 64 combinations of frequencies.

   Frequency coding of nucleotides however leads to a problem. The first two letters of the codon are known to determine the amino-acid coded by it to a high degree since the third letter typically distinguishes between 1 or 2 amino-acids only, and labels codons at the orbit of DNA codon defining amino-acid. Therefore for DNA codons coding same amino-acid the first two frequencies should be same. This is not the case for bio-harmony for the simple reason that the frequencies of 3-chords along the orbit defining amino-acids are different. Only the frequency ratios defining the type of the chord are same along the orbit.

   The frequency ratios determine the correspondence so that the correspondence can be only between *entire* dark and ordinary codons, and cannot be reduced to correspondence between frequencies and letters. Holism does not reduce to reductionism.

5.3.2 Does the impossibility of frequency coding of nucleotides lead to problems with the models of replication and transription?

This becomes a potential problem in the model for DNA replication and transcription to RNA.

1. The basic picture about bio-catalysis in TGD framework is following. U-shaped magnetic flux tubes emanate from the reactants and can reconnect to form a pair of flux tubes connecting the reactants. The shortening of the flux tube pair by a reduction of h_{eff} brings the reactants together and liberates the energy needed to kick the reactants over the potential wall making the reaction rate extremely low otherwise.

   The U-shaped flux tubes or flux tube triplets would be associated with dark codons of dark DNA accompanying DNA strand, and would be formed as the flux tube pair(s) connecting the strands split by the reversal of reconnection. The h_{eff} associated with resulting U-shaped flux tubes associated with replicating strands would increase requiring metabolic energy. They would get longer and could act as tentacles scanning the environment to spot similar flux tubes assignable to nucleotides or codons by resonance.

2. In the standard picture one assumes that nucleotides defining the letters of the codons appear as non-correlated molecules in the environment, and that each codon is built by a stepwise process in which letters attach to it. The letters can respond only to single frequency and cannot "know" which position to attach to. Thefrequency coding is not consistent with the idea that dark photon triplet assigned with the dark codon gives rise to energy resonance with the letters one by one.

   Could the triple resonance occur as single step and attach all 3 nucleotides in single step? Or could the triple resonance be a collective frequency resonance with dark codon already attached to the ordinary codon in the environment. Ordinary-dark pairing by energy resonance would sustain rather than generate DNA strand since otherwise the Coulomb repulsion due to the large negative charge of DNA does not allow stability.

3. The problem is that it is nucleotides seem to appear in the environment rather than codons. Could the nucleotides of the environment actually form loose codons connected to dark codons by long flux tubes with large value of h_{eff}? Could the reduction of h_{eff} bringing nucleotides together induce the reduction of flux tube lengths giving rise to ordinary codon? If the reduction of h_{eff} for flux tubes occurs nucleotide-by nucleotide, one would have consistency with the standard picture. The simplest picture is following.

   Dark codons are paired with the loose variants ordinary codons. The opening of DNA double strand leads to the splitting of the flux tube pairs connecting the ordinary codons of strands to U-shaped flux tubes, which reconnect with U-shaped flux tubes coming dark codons paired with loose ordinary codons. The reduction of h_{eff} d pairs nucleotides of loose codons with those of ordinary codons.

4. The pairs of dark codons and loose codons would be analogous to tRNA molecules. One can imagine even pre-tRNA molecules with loose coupling of RNA and amino-acid so that replication and transcription would be very similar topological processes. Also RNA transcription and translation of RNA to amino-acids would rely on similar mechanism. The only difference would be that only the second - active - strand would form U-shaped flux tubes connecting with dark RNA codons.

5.3.3 What about remote DNA replication

This model could also explain remote replication of DNA for which Montagnier *et al* have reported evidence [I10]. Also remote transcription is predicted to be possible. I have already earlier considered a model of remote replication [K9] in an article written together with Peter Gariaev who has reported this kind phenomenon already earlier. I have discussed the findings of Montagnier *et al* in [L1].

1. The experiment involves two vessels, call them A and B. A contains genes and B only nucleotides - at least according to the standard picture. There is irradiation using 7 Hz frequency

not far from the lowest Schumann frequency having a nominal value of 7.8 Hz. What happens is that the replicas of genes appear in B. It is also reported that the DNA generates em radiation possibly responsible for the information transfer.

2. The proposed model for the ordinary DNA replication generalizes easily to describe also remote replication. The new element would be that the U-shaped flux tubes from A would extend to B - here 7 Hz radiation could be essential - , would be parallel to each other, and have same average length, which is natural if they have same value of h_{eff}. Also the experimental arrangement could favor parallel flux tubes. In B the dark codons paired with loose codons formed from ordinary nucleotides would be present, and their U-shaped flux tubes would reconnect with those coming from A. Remote replication could take place: here it is essential that the U-shaped flux tubes are parallel and have very nearly the same length.

The TGD interpretation would be that the Earth's magnetic body is involved and generates quantum coherence in the length scale at least the size of the system studied. The reported em radiation would naturally relate to the dark photon triplets representing the codons.

5.3.4 Is ZEO needed to understand the replication?

In TGD one must give up thinking in terms of standard ontology of bio-chemistry in which the process is a kinetic process governed by differential equations for the populations of molecules and proceeding in step-wise manner nucleotide by nucleotide. ZEO suggests temporal holism - at least at the level of single dark codon, which cannot be built building brick by building brick.

1. An open question is in which time scale this temporal quantum holism holds true: in the time scale of addition of single codon or in the time scale of replication of gene or something else? In the following the possibility that temporal holism holds in the time scale for the pairing of dark codons.

2. In ZEO one could have state function reduction in which initial state corresponds to dark codon plus population of nucleotides and final state to dark codon paired with the ordinary codon formed from 3 nucleotides in energy resonance with the codon formed from nucleotides. What matters are only the initial and final states.

3. If "big" state function reduction (BSFR) is in question, the final state would correspond to a superposition of deterministic time evolutions leading from the outcome of the reduction to geometric past, possibly but not necessary to a state in which nucleotides do not form codon paired with the dark codon.

4. The process would create strong correlations between the position of nucleotides of the codon and between the positions of codon and its dark variant and therefore a generation of entanglement. Unitary evolutions followed by "small" state function reductions (SSFRs) would generate a state as a superposition of the states satisfying the criteria of the desired final state and other states and BSFR would select the desired final state. It could be followed by BSFR returning the original arrow of time but doing nothing for the state.

6 How to compose beautiful music of light in bio-harmony?

The topic of this section is the detailed definition of the notion of bio-harmony [L4, L5, L27]. A sequence of 3-chords of bio-harmony defines a music piece: what rules guarantee that this piece is beautiful? This question is interesting because the chords of bio-harmony correspond to DNA codons.

6.0.1 Bio-harmony as a realization of genetic code

TGD leads to a notion of bio-harmony in terms of icosahedral and tetrahedral geometries and 3-chords made of light assigned to the triangular faces of icosahedron and tetrahedron [L4, L5, L27]. Bio-harmonies are associated with the so-called Hamiltonian cycles , which go through every vertex

of Platonic solid once. For icosahedron the number of vertices is 12, the number of notes in 12-note scale. The 64 codons of bio-harmony represented as light 3-chords formed by dark photon triplets are formed from 3 20-chord harmonies associated with icosahedron and the unique 4-chord harmony associated with tetrahedron.

The surprise was that vertebrate genetic code emerged as a prediction: the numbers of DNA codons coding for a given amino acid are predicted correctly. DNA codons correspond to triangular faces and the orbit of a given triangle under the symmetries of the bio-harmony in question corresponds to DNA codons coding for the amino acid assigned with the orbit.

Codon corresponds to 6 bits: this is information in the usual computational sense. Bio-harmony codes for mood: emotional information related to emotional intelligence as ability to get to the same mood allowing to receive this information. Bio-harmony would be a fundamental representation of information realized already at molecular level and speech, hearing and other expressions of information would be based on it. For emotional expression at RNA level possibly involved with conditioning at synaptic level see [L17].

6.0.2 About generalizations of the notion of bio-harmony

One can consider several generalizations for the notion of bio-harmony.

1. All Platonic solids, in particualr tetrahedron, cube, octahedron and dodecahedron are possible and one can consider the possibility that they also define harmonies in terms of Hamiltonian cycles. Dodecahedron would have 5-chords (pentagons as faces) as basic chords and there is only single harmony. Same mood always, very eastern and enlightened as also the fact that scale would have 20 notes.

   Also octahedron gives 3-chords (triangular faces) whereas cube gives 4-chords (squares as faces). One can of course speculate with the idea that DNA could also represent this kind of harmonies: sometimes the 3N rule is indeed broken, for instance for introns.

2. Galois confinement [L33] allows the possibility to interpret dark genes as sequences of N dark proton triplets as higher level structures behaving like a single quantal unit. This would be true also for the corresponding dark photon sequences consisting of 3N dark photons representing the gene in bio-harmony as an analog of a music piece consisting of 3-chords and played by transcribing it to mRNA.

   Basic biomolecules (DNA, RNA, tRNA, amino acids) would have names represented as a sequence of light 3-chords representing a piece of music and dark biomolecules with the same name could recognize and communicate with each other in 3N-resonance. Dark-ordinary communications could transform dark 3N-photon to single bio-photon so that resonance would be possible when the sum of energies coincides with a transition energy of the ordinary biomolecule. The resonance condition would very effectively select survivors in the fight for survival.

3. The picture can be viewed even more generally. Any discrete structure, defining graph, in particular cognitive representation providing a unique finite discretization of space-time surface as points with the coordinates of the 8-D embedding space coordinates in the extension of rationals, defines harmonies in terms of Hamiltonian cycles. Could also these harmonies make sense? The restrictions of the cognitive representations to 2-D partonic 2-surfaces would define something analogous to bio-harmony as Hamiltonian cycle of 2-D graph (Platonic surfaces solids can be regarded as 2-D graphs). The interpretation as representations of Galois groups and the notion of Galois confinement is possible although one loses the symmetries of the Platonic solids allowing to identify genetic code.

During years I have indeed considered some modifications of the original bio-harmony base on the fusion of 3 icosahedral harmonies and tetrahedral harmony in partcular so called E_8 harmony and toric harmony [L7, L16] but the overall conclusion [L22] is that the original model is the most plausible candidate.

6.0.3 The challenges of the model

The model of bio-harmony is far from complete and this article discusses a more detailed definition. Also the question about the rules defining beautiful music by posing rules on chord sequences are considered. These aesthetic rules are also rules for the corresponding DNA and amino-acid sequences.

1. The fusion of the three harmonies having symmetry groups Z_n, $n = 6, 4, 2$ has been considered but not in the required detail. The Hamiltonian cycles of icosahedron are fixed only modulo isometries of icosahedron preserving the shape of the cycle, scalings of the cycle by a power of quint forming group Z_{12} leaving the cycle of invariant but inducings transponation (change of the key), and the change of the cycle orientation possibly related to minor-major dichotomy correlating with joyful-sad dichotomy. For a single icosahedral cycle these transformations do not change anything but for the fusion of 3 cycles realized at the same icosahedron the situation changes, and the number of harmonies increases dramatically.

   Are all combinations of icosahedral harmonies allowed or are there some natural restrictions on them? I have considered this question but it seems that there is no good reason for posing any restrictions. The spectrum of harmonies determined by dark genetic codons and therefore the spectrum of emotions at the molecular level would be surprisingly rich.

2. Is it possible to reproduce the basic harmonies of the western music based on the 12-note system which inspired icosahedral harmonies? In particular, can one understand the chords C, F, G of C-major scale? By octave equivalence the nearest neighbors of the Hamiltonian cycle are related by quint scaling scaling frequency by factor 3/2 scaling C to G. The 3-chords containing at least one cycle edge contain quint (C→ G) and quint is the basic aspect of bio-harmony. For harmonies with opposite orientation quints become perfect fourths (C→ F) and FCG corresponds to transponantion of F by two quints.

   For a single icosahedral harmony the chord-pairs analogous to C-F or C-G do not appear in any obvious manner. If the 3 icosahedral harmonies are related by quint scalings (FCG) the analogs of these chord pairs become natural. Could this be the solution to the problem?

3. What are the rules producing aesthetically satisfying music? I experimented with the ultraconservative assumption that only chord pairs containing common quint are allowed: the result was not ugly but it was boring. Already the transitions of CFG major scale are too radical for this option!

   An attractive idea is that the sequence of 3-chords is continuous in some sense. Could the sense be strictly geometric: could chord pairs be nearest neighbors in some sense. For Option I nearest neighbors have a common edge (3 nearest neighbours). For Option II they have a common vertex (10 nearest neighbors). These options do not allow all 3-chord pairs and thus not all possible DNA pairs and all possible amino-acid pairs. A more abstract definition identifies the nearest neighbors with the orbits of nearest neighbors for Option I or II under the symmetry group Z_n ($n = 6, 2$). Codon is replaced with the codons coding for the same amino-acid. For Option II this allows to have all possible chord pairs and therefore DNA and amino-acid pairs.

4. Also the role of tetrahedral harmony and its relation to start and stop codons is interesting. One wants also to understand why the genetic code at the bio-chemical level is not quite complete and why there are several variants of it.

6.1 About bio-harmonies

The set of allowed 3-chords define music harmony. The 12-note scale is essential for the western view about harmony. The TGD inspired geometric model for music harmony identifies bio-harmony as a fusion of 3 icosahedral harmonies with 12-note scale represented geometrically as a Hamiltonian cycle at icosahedron and 1 tetrahedral harmony represented as a unique Hamiltonian cycle of tetrahedron. Each icosahedral harmony has 20 3-chords identifiable as triangular faces of the icosahedron whereas tetrahedral harmony 4 3-chords. This gives 20+20+20+4=64 chords - the number of genetic codons.

Symmetry	#(class)	#(repr)
Z_6	1	8
Z_4	2	12
$Z_{2,rot}$	3	24
$Z_{2,refl}$	5	24

Table 1: The number $\#(class)$ of equivalence classes of Hamiltonian cycles ad the number $\#(repr)$ of representatives in the class for icosahedral Hamiltonian cycles. If the orientation is not taken into account the number of representatives reduces to $\#(repr)/2$

6.1.1 Symmetries of icosahedral harmonies

There are 3 types of icosahedral harmonies with symmetries characterized by a subgroup of icosahedral isometries, which is Z_6, Z_4 or Z_2 acting either as a rotation by π or as a reflection. The orbits of triangles are identified as counterparts of amino-acids coded by the DNA codons assigned with the triangles of the orbit.

1. For Z_6 given triangle gives rise to 3 6-orbits with 6 triangles and 1 2-orbit: Z_3 subgroup of icosahedral group permutes the 3 6-orbits and acts trivially to 2-orbit.

2. For Z_4 there are 5 4-orbits and Z_5 permutes these orbits.

3. For Z_2 there are 10 2-orbits and Z_{10} permutes them. Z_2 can act either as reflections or rotations.

There are also 6 cycles without any symmetries perhaps identifiable as dis-harmonies. They will not be considered in the sequel. For them the number of amino-acids coded by codon would be one.

Table 1 summarizes the numbers of equivalence classes of cycles and under icosahedral rotation group for various symmetry groups as well as the numbers of representatives in the class. These numbers allow to deduce the number of bio-harmonies by fixing one of the icosahedral harmonies, most naturally the Z_6 harmony for which one has only one class.

Remarkably, the combination of 3 icosahedral cycles with symmetries Z_k, $k = 6, 4, 2$ with the tetrahedral Hamiltonian cycle gives 64 codons and the model correctly predicts the numbers of DNA codons coding for a given amino acid. Could there be a connection between music and genetic code? Could one speak of bio harmonies as correlates of emotions at the molecular level?

The natural expectation is that the symmetries Z_n of a given harmony leave the ratios of frequencies of 3-chords invariant. This is true if the edge connecting nearest neighbors along Hamiltonan cycle corresponds to a quint that is scaling of frequency by 3/2 and projection to the basic octave (octave equivalence). Therefore the chords at the orbit of a given chord coding for the same amino-acid are replaced by a scaling by power of 3/2 so that the scalings are mapped to unitary rotations.

The factors of 12 include indeed 6, 4, and 2 so that the 12-element group of scalings modulo octave equivalence can be mapped to Z_{12} rotations. There is however a problem with rational quints due to the fact that - as already Pythagoras found - $(3/2)^{12} = 129.746...$ does not correspond exactly to $2^7 = 128$. One reason for introducing icosahedron could be that this brings additional note allowing to get rid of the problem. One can also construct the notes by powers of $2^{1/12}$ applied to the basic frequency but now the frequencies are not rational. Furthermore, people with absolute pitch favor rational frequency ratios, which suggests that rational numbers and roots of unitary assignable with adelic physics as physics of cognition are really important.

6.1.2 Fusion of 3 icosahedral harmonies and tetrahedral harmony to bio-harmony

There is quite a large number of icosahedral Hamiltonian cycles and therefore of bio-harmonies. Although the isometries of icosahedron and their transponations do not matter for given icosahedral harmony, they matter when one has 3 icosahedral harmonies. A simple example from physics helps

to understand this: although rotations are symmetries of an N-particle system the rotations of a single particle are not symmetries anymore and represent new degrees of freedom.

1. Bio-harmony assigns to the same icosahedron 3 Hamilton cycles with symmetries Z_k, $k = 6, 4, 2$. This means assigning to the same icosahedron 3 Hamiltonian cycles giving rise to 3 representations of 12-note scale each giving 20 chords so that one 20+20+20 chords coding 3 classes of amino acids. Tetrahedron gives the remaining 4 chords.

   There are N_i, $i = 1, 2, 3$ cycles corresponding to $Z_{k(i)}$, $k(i) = 6, 4, 2$: for the values of N_i and detailed 3-chord contents of icosahedral harmonies see [L2]. From the table **Table 1** one has for $(Z_6, Z_4, Z_{2,rot})$ #$(class)$ = (#$(class)_1$, #$(class)_2$, #$(class)_3$) = $(1, 2, 3)$ giving 6 different classes and $(Z_6, Z_4, Z_{2,refl})$ (#$(class)_1$, #$(class)_2$, #$(class)_3$) = $(1, 2, 5)$ giving 8 different classes. This gives $N = 14$ different icosahedral Hamiltonian cycles.

   The numbers of reresentatives for given equivalence class are for both $(Z_6, Z_4, Z_{2,rot})$ $(Z_6, Z_4, Z_{2,rot})$ #$(repr)$ = $(2, 12, 24)$.

2. The 3 cycles go through all points of the icosahedron. This means that for each point of icosahedron there are 3 cycles going through that point. There can be however situations in which there are common edges. 5 edges arrive at given icosahedral vertex. There are 3 cycles entering and leaving the vertex: this makes 6 cycle edges. There is necessarily one edge shared by two cycles. If the edge is shared by 3 cycle edges, one edge has no cycle edge. This kind of situation - 3-edge - is achieved by performing a suitable Z_5 rotation for the third cycle.

   Do all bioharmonies have 3-edges? Could 3-edges have a special role concerning bio-harmony and music experience? Could they define chords with preferred quints such as chords C, F, G in C major scale? The bio-harmonies having chord(s) with 3-edge could give rise to simple CFG type harmonies. Fusion of 3 icosahedral harmonies differing by quint scalings gives a CFG type situation, and one could assign all these 3 types of chords with a triangle with 3-edge. Geometrically the chord progression would reduce to a repetition of the same triangle! Allowing also the triangle at the other side of the 3-edge, the chord progression involving only these 2 triangles consists of 3+3=6 chords.

3. One can assume that the 3 Hamiltonian cycles start at the same almost arbitrarily chosen vertex of the icosahedron. As a special case one can assume that it corresponds to the same basic note (C). Since Z_6 allows only a single cycle, it is natural to fix it: the fact this cycle has 2 orientations gives degeneracy factor 2.

   The other other cycles are determined apart from the rotation group Z_5 leaving the base point invariant. Therefore the Z_4 and Z_2 harmonies give rise to an additional $5^2 = 25$-fold degeneracy of bio-harmonies $N \to 25N$. If the cycles are required to have a common first edge besides the base point, one does not obtain the degeneracy factor. This argument shows that common edges are possible and the vertices associated with them are definitely special.

   Fixing the cycle types and the Z_6 cycle one can calculate the number of bioharmonies for a given equivalence classes as the number #$(repr(Z_4))$#$(repr(Z_2))$ One obtains 12×24 representatives for both choices of Z_2. For r $Z_2 = Z_{rot}$ the total number of bioharmonies is

   $$N(harmony, rot) = 2 \times 2 \times 12 \times 3 \times 24 = 2^7 \times 3^2$$

   $$N(harmony, refl) = 2 \times 2 \times 12 \times 5 \times 24 = 2^7 \times 3 \times 5 \ .$$

   The first factor of 2 comes from the two orientations for the fixed Z_6 cycle.

4. The transponations realized as scalings along the Hamiltonian cycle define 1-to-1 map of icosahedral vertices which is however not an isometry but preserves the harmony. This gives a degeneracy factor 12^2 and one has

   $$N(harmony, ...) \to 12^2 \times N(harmony, ...) \ .$$

The formula for the total number of bioharmonies is

$$
\begin{aligned}
N(harmony) &= N(harmony, rot) + N(harmony, refl) = 2^{14} \times 3^3 \ , \\
N(harmony, rot) &= 2^{11} \times 3^4 \ , \\
N(harmony, refl) &= 2^{11} \times 3^3 \times 5 \ .
\end{aligned}
\tag{6.1}
$$

$$\tag{6.2}$$

6.1.3   How to understand the tetrahedral code and symmetry breaking of the perfect code?

The precise understanding of the relationship between tetrahedral and icosahedral codes has been a long standing challenge andI have considered several scenarios. The geometric idea has been that tetrahedron is somehow glued to icosahedron along on faceand selects a unique codon of the icosahedron defining the basic chord. As found, another manner to fix this chord as a chord to which one can assign 3 cycle edges. There might be other faces with the same property.
  One can get information about the situation by looking at the code table.

1. There are 10 unbroken icosahedral Z_2 doublets   containing (stop,stop) plus 1 symmetry broken doublet (stop,tyr). What could cause the symmetry breaking? The energy resonance condition associated with the pairing of dark mRNA codons with dark tRNA codons could explain the presence of stop codons: translation would stop when no tRNA in energy resonance is found.

    Dark 3-photon representing the dark stop codons could not couple to tRNA codon in energy resonance since there would not be tRNA with cyclotron resonance energy triplet resonating with that of dark stop codon.   This would be the case for the (punc,punc) doublet and also for punc member of (puc,trp) doublet. The mimicry of dark level by biochemical level would not be complete. For   the variants of the code it would be even less complete.

2. From the table one learns that both Z_6 and Z_4 codons are realized completely for the vertebrate code. This leaves only one conclusion: (ile,ile,ile,met) must correspond to a Z^4 symmetry breaking for tetrahedral rather than icosahedral 4-plet.   The AGG coding for met, which is   unique in the sense that it serves as a mark for the beginning of genes, would correspond to a tetrahedral face.

    The failure of energy resonance could force the splitting of unbroken tetrahedral ile 4-plet to (ile,ile,ile,met). Fourth codon in Z_4 4-plet would be in energy resonance with tRNA associated with met. Note that icosahedral code gives rise to 4+5+10=19 amino-acids and met provides   the 20th amino acid.   Symmetry breaking would be necessary to mark the starting and stopping points of transcription and translation.

    3-chords also depend on the icosahedral harmony and for some icosahedral harmonies energy resonance could fail so that the emotional state of at dark matter level would reflect itself at the biochemical level. The number of icosahedral harmonies is (1,2,3,5) for $(Z_6, Z_4, Z_{rot,}, Z_{2,refl})$. For Z_4 and Z_2 the failure of energy resonance is possible.

    Remark: I must confess that many earlier texts about the problem contain a stupid error.   I have considered the proposal that (ile,ile,ile,met) could correspond to symmetry broken icosahedral 4-plet. Vertebrate code has however 5 unbroken 4-plets corresponding to (val,pro,thr,ala,gly) as also 3 unbroken 6-plets (leu,ser,arg)! For vertebrate code the symmetry breaking can therefore occur only for icosahedral Z_2 doublets and tetrahedral Z_4 4-plet.

6.1.4   Variations of the genetic code

There exists also as many as 31 genetic codes (see `http://tinyurl.com/ydeeyhjl`) and an interesting question is whether this relates to the context dependence. Mitochondrial codes differ from the nuclear code and there are several of them. The codes for viruses, prokaryotes, mitochondria

and chloroplasts deviate from the standard code. As a rule, the non-standard codes break U-C or A-G symmetries for the third code letter.

In the proposed framework the failure of energy resonance conditions could be at the level of tRNA. The dark tRNA analog of RNA could be in energy resonance with "wrong" amino acid.

Some examples are in order (see `http://tinyurl.com/puw82x8`).

1. UUU can code Leu instead of Phe (symmetry breaks for Phe doublet) and CUG can code Ser rather than Leu (symmetry breaks for leu 6-plet). In this case it seems that the "problem" is at the level of tRNA. The dark RNA codon could couple with a "wrong" amino acid.

2. In bacteria the GUG and UUG coding for Val and Leu normally can serve as Start codons. In this case symmetry breaking for Z_4 4-plet would be in question. The problem could be also at tRNA level. Note however that both tetrahedral codons and icosahedral Z_4 codons have the same symmetry group. Could tetrahedral codons correspond to a different frequency scale and correspond to Leu and Val 4-plet instead of symmetry broken ile 4-plet.

3. UGA can code to trp rather than punc: in this case the broken symmetry would be restored since also UGG codes for trp. Both codons for (trp,trp) doublet would be in resonance: this supports the explanation for the emergence of the third stop codon.

4. There is variation even in human mitochondrial code (see `http://tinyurl.com/puw82x8`). In 2016, researchers studying the translation of malate dehydrogenase found that in about 4 per cent of the mRNAs encoding this enzyme the UAG Stop codon is naturally used to encode the AAs trp and arg. This phenomenon is known as Stop codon readthrough [I9]. Also this phenomenon could be understood at tRNA level.

5. There is also a variant of genetic code in which there are 21st and 22nd AAs Sec and Pyl coded by Stop codons. UGA in (punc,trp) doublet can code for Sec and punc in the same organism. UAG can code for (punc,punc) doublet Pyl instead of punc and UAG. This introduces additional breaking of A-G symmetry for the third letter of codon. Energy resonance at the level of tRNA could explain these deviations from the vertebrate code.

Peter Gariaev has introduced the notion of homonymy of genetic code meaning that the same codon can code for several amino-acids and the coding depends on context. I have considered this phenomenon from the TGD point of view in [L20]. Resonance could explain this phenomenon.

Dark mRNA codon could be in frequency resonance with dark tRNAs coding for different amino acids. The fraction of particular synonymous amino-acid produced in translation would naturally depend on how well the energy resonance condition is satisfied. Homonymy could also reduce to the level of tRNA: this happens if the coupling of the tRNA analog of RNA codon has energy resonance with several amino-acids.

6.2 How to produce beautiful bio-music?

Music expresses and produces emotions and harmonies in music correspond to emotions. Chemical representation of the genetic code should be the same irrespective of the emotional state of the gene represented at the magnetic body in terms of dark proton triplets also representing genetic codons and by music of light represents 3-chords of light with frequency ratios determined by one of the bio-harmonies.

This is achieved naturally. The correspondence between the chords of harmony and DNA and amino-acids does not depend on what vertex of icosahedron the base note (C for definiteness in the sequel) corresponds to. It also depends only on the shape of the Hamiltonian cycle invariant under isometries of the icosahedron. Furthermore, transpositions of the scale by power of 3/2 plus projection to the basic octave do not affect the Hamiltonian cycle and therefore leave the correspondence with DNA codons and amino acids invariant.

The sequences of 3-chords would correspond to sequences of DNA codons mapped to sequences of amino-acids. Genes would be like music pieces. These music pieces would also serve as kind of names of passwords in 3N-fold resonance in communications between dark variants of basic

biomolecules and between them and ordinary basic biomolecules. They would be like theme songs of TV series catching the attention or names essential for symbolic dynamics at the level of the basic biomolecules. The basic biomolecules in the same emotional state - that is having the same bio-harmony - could resonate and therefore couple.

What the rules for a beautiful bio-music could be? Could these rules select particular bio-harmonies and/or particular DNA sequences as allowed chord progressions and allow a deeper understanding of why particular genes are selected? Note that the condition that the chords of bio-harmony define 3N-resonances assignable to transitions of the basic biomolecules could lead to the selection of both harmony and biomolecules. A weaker condition is that ordinary biomolecules couple only to the sum of frequencies appearing in 3N-frequency assignable to dark codon.

6.2.1   Are beautiful chord sequences continuous in some sense?

The original model discussed in [L2, L22] started from a very conservative idea for what harmonic change of chord could be. The two chords should have at least a single quint. This fails for the chords with no quints. The resulting music pieces were also boring which is not a surprise: for instance, the transitions between basic chords C, F, G of C major scale are not possible.

This suggests that one should not start from music but from geometry. Let us consider isohedral geometry for simplicity and the proposed picture for the bio-harmonies.

1. Continuity in some sense is a natural requirement. The natural definition of continuity is that the sequence of 3-chords of progression should define a sequence of neighbouring triangles at the icosahedron. But how should one define neighborhood?

2. Concerning the notion of nearest neighbor, there are 3 options to consider.

   Option I: The strong form of continuity is that neighboring triangles have at least one common edge. This allows 4 different chord pairs. This would mean 4 possible DNA codon pairs for a given Hamiltonian cycle. For bio-harmony the symmetry of icosahedral harmony determined by Z_n ($n = 6, 4, 2$) can change and one would have 4+4+4=12 codon pairs. This kind of correlation for codon sequences would have been observed.

   Option II: For a weaker option the neighboring triangles would have at least 1 common vertex. A given triangle would have 4+3+2+1 =10 neighbors ("1" corresponds to the triangle itself as a neighbor). This would give 10+10+10 =30 possible codon pairs.

   Tetrahedral harmony gives further pairs but since one triangle of tetrahedron should correspond to a fixed triangle of icosahedron, this can change the situation for only a single chord. It is known that the minimum of 32 two codons are needed to code amino acids. The optimum situation very probably not reached for all bio-harmonies (if any), would be that the amino acid associated with the next codon can be any aminoacid. It should be easy to demonstrate by studying a sample of genes or more general DNA codon sequences to find that this prediction is wrong.

   Option III: For the weakest option the nearest neighbors would correspond to triangles at the orbits of the nearest neighbors in the sense of **Option II** or perhaps even **Option I** under the symmetry group Z_n of a given cycle. For instance, the transitions which would not change the codon would be replaced with all codons coding for the same amino-acid. The notion of nearest neighbor would reduce to the level of amino-acids: only the transitions to codons coding for the same amino-acid would be possible.

   For the generalization of **Option I** Z_6 cycle would give 4 orbits of which several must be identical so that there are no problems. Z_4 cycle would give 4 orbits with 4 codons so that one amino acid is missing. For the Z_2 option one obtains only 4 2-origi so that 6 amino-acids are missing.

   For the generalization of **Option II** 10+10+10 nearest neighbours would be replaced with their orbits. For the Z_6 cycle there are nearest neighbor 10 orbits and since there are only 4 orbits, there are no problems. For the Z_4 cycle one there are 5 4-orbits so that the minimal degeneracy of a given orbit is 2.

   For the Z_2 cycle there are 10 2-orbits, and this number is obtained unless some 2-orbit occurs more than once. The 10 nearest neighbor triangles must correspond to different amino-acids:

whether this is possible for all bioharmonies, remains an open question. In any case, it is plausible **Option III** can produce all possible codon pairs although this need not be the case for all bioharmonies. Could preferred bioharmonies be selected by the condition that all codon pairs are possible?

6.2.2   What about melody?

Melody is also an important part of music. A rough rule of thumb is that a beautiful melody tends to contain notes of the chord accompanying it. Dissonance is of course what makes music really interesting. This can be understood as a resonant coupling of the notes of the melody with the notes appearing in the accompanying chords.

Can one apply this picture to the music of light? Could the dark 3-photon states bound to a single unit by Galois confinement tend to decay to ordinary 3-photon states (bio-photons) and could melody represented as a sequence of single photon states couples resonantly to these photons? Could melody correspond to as sequence dark photons 1-plets decaying to ordinary bio-photons coupling to the decay products of dark photon triplets representing genetic codons?

6.2.3   Summary

The basic results of the article are a precise definition of bio-harmony allowing to obtain the analogs of ordinary simple harmonies as special cases and a proposal that the 3-chord sequence defines a beautiful music piece if it corresponds to a continuous sequence for icosahedral faces. In principle this criterion allows bio-harmonies for which all possible codon pairings appear in chord sequences but some bio-harmonies might be excluded.

7   Is genetic code part of fundamental physics in TGD framework?

7.1   3 basic realizations of the genetic code

Topological Geometrodynamics (TGD) proposes 3 basic realizations of the genetic code [L22]. The first realization is the standard chemical realization. The second realization is in terms of dark proton sequences (dark nuclei) with proton triplet representing a codon. Ordinary DNA strands would be accompanied by dark magnetic flux tubes carrying the dark proton triplets. Also RNA, amino-acids and tRNA would have dark proton analogs.

The third realization is in terms of dark photon triplets and involves the notion of bio-harmony described in terms of icosahedral and tetrahedral geometries with 3-chords of light (perhaps also sound) assigned to the triangular faces of icosahedron and tetrahedron. 12-note scale is realized as a Hamiltonian cycle for icosahedron with the step between nearest neighbor vertices for the cycle realised as quin (scaling of frequency by factor 3/2). The 3-chords correspond to the triangular faces of the icosahedron. Also tetrahedral realization of 4-note scale is necessary in order to obtain genetic code. DNA codons correspond to triangular faces and the orbit of a given triangle under the symmetries of the bio-harmony corresponds to DNA codons coding for the amino acid assigned with the orbit. Vertebrate genetic code emerges as a prediction.

The 3-chords of dark photon triangles are assigned with the triangular faces of icosahedron and tetrahedron [L2, L22, L31] such that their corners are labelled by the notes of the 12- and 4-note scales realized as a icosahedral and tetrahedral Hamiltonian cycles, which are closed paths connecting vertex to neighboring vertex and going through every vertex once.

Genetic code corresponds to a fusion of tetrahedral harmony with 4 chords and of 3 icosahedral harmonies with 20 3-chords having as group of symmetries Z_6, Z_4 and Z_2 - Z_2 can correspond either to reflection or rotation by π. There are also 6 disharmonies without any symmetries (Z_1) with single DNA codon coding for single amino-acid. There is a considerable number of different icosahedral harmonies and the 3 icosahedral harmonies can be in different key so that a large number of bio-harmonies is possible [L31]. The details of the model of bio-harmony are not completely fixed. In particular, the understanding of stop codons is not completely satisfactory. The small deviations from the vertebrate code (say bacteria and mitochondria) could be understood

as being due to the incomplete mimicry of the dark code by chemical code in accordance with the idea that the mimicry has gradually evolved more complete.

Dark photon 3-chords mediate interaction between various realizations. Both dark proton and dark photon triplets would be dynamical units analogous to protons as color confined states of 3 quarks and in the adelic vision the notion of color confinement is replaced with Galois confinement [L31, L38]. Also genes could be seen as Galois confined states of 3N dark protons and dark photons. 3N-photon exchange would be realized as 3N-fold frequency - and energy resonance (mere energy resonance) between dark levels with the same value (different values) of h_{eff} . The possibility to modify the value of h_{eff} for flux tube makes it possible to have for a given codon single resonance energy [L38, L36, L37].

There are several questions relating to the bio-harmony.

1. The gluing of icosahedron and tetrahedron along the face looks ugly in the original model. Why both icosahedron and tetrahedron and why the gluing? The recent progress with M^8-H duality [L28, L29] suggests an answer. The tessellations (honeycombs) of hyperbolic 3-space H^3 appear at the fundamental level and induce sub-tessellations of the magnetic flux tubes. One of these honeycombs- tetrahedral-icosahedral honeycomb (TIH)- involves all Platonic solids with triangular faces - tetrahedron, octahedron, and icosahedron. Could genetic code relate to TIH?

   Cognitive representation [L14, L25, L26] as a set of points of space-time surface in the space of complexified octonions O_c with points having O_c coordinates in extension of rationals associated with the polynomial defining the space-time surfaces are central for for both quantum TGD and TGD inspired theory of cognition leading to adelic physics [L12]. The cognitive representation is mapped to $H = M^4 \times CP_2$ by $M^8 - H$ duality [L28, L29].

   Could the genetic code be realized at the level of fundamental physics as a TIH in H^3 emerging as a cognitive representation [L14, L25, L26, L33] for the space-time surfaces in M^8 and by $M^8 - H$ duality also in $H = M^4 \times CP_2$. If so, the biological realization could be only one particular realization of the code.

2. Why there should ber 3 icosahedral harmonies and one tetrahedral harmony? There is a partial answer to this question. The correspondence with 64 dark proton triplets representing codons and triangles requires 3 icosahedral harmonies. What distinguishes stop codons from other codons? It turns out that stop codons could be dark proton triplets for which the corresponding triangle does not exist in THI realization! The lack of dark proton triplet would mark the end of the gene.

It should be possible to unify various TGD inspired models of genetic code to a single unified description. Is the time ripe for this?

1. The realizations in terms of dark protons and dark photons are related: dark photon 3N-plets would be emitted by dark proton 3N-plets in 3N-proton cyclotron transitions. In the 3N-resonance interaction with DNA, RNA, amino-acids, and tRNA the dark photon 3N-plet would transform to ordinary photons (bio-photons). Energy resonance could select the basic information molecules.

2. How the dark level interacts with the ordinary matter? Music expresses and creates emotions. Light 3-chords for a given bio-harmony could therefore represent an emotional state of MB (emotions as sensory perceptions of MB?). Fourier transform in terms of frequencies represents non-local holistic information and emotional information indeed is holistic information. Codons as units of 6 bits would represent ordinary temporily local, reductionistic information.

   Each emotional state corresponds to a particular collection of 3-chords as allowed chords of the bio-harmony and therefore the resonance occurs with different biomolecules or induces different transitions of these bio-molecules. Could this serve as a universal mechanism of bio-control? Could epigenesis as a control of DNA transcription rely on this mechanism? As a matter of fact, the model described in this article emerged from an attempt to understand epigenesis in the TGD framework.

3. Is it possible to unify all models of the genetic code to single model so that the representation of a codon as dark proton triplet is assigned to a representation as an "activated" triangle of icosahedron or tetrahedron of TIH containing at it vertices dark protons defining the same codon as the triangle as 3-chord for a given icosahedral harmony. Could these "activated" triangles be selected faces of TIH. Could genes correspond to sequences of these icosahedron-tetrahedron pairs at magnetic flux tubes?

In the sequel the questions raised above are discussed.

7.2 Genetic code and hyperbolic tessellations

Why 3 different icosahedral harmonies with symmetries Z_6, Z_4, and Z_2 plus one (there is only one) tetrahedral harmony is needed to get $3 \times 20 = 60 + 4$ chords in correspondences with 64 codons of the genetic code?

7.2.1 Hyperbolic tessellations and genetic code?

What comes into mind, are fundamental lattice like structures - tessellations - having as basic building bricks icosahedron and tetrahedron - at least these. This would make sensical to speak about gluing of tetrahedron to icosahedron, which looks a strange operation in the original formulation of the model.

1. Platonic solids correspond to finite tessellations at 2-sphere or equivalently 3-D solid polyhedrons in 3-D space Euclidian space E^3. Maybe one could answer the question by increasing dimension and by studying 3-D polyhedrons of 4-D space defining tessellations of the hyperbolic space H^3.

   By $M^8 - H$ duality [L28, L29], these tessellations appear at the fundamental level TGD as cognitive representations since the 3-D mass shells with the geometry of H^3 appear naturally in the solutions of dynamical equations as algebraic equations at the level of M^8 identifiable as real section of complexified octonions O_c. The dynamics reduces to the associativity of the normal space of the space-time surface determined as a root for the real part of an octonionic polynomial obtained as an algebraic continuation of a real polynomial. Real part is defined in quaternionic sense by decomposing octonion to two quaternions in the same manner as a complex number is decomposed to its real and imaginary parts.

   The algebraization of the octonionic counterpart of Dirac equation forces its identification as the counterpart of momentum space version of the ordinary Dirac equations and the identification of M^8 as an analog of momentum space so that space-time surface is analog of Fermi ball.

2. The tessellations of H^3 are analogs of lattices in an Euclidian momentum space E^3. In adelic physics they define cognitive representations providing unique discretizations of space-time surface both at the level of M^8 and H. $M^8 - H$ duality maps tessellations to their analogs of $H = M^4 \times CP_2$. Contrary to my long held belief, Uncertainty Principle forces the map to be instead of a direct identification an inversion for $M^4 \subset M^8 \to M^4 \subset H$ [L28, L29]. Mass hyperboloids correspond in H to light-cone proper time constant sections of space-time surface: light-cone proper time defines Lorentz invariant cosmic time.

3. The tessellations of H^3 can have several different analogs of unit cells glued together along their 2-D faces. The positive curvature of sphere forces Platonic solids as tessellations of 2-sphere to be closed and be finite. H^3 as a negative curvature space does not allow a closure. This implies a large number of tessellations as infinite analogs of regular solid polyhedra. Both icosahedron, octahedron and tetrahedron have triangular faces so that they might allow gluing together for the simplest tessellations. Also more complex tessellations are possible.

7.2.2 Details about hyperbolic tessellations

Consider now in more detail some tessellations of H^3 possibly relevant for the bio-harmony [L2, L22, L31] involving icosahedral and tetrahedral geometries.

Some basic concepts and notations are necessary to help the reader to understand the Wikipedia articles, which give detailed explanations and illustrations.

1. Regular polytopes are tessellations consisting of single polytope. There are subtle differences between tessellations and honeycombs: tessellations are more general than honeycombs. These differences are not relevant for what follows so that I will use both terms interchangeably.

2. Schläfli symbol [A7] `https://cutt.ly/7jagV1T` $(p, q, r, ..)$ characterizes regular polytopes in both Euclidian spaces and hyperbolic spaces locally but does not tell anything about the object globally. For a 3-D regular polytope (p, q, r) in 4-D space (say tessellation of H^3 the faces have p vertices, q identical faces meet at given vertex, and r identical 3-cells meet along given edge. For instance, $(3, 5, 3)$ characterizes a regular tessellation having icosahedron as fundamental cells with 3 icosahedrons meeting along given edge.

3. Vertex figure [A10] `https://cutt.ly/yjagMQn`) represents the neighboring vertices as seen from a given vertex. Formally it is defined by contracting all edges emanating from the vertex to their middle points and connecting these points by lines along faces. For a n-D polytope (p,r,s,..) the vertex figure is n-1-D polytope (r,s,...). For instance, for icosahedron $(3,5)$ the vertex figure is (5) telling that 5 edges meet at vertex. For the regular honeycombs in H^3 the vertex figure is a regular polyhedron. For instance, for $(3, 5, 3)$ it is $(5,3)$ identifiable as dodecahedron. Second notation for the vertex figure is as the list of numbers of edges meeting at the vertices of the face: For icosahedron this list is 3.3.3.3.3 telling that the faces of the edge figure has 5 vertices at which edges meet.

4. Edge figure [A10] (`https://cutt.ly/djag9Q9`) is the vertex figure of the vertex figure of the polytope. For D-dimensional polytope it is polytope of dimension D-2. For a regular polytope $(p, q, r, ..., s)$ the edge figure is $(r, ..., p)$: for Platonic solids (r,s) edge figure is () telling that two faces meet along a given edge. For the regular polytope (r,s,p) the edge figure tells the number of identical 3-cells meeting at given edge. For cubic lattice it is 4. For semiregular honeycombs the 3-cells need not be identical.

5. The notion of dihedral angle (see `https://cutt.ly/vjs2OBI`) is very useful in trying to understand whether a given tessellation of E^3 and H^3 is possible. Dihedral angle is defined as the angle between the faces of the polytope meeting along a given edge. For tetrahedron it is 120 °, for octahedron 90 ° and for icosahedron 138.19 °. Since at least 3 polyhedra must meet at a given edge, the sum of these angles must be smaller than 360 degrees in E^3. This prevents icosahedral tessellations in E^3.

   In H^3 negative curvature allows the sum to be larger than 360 ° (think of polygons at a saddle surface as a visualization) so that 3 icosahedra might meet at a given edge as indeed occurs for $(3, 5, 3)$ tessellation. The sum of the dihedral angles of T, O, and I assignable to to tetrahedral-icosahedral honeycomb in H^3 is 348.19 ° and smaller than 360 ° but rather near to it.

6. An important notion is Coxeter group [A3] (`https://cutt.ly/FjdEJeG`) acting as the symmetry group of the honeycomb. Coxeter group is generated by reflections meaning that honeycombs can be generated by reflections in suitable mirror planes. Honeycomb is constructed kaleidoscopically: a concretization of Leibniz's monadology is in question. Coxeter group and therefore also the honeycomb is characterized by Coxeter diagram [A2] (`https://cutt.ly/SjdEZiH`) having as its nodes the mirrors and connected by edges labelled by the dihedral angles $\phi = \pi/n$ between the mirror planes. The value of n is written explicitly to the diagram except when it is the minimal value $n = 3$. For instance, the sequence [(5,3,3,3,3)] characterizing tetrahedral-icosahedral honeycomb in H^3 tells that the dihedral angles between the 5 mirror planes are $(\pi/5, \pi/3, \pi/3, \pi/3, \pi/3)$.

Consider now honeycombs in hyperbolic space H^3.

1. The simplest tessellations - regular honeycombs - of H^3 consist of icosahedra and dodecahedra having the same isometry group. That 3 of the 4 most symmetric honeycombs in H^3 have

icosahedral symmetries whereas the fourth has cubic symmetries, is a highly encouraging sign. These 4 regular honeycombs are icosahedral honeycomb $\{3, 5, 3\}$ with 3 icosahedrons meeting along edge; order-5-cubic honeycomb $\{4, 3, 5\}$ with 5 cubes (rather than 4 as in E^3) meeting along a given edge; and dodecahedral honeycombs of order 4 (5) with 4 (5) dodecahedra meeting along edge. In all these cases the sum of the dihedral angles is larger than 360 ° so that the negative curvature of H^3 is essential for the existence of these honeycombs.

2. What about the combinations of Platonic solids having triangles as faces - tetrahedron, octahedron, and icosahedron? From Wikipedia article [L35] (`https://cutt.ly/cjaheWC`) one learns that there exists honeycombs of H^3 characterized by Schläfli symbol $\{(3, 3, 5, 3)\}$ and Coxeter group with symbol $[(5, 3, 3, 3)]$ consisting of reflections and generating the honeycomb. The regular honeycombs are characterized by 3 integers (say $(3, 5, 3)$) and the meaning of the code is not quite clear to me but must reflecs the fact that the honeycomb is semiregular.

Tetrahedron corresponds to (3,3) and icosahedron to (3,5) and octahedron (3,4) as a rectified tetrahedron obtained by contracting edges to their middle points and expanding vertices to faces, has symbol $r(3, 3)$. Perhaps (3,3) in (3,3,5,3) refers tCoxetergroupo both tetrahedron and its rectification and (3,5) in (3,3,5,3) to icosahedron. The last "3" tells that 3 identical solid icosahedra, tetrahedra, or octahedra meet at given edge.

In particular, the tetrahedral-icosahedral honeycomb (TIH) is a compact uniform but not a regular honeycomb, having icosahedra, tetrahedra, and octahedra, all of which have triangular faces, as analogs of unit cells [A5, A4, A9] (see `https://cutt.ly/xhBwTph`, `https://cutt.ly/lhBwPRc`, and `https://cutt.ly/0hBwUOO`). The Wikipedia article [L35] contains beautiful illustrations of these honeycombs.

One can wonder why "tetrahedral-icosahedral honeycomb" does not involve octahedron. This is said to reflect the fact that only tetrahedral and icosahedral cells of the tessellation are regular 3-cells. All these polyhedra are regular as Platonic solids, and it remains unclear to me what the lacking regularity of the octahedron as 3-cell means in the recent context.

For TIH $\{(3, 3, 5, 3\}$ the vertex figure is rhombicosidodecahedron (RID) [A6] (`https://cutt.ly/yjahitS`) discovered already by Kepler. Kepler talked about Harmonices Mundi and I cannot but smile as I recall how I read as a young man a book having fun with Kepler's medieval belief on celestial harmonies and laughed also! Maybe the celestial harmonies are making a glorious comeback!

RID is an Archimedean solid [A1] (`https://cutt.ly/njahaGN`) having 60 vertices corresponding to 12 disjoint pentagons and 20 disjoint triangles with 60 vertices both. RID has as faces 20 triangles assignable to icosahedron, 12 pentagons assignable to dodecahedron plus 30 squares - 62 faces altogether. RID is obtained by radially scaling the distance of icosahedral and dodecahedral faces from origin but keeping the area of the spherical faces the same: this yields squares as additional faces. Triangles and pentagons have only squares as edge neighbors.

Edge figure tells the number of edges meeting at given edge. For TIH it is 3. Regular and single-ringed Coxeter diagram uniform polytopes to which also TIH belongs have a single edge type. Therefore icosahedron, tetrahedron, and octahedron must meet at given edge. That vertex figure contains 3 types of faces (triangles, and squares, and pentagons) presumably reflects this. Recall that the sum of the dihedral angles of T,O, and I is 348.19 °.

One can try to build a more concrete picture about how the Platonic solids are glued together along their triangular faces in the icosahedral-tetrahedral honeycomb.

1. Must to make this concrete, one can regard Platonic solid as a kind of mini Earth with two other Platonic solids glued to its surface like mountains. In all cases one has Platonic analog of a planar lattice of triangles at this mini Earth. To minimize typing call the 3 different Platonic solids T, O, and I.

2. Due to the symmetries one expects that for O and I the triangles correspond to different Platonic solids if they are edge neighbors. For T this is not possible since all faces are

edge neighbours. All 6 2+2 configurations of B and C are however related by a rotational symmetry. This already gives a rather satisfactory picture about what the situation looks like at the surface of each mini Earth (I cannot avoid the analogy with inner planets, the living Earth as the largest one would correspond to I!).

3. The radius R of circumscribed inner or or outer sphere gives an idea about the size scales of these Platonic solids when the edge length a is the same for them as it is in the recent case. The following gives the radii of the outer sphere.

$$
\begin{array}{llll}
\text{tetrahedron} & \frac{R_{T,out}}{a} = \sqrt{\frac{1}{2}} \ , & & \frac{R_{T,in}}{a} = \sqrt{\frac{1}{24}} \\[2mm]
\text{octahedron} & \frac{R_{O,out}}{a} = \sqrt{\frac{3}{4}} \ , & & \frac{R_{O,in}}{a} = \sqrt{\frac{1}{6}} \ , \\[4mm]
\text{icosahedron} & \frac{R_{I,out}}{a} = \frac{1}{2}\sqrt{\phi\sqrt{5}} \ , \phi = \frac{(1+\sqrt{5})}{2} \ , & \frac{R_{I,in}}{a} = \frac{\sqrt{3}}{12}\sqrt{3+\sqrt{5}} \ .
\end{array}
\tag{7.1}
$$

4. The ratios of the outer radii are given by $R_{I,out} : R_{O,out} : R_{T,out} = \sqrt{\phi\sqrt{5}} : \sqrt{\frac{3}{4}} : \sqrt{\frac{1}{2}} \simeq$ 1.9021 : 0.8660 : 0.7071. The ratios of the inner radii are given by $R_{I,in} : R_{O,in} : R_{T,in} = \sqrt{\phi\sqrt{5}} : \sqrt{\frac{3}{4}} : \sqrt{\frac{1}{2}} \simeq .756 : 0.408 : 0.2041$. That icosahedron has the largest size, is natural since the total solid angle defined as a sum of the solid angles of the 20 triangles is $4/pi$ and the contribution of an individual triangle is smallest for I and largest for the 4 triangles of T.

7.2.3   Could TIH allow to unify the models of genetic code?

Does this picture help to say anything interesting about the model of bio-harmony and even to unify the models of genetic code?

1. tessellations define in a natural manner discretizations of MB defining cognitive representations suggested to relate to the geometric representations for the states of the brain at MB and more generally, for the states of various parts of the biological body at MB. There is evidence for an effective hyperbolic geometry of brain realized in a statistical sense [**?**] (`http://tinyurl.com/ybghux6d`) : functionally similar neurons are near to each other in this effective hyperbolic geometry. This evidence is discussed from TGD point of view in [L30]: one ends up with a proposal that the MB of the brain provides a geometric representation for the statistical aspects of the brain - kind of abstraction? Information from the brain would be sent by dark Josephson radiation from similar neurons to positions of MB near to each other. This model could generalize to other parts of organism. MBs could form a kind of abstraction hierarchy representing more and more abstract data about the state of organism.

2. Could the icosahedral-tetrahedral tessellation allow a justification for the fusion of 3 icosahedral harmonies with the tetrahedral harmony? Why does the octahedral harmony disappear? Octahedral harmony would mean 6 additional notes assignable to the vertices of octahedron and 8 3-chords and this does not fit with facts.

   Remark: In the Wikipedia article about TIH it is said that octahedrons of TIH are not regular, unfortunately in the sense that I do not understand. Note also that tetrahedral and octahedral harmonies are unique because there is only a single Hamiltonian cycle.

3. Geometrically the tessellation means identification of the neighbouring faces, which gives a justification for the strange looking proposal of gluing tetrahedron to icosahedron in order to fuse 3 icosahedral and one tetrahedral harmony. If also the 3-chords associated with the faces are identified, one can ask whether only icosahedral and tetrahedral harmonies are needed and the chords of the octahedral harmony are determined by them.

   2 3-chords of tetrahedral harmony are the same as those for icosahedral harmony but the 2 3- chords associated with the 2 T-O faces are independent. This would give 62 independent chords (amusingly, 62 happens to be the number of faces of RID).

One of the tetrahedral chords is necessary since purely icosahedral harmony allows to get only 19 amino-acids identified as the orbits of the chords under the symmetries of a particular icosahedral harmony with 20 chords: one additional chord is needed for the missing amino-acid. Since two icosahedral triangles facing the tetrahedron "eat" 2 further tetrahedral chords, this leaves 1 tetrahedral chord from 4: 3 chords as tetrahedral codons are missing. Could the 3 missing tetrahedral 3-chords correspond to the ordinary DNA codons acting as stop codons? Could the stop codons lack a representation as dark photon triplets or could their frequencies be such that they do not allow 3-resonance with any tRNA?

4. How genes would be realized in the tessellation? Could dark genes correspond to flux tubes forming 1-D sub-tessellations of H^3 induced to the flux tubes? Could gene correspond to a sequence of icosahedron-tetrahedron pairs such that neighboring codons are associated with icosahedron-tetrahedron pairs as cell-neighbors. Two subsequent icosahedrons would have a tetrahedron between them.

   Could the tessellation induced from H^3 to MB be dynamical involving an "activation" of a particular triangle as a codon inside each icosahedron and tetrahedron? Could dark genes at the flux tubes have these codons as induced dark codon sequences? Could "activation" mean that the triangle representing particular codon is accompanied by 3 dark protons at its vertices and representing the same genetic codon? The representations in terms of dark protons triplets, as triangles of icosahedron and tetrahedron, and as dark photon triplets would fuse to single representation. There could be a representation also for stop codons in terms of 3 dark protons but there would not be no triangle where to locate them so that coding would stop! The missing dark codon would signify the end of the gene.

   This would give the long-sought connection between dark codons realized as dark triplets and dark codons realizing bio-harmony and dark codons realized as dark photon triplets generated in the cyclotron transitions of dark codons. An essential role would be played by Galois confinement [L31] stating that these triplets behave like dynamical units - just like 3 confined quarks forming a baryon. Galois confinement generalizes to the level of genes.

5. This proposal is of course one of the many variations of single theme developed during years. What is new that the proposal would make the roles of the icosahedral and tetrahedral geometries concrete, not at the level of bio-molecules but at the level of their MBs. A profound dramatic generalization of the notion of genetic code from biology to the level of fundamental physics is also suggestive. Even a hierarchy of genetic codes in various scales can be considered.

   The interpretation of various harmonies as correlates of emotions implies that each icosahedral-tetrahedral unit of the tessellation would have its own varying emotional state expressed and affected by biochemical level via different interaction actions with ordinary biomatter realized in terms of dark photon N-resonance with targets depending on the emotional state [L38, L36, L37]. This could serve as a universal mechanism of bio-control by MB applying also to epigenesis.

   There are still several open questions: in particular, what is the deeper reason for the fusion of just 3 icosahedral bio-harmonies. That the number of the dark codons is 64 is a partial reason but is this enough.

6. There are reasons to ask whether the cell membrane and microtubuli could provide a 2-D realizations of the genetic code [L38]. If genes are induced as 1-D sub-tessellations from that of MB, there is no reason to exclude 2-D or even 3-D induced tessellations.

7. I cannot avoid the temptation of mentioning the notion of memetic code [K1], which was my first idea about genetic code and proposed as a generalization of genetic code by starting from a speculated hierarchy of Mersenne primes, whose members would come as $M(n+1) = M_{M(n)}$, $M_n = 2^n - 1$, ($M(2) = 2$. This gives the Mersenne primes $M(2) = M_2 = 3$, $M(3) = 2^3 - 1 = 7$, $M(4) = M_7 = 2^7 - 1$, $M(5) = M_{127} = 2^{127-1}$. It is not known whether the hierarchy continues. M_7 would correspond to the ordinary genetic code and M_{127} to memetic code with codons realizable as sequences of 20 codons.

Could memetic code be realized by TIH? Could one consider a planar or cylindrical sub-tessellation with a width of 20 tetrahedral-icosahedral pairs? If the size assignable to single pair is that of DNA codon - 1 nm roughly - the width would be about 20 nm which might relate to the radial scale of the microtubuli.

8   Galois groups and genetic code

Galois groups, in particular simple Galois groups acting on cognitive representations consisting of points, whose coordinates in a number theoretically preferred coordinate system of octonions belong to EQ, play a fundamental role in the TGD view of cognition [L33]. The TGD based model of genetic code [L2, L32] involves in an essential manner the groups A_5 (icosahedron (I)), which is the smallest non-abelian simple group, and A_4 (tetrahedron (T)). Genetic code has as building bricks Hamiltonian cycles of I and T. Genetic code relates to information and therefore to cognition so that the interpretation of these symmetry groups as Galois groups is suggestive.

The most recent step of progress was the realization that genetic code can be represented in terms of icosa-tetrahedral tessellation of a hyperbolic 3-space H^3 [L35] and that the notion of genetic code generalizes dramatically. Also octahedron (O) is involved with the tessellation but plays a completely passive role. The question why the genetic code is a fusion of 3 icosahedral codes and of only a single tetrahedral code remained however poorly understood.

The progress in the understanding of the role of Galois groups inspired by a summary of inverse Galois problem [A13] (`https://cutt.ly/jmjpyDS`) in TGD framework [L34] made it possible to answer this question. The proposal is that the symmetry groups of the I, O, and T can be identified as Galois groups.

Icosa-tetrahedral tessellation can be replaced with its 3-fold covering replacing $I/O/T$ with the corresponding symmetry group acting as a Galois group. Octahedral codons can be regarded as icosahedral and tetrahedral codons so they do not contribute to the code. T has only only a single Hamiltonian cycle and its 3-fold covering behaves as a single cycle. T has only only a single Hamiltonian cycle and its 3-fold covering behaves effectively as a single cycle.

8.1   Could the symmetries of icosa-tetrahedral realization of the genetic code correspond to Galois symmetries?

Abelian groups Z_p, p prime, are simple and the alternating group A_5 with order 60 is the smallest non-Abelian simple group. All groups A_n, $n \geq 5$ are simple and have $n!/2$ elements. A_5 corresponds to the icosahedral group isomorphic with the symmetry group of the dodecahedron.

The TGD based model of genetic code [L2, L32, L35] involves in an essential manner the groups A_5 (icosahedron) and A_4 (tetrahedron). Simple groups play a fundamental role in the TGD view of cognition. Could this mean that genetic code represents the lowest level of an infinite cognitive hierarchy?

8.1.1   The TGD inspired model model of genetic code, cognition, and Galois groups

TGD based model of bioharmony [L2, L32, L35] provides a model of genetic code as a fusion of 3 icosahedral Hamiltonian cycles and the unique tetrahedral Hamiltonian cycle (what "fusion" precisely means is far from clear and I have considered several options).

Icosahedral Hamiltonian cycles is a non-self-intersecting path at icosahedron connecting nearest points if icosahedron going through all 12 points of the icosahedron. It is interpreted as a representation of a 12-note scale with a scaling by quint assigned to a given step along the cycle. For a given Hamiltonian cycle, the allowed 3-chords of icosahedral harmony are identified as chords defined by the triangular faces of the icosahedron.

Remark: In the sequel I will use the shorthands IH, OH, and TH for icosahedral, octahedral, and tetrahedral harmonies. Also the notation $I/O/T$ will be used for icosahedron/octahedron/tetrahedron

unless there is a danger of confusing them with their symmetry groups with identical shorthand notations.

Galois groups are essential for cognition in the TGD framework. In particular, simple groups as primes for groups are also primes for cognition [L33]. Genes represent information and Galois groups are crucial for cognition in the TGD framework. Genes would correspond to sequences of 3-chords of bioharmony. This raises several questions.

Could genetic code relate to Galois group A_5 as the smallest simple non-abelian Galois group (and also to the fact that the only polynomials of order smaller than 5 are generically solvable)? Could genetic code correspond to the lowest level in a hierarchy of cognition and of analogs of genetic code?

The order $n = 60$ for A_5 suggests a fusion of 3 icosahedral codes to give $20+20+20 = 60$ codons.

1. 3 Platonic solids, - icosahedron (I), tetrahedron (T) , and octahedron (O) - which have triangles as faces so that one can consider the possibility of constructing a lattice like structure by gluing these Platonic solids together along their faces. Hyperbolic space H^3 indeed allows isosa-tetrahedral tessellation, which also involves O:s. I have proposed that this allows a realization of genetic code and also of genes [L35]. The notion of gene generalizes so that genes can also be 2- or 3-D lattice-like structures.

2. A_5 has $A_3 = Z_3$ as a subgroup and I(cosahedron) corresponds to A_5/Z_3. I has several Hamiltonian cycles having as a symmetry group Z_6, Z_4 or Z_2. Z_2 can act either as rotations or reflections.

   Q: Could A_5 as a Galois group as 3-fold covering of I make it possible to understand why the fusion of just 3 icosahedral codes is possible?

3. Tetrahedral group T corresponds to the alternating group $A_4 = S_4/Z_2 = Z_4 \times Z_3$ with 12 elements and tetrahedron identification as A_4/Z_3. The tetrahedral Hamiltonian cycle (4-scale) is unique and has 4 3-chords. The 3-fold copy would correspond to A_4. Information about the unique Hamiltonian cycles of O and T can be found in [A11] (`https://cutt.ly/9mlMiV8`).

   Q: Could the factor that there is only one tetrahedral cycle explain why only a single tetrahedron contributes?

4. Octahedral group O has 24 elements and is the wreath product of Z_3 and Z_2^3 and has also the decomposition $O = S_2 \times S_4$. Octahedron can be identified as O/Z_3. Also octahedral Hamiltonian cycle representing 8-scale with 8 chords is unique.

   Q: Why don't octahedral codons contribute?

8.1.2 A model of the genetic code based on icosa-tetrahedral tessellation of hyperbolic 3-space

TGD leads to a proposal for a geometric representation of the genetic code in terms of icosa-tetrahedral tessellation of the hyperbolic 3-space H^3 (mass shell or light-cone proper time $a = constant$ hyperboloids of M^4) [L35]. Both I, O, and T having triangular faces appear in the tessellation. Recall that the corresponding harmonies are denoted by IH, OH and TH.

I do not completely understand the details of the icosa-tetrahedral tessellation. The following picture satisfies the constraints coming from the notion of harmony but I have not proven that it is correct. Here the help of a professional geometrician knowing about tessellations of H^3 would be needed.

1. The analog of the discrete translational symmetry for lattices can be assumed: all I:s , O:s and T:s are equivalent as far as common faces with neighboring Platonic solids are considered.

2. The term icosa-tetrahedral tessellation suggests that all octahedral faces are glued to tetrahedral and icosahedral faces so that octahedral chords reduce to either icosahedral or tetrahedral chords. OH would not be an independent harmony. This requires that the number of common faces between two O:s vanishes: $n_O^O = 0$.

3. T shares at least 1 face with a given I so that the number of tetrahedral chords is reduced to at most 3 for given T. 4 purely tetrahedral faces (not shared with I) are needed. I would have $n_{IT} \leq 4$ purely tetrahedral faces in such a way that the total number of purely tetrahedral 3-chords is 4.

   The simplest possibility is that I shares a common face with 2 T:s. Each T shares 2 faces with O providing 2 purely tetrahedral 3-chords and shares the remaining 2 faces with distinct I:s. One would have $n_T^I = 2$, $n_T^O = 2$, $n_T^T = 0$.

   Since each I defines independently 20 chords, 2 I:s cannot have common faces. One would have $n_I^T = 2$, $n_I^I = 0$ and $n_I^O = 18$ to give $n_I^T + n_I^O + n_I^I = 2 + 18 + 0 = 20$.

4. What remains to be fixed are the numbers n_O^I and n_O^T satisfying $n_O^I + n_O^T = 8$. The conditions $n_O^T \geq 1$ and $n_O^I \geq 1$ must be satisfied since both T and I share faces with Os.

   Music comes to rescue here. The 8 3-chords of OH could define OH sub-harmony of IH. Analogously, the 4 3-chords of TH could define TH as a sub-harmony of OH.

   Could IH sharing 18 3-chords with OH contain 2 transposed copies of OH plus 2 chords of TH? IH cannot of course contain the entire TH as a sub-harmony.

   Could OH contain one copy of TH? This would give $n_O^I = n_O^T = 4$. Could the IH part of OH actually be TH as a sub-harmony of IH so that OH would reduce to 2 copies of TH?

To sum up, if the answers to the questions are positive, the incidence matrix n_i^j, $i, j \in \{I, T, O\}$, telling how many faces i shares with j would be given by

$$
\begin{bmatrix}
n_I^I & n_I^O & n_I^T \\
n_O^I & N_O^O & n_O^T \\
n_T^I & N_T^O & n_T^T
\end{bmatrix}
=
\begin{bmatrix}
0 & 18 & 2 \\
4 & 0 & 4 \\
2 & 2 & 0
\end{bmatrix} . \tag{8.1}
$$

8.1.3 3-fold cover of the icosa-tetrahedral tessellation

The proposed model does not yet explain the fusion of 3 icosahedral Hamiltomnian cycles. A 3-fold cover of the icosa-tetrahedral tessellation which replaces Platonic solids with their symmetry groups is highly suggestive. This raises a series of questions.

1. How could this representation relate to a possible interpretation in terms of the Galois groups $I = A_5$ and $O = S_2 \times S_4$ and $T = A_4$? Z_3 appears as a sub-group of all these groups and these Platonic solids are coset spaces I/Z_3, O/Z_3, and T/Z_3.

2. Could one lift the icosa-tetrahedral tessellation to a 3-sheeted structure formed by the geometric representations of the Galois groups of this structure acting as symmetry groups? Platonic solids would be replaced with their symmetry groups acting as Galois groups.

3. Could the 3 different icosahedral Hamiltonian cycles correspond to different space-time sheets - roughly CP_2 coordinates as 3-valued functions of M^4 coordinates whereas 20 regions representing icosahedral vertices would correspond to different loci of $E^3 \subset M^4$ just as one intuitively expects?

4. Same should apply to the tetrahedral and octahedral parts of the tessellation. But don't the 3 identical copies of the tetrahedral Hamiltonian cycle give 64+8=72 codons? How can one overcome this problem?

The following is a possible answer to these questions.

1. $h_{eff} = 60h_0$ corresponds to 60-sheeted space-time (here also $60k$-sheeted space-time is possible if 60-D extension of k-dimensional extension is in question). For T and O an analogous picture would apply. One could say that the projections of I and O and T are in M^4. At each sheet one would have icosa-tetrahedral tessellation.

2. *I* has 3 types of Hamiltonian cycles with symmetry groups Z_6, Z_4, and Z_2 and can give 3 different copies. However, only a single copy of tetrahedral harmony appears in the model: otherwise the number of codons would be larger than 64. Could the 3 identical Hamiltonian cycles for *T* and *O* effectively correspond to a single Hamiltonian cycle?

3. The fusion of Hamiltonian cycles is analogous to a formation of many-boson states. For *T* and *O* all Hamiltonian cycles would be identical: one would have only one Hamiltonian cycle effectively. The 3-chords associated with the 3 octahedral and tetrahedral cycles are identical so that only single tetrahedral harmony would be present.

To sum up, the lift of the icosa-tetrahedral complex to that defined by the respective Galois groups could explain why just 3 icosahedral Hamiltomian cycles and effectively only 1 tetrahedral cycle.

9 MeshCODE theory from TGD point of view

Benjamin Goult has made an interesting proposal in the article *The Mechanical Basis of Memory the MeshCODE Theory* [**?**] (`https://cutt.ly/WzlrmrM`) published in Frontiers of Molecular Neuroscience in 25 February 2021.

The proposal is that the cell or at least synaptic contacts realize mechanical computation in terms of adhesive structures consisting of hundreds of proteins known as talins, which act as force sensors. Talins are connected to integrins in the extracellular matrix, to each other, and to the actins in the cell interior.

This proposal does not conform with the TGD vision but inspires a series of questions leading to a rather detailed general vision for how magnetic body (MB) receives sensory input from biological body (BB) coded into dark 3N-photons representing genes with N codons and as a response activates same but differently realized genes, RNA or corresponding proteins as a reaction [L38, L2, L22, L32, L35]. This would mean a universal response function assigning to sensory input a unique response. Sensory input would code the response to it in terms of dark genes, which also generalize in TGD framework.

9.1 Some basic facts

The role of a protein known as talin [I7] (`https://en.wikipedia.org/wiki/Talin_(protein)`) is the topic of the article. Talin is associated with the cell-substratum contact and mechanically couples cytoskeleton and extracellular matrix (ECM) together. Adhesion units formed by integrin coupling to ECM, talin, and actin at cytoskeleton side form adhesion structures consisting of hundreds of adhesion units.

It is good to begin with by listing some basic definitions and facts.

1. Cytoskeleton [I2] (`https://en.wikipedia.org/wiki/Cytoskeleton`) consists of microfilaments (actin), intermediate filaments, and microtubules (MTs) which in neurons are called neurotubules. Neurons contain neurotubules [I6] (NTs)(`https://en.wikipedia.org/wiki/Neurotubule`) generated at MT organizing center (MTOC) and transferred to dendrites and axon, where they are parallel to the neuronal surface.

   The cytoskeleton of an ordinary cell has as basic building bricks MTs and microfilaments and intermediate filaments. Both MTs and NTs are polarized. The + ends of MTs are at MTOC. + ends of NTs point towards the axon terminal and - end to the parent neuron. NTs in dendrites have mixed polarities.

2. ECM [I3] (`https://cutt.ly/5zNYtP6`) is a three-dimensional network consisting of extracellular macromolecules and minerals, such as collagen, enzymes, glycoproteins and hydroxyapatite that provide structural and biochemical support to surrounding cells. Cell adhesion, cell-to-cell communication and differentiation are common functions of the ECM.

3. Integrins [I4] (`https://cutt.ly/xzNYk7n`) are transmembrane receptors that facilitate cell-cell and cell-extracellular matrix (ECM) adhesion. Upon ligand binding, integrins activate signal transduction pathways that mediate cellular signals such as regulation of the cell

cycle, organization of the intracellular cytoskeleton, and movement of new receptors to the cell membrane. The presence of integrins allows rapid and flexible responses to events at the cell surface (e.g. signal platelets to initiate an interaction with coagulation factors).

4. Actins [I1] (`https://cutt.ly/LzNYEo9`) are a family of globular multi-functional proteins that form microfilaments. It is found in essentially all eukaryotic cells, where it may be present at a concentration of over 100 μM; its mass is roughly 42-kDa, with a diameter of 4 to 7 nm. An actin protein is the monomeric subunit of two types of filaments in cells: microfilaments, one of the three major components of the cytoskeleton, and thin filaments, part of the contractile apparatus in muscle cells.

One can visualizetalin as a spring between cytoskeleton and ECM. Talincouples directly to integrins at ECM side and either indirectly or directly to actin at cytoskeleton side. Talin's role is to be a rope in a "tug-of-war" between integrins at ECM and actin and it acts as a force sensor and could give rise to a molecular sense of touch based on force.

The part of talin subject to forces from the cellular interior and environment consists of 13 proteins domains which can be in two thermodynamically stable states analogous to the opposite magnetizations of ferromagnet and the domain exhibits hysteresis curve under a varying external force. The phases correspond folded and unfolded configuration looking like a straight bar. The two phases can be labelled by a bit and the proposal is that the talin conformations define 13 bits.

The domains are not identical so that each equilibrium state under varying external net force could correspond to a unique configuration in which domains are folded or unfolded. If so, talin would serve as a 13-bit force sensor of external forces with finite resolution corresponding to 13 octaves in linear scale. It will be found that the response could actually be determined by 6 bits and correspond to genetic codon.

The abstract of [I13] summarizes the functions of talin.

> ... Talin forms the core of integrin adhesion complexes by linking integrins directly to actin, increasing the affinity of integrin for ligands (integrin activation) and recruiting numerous proteins. It regulates the strength of integrin adhesion, senses matrix rigidity, increases focal adhesion size in response to force and serves as a platform for the building of the adhesion structure. Finally, the mechano-sensitive structure of talin provides a paradigm for how proteins transduce mechanical signals to chemical signals.

It is clear that talin does not look only a passive sensory receptor. That integrins are not necessary for talins to function implies that they have emerged before integrins in the evolution. It is clear that talins are essential aspect of multicellular life.

9.2   Could adhesion structures act as classical computers?

The proposal of the article [?] relies on computationalism and suggests that talin could be more than a sensory receptor and adhesion structures could act as a computer. The structures formed by the adhesion units consisting of integrin-talin-actin triplets would serve as 13-bit units. Adhesion units would perform mechanical computation based on what authors call MESHcode.

One can argue that mechanical computation requires that adhesion units are isolated from the environment during the computation. This is in conflict with the role as force sensors. A weaker proposal would be that computation occurs only in the synaptic contacts which should be isolated during the computation. The same could take place also in the contacts between neurons and glial cells.

Concerning the synaptic level, a more realistic view to my opinion is that learning as a strengthening of the synaptic strengths corresponds to a development of force equilibrium of adhesion units. Learning could be described as the change of the resting states of the talin units and lead to a higher tension and larger number of unfolded protein domains. Nerve pulse patterns could cause temporary changes of this pattern.

9.3   TGD interpretation of adhesion units as quantal force sensors

In the TGD framework all communications and control in biology should rely on genetic code whose fundamental realization would be at the level of dark proton sequences forming dark nuclei

with $h_{eff} = nh_0 > h$ and dark photons.

Dark proton triplets - light 3-chords - would represent the counterparts for dark DNA, RNA, tRNA, and aminoacids and dark photon triplets could represent dark DNA codons [L2, L22, L32, L35]. Number theoretic vision [L12, L13] leads to a proposal that not only dark 3-photon 3-proton units act as single particle like units but also dark 3N-photons and 3-N protons do so and represent a gene consisting of N codons. Galois confinement would bind the photons and protons to larger particle units analgous to baryons as composites of 3-quarks.

All communications to MB would use dark 3N-photons coupling to corresponding dark 3N-proton by cyclotron resonances [L38, L36, **?**]. Therefore 3N-photon as a dynamical gene with N codons would define its own address. Frequency modulation of frequencies of 3N-photon would give rise to a sequence of resonance peaks and the continuous signal would be transformed to a signal analogous to nerve pulse sequence and could realize motor action as a response.

9.3.1   Magnetic body containing dark matter as the master

MB has a hierarchical onion-like structure with levels labelled by the value of $h_{eff} = nh_0$ giving rise to increasing scales. The dark analogs of DNA, RNA, tRNA, and amino-acids define flux tubes accompanying their ordinary variants with codons realized as dark 3-proton units.

In TGD genetic code in terms of 3-chords would be realized in a universal manner for the simplest tessellation of hyperbolic space known as icosa-tedrahedral honeycomb involving icosahedrons and tetrahedrons (also octahedrons are involved but they would be in passive role) [L35]. This would suggest that genetic code using dark proton- and dark photon triplets is realized at all layers of MB. Chemical realization would represent the lowest level in the hierarchy.

The layers of MB with increasing value of h_{eff} would define a hierarchy of abstractions. There is evidence for an effective statistically determined hyperbolic geometry [**?**] in the sense that neurons functionally but not necessarily spatiall near to each other are near to each other in this effective geometry. This hyperbolic geometry would be realized quite concretely at the level of MB [L30] for which hyperbolic geometry of proper time constant hyperboloid of the light-cone gives a concrete meaning.

One particular implication could be that sensory receptors of a given structure (say adhesion units of given cell-environment pair) could communicate their sensory data to neighboring icosa-tetrahedral units of the honeycomb of some layer of MB representing the codons of genetic code. The states of the icosahedrons and tetrahedrons of the honeycomb would be dynamical and selected by the 3-chord (actually pair of 3-chord and conjugate) to actualize genetic codon as 3-quark units assignable to the corresponding triangle of icosahedron or tetrahedron.

This would define sensory representation at MB, and the simplest option is that it automatically determines motor response as a sequence of resonance peaks communicated back to the biological body (BB) where they would initiate gene expression, RNA or protein activity, MT activity, or nerve pulse activity. The feedback would be directly to DNA (or RNA, amino-acid of protein, or even tRNA, microbuli, or cell membrane).

The biochemical motor actions of MB would be realized as bursts of dark cyclotron 3N-photons induced by the cyclotron resonances at MB transforming to ordinary photons (biophotons or IR photons with energy above thermal energy) controlling biochemistry by inducing molecular transitions.

This condition constrains the value of h_{eff} for a layer of MB. The size of the layer should be of the order of wavelengths involved. For valence bonds the values of $h_{eff} = h_{em}$ would be rather small and assignable with small layers of MB. For frequencies in EEG range the large value of gravitational Planck constant $h_{eff} = h_{gr}$ [L15, L38] assignable to the gravitational flux tubes would guarantee that the energies are in the required range.

The following picture about how sensory input induces gene expression or some other activity with communication and control realized in terms of genetic code might apply completely generally, not only in the case of adhesion units.

1. Suppose the sensory receptors of a given structure (say adhesion units of a given cell) are organized into coherent structures in the sense that the signals from them go along flux tubes to nearby cells of icosa-tetrahedral honeycomb at some layer of MB.

Adhesion structures consting of few hundred adhesion units are indeed connected to each other. Coherence would be forced by the quantum coherence at the level of MB as a forced coherence. One could assume that the cells of the honeycombinvolved are organized linearly but even 2-D and 3-D structures are possible.

For a structure consisting of N units, the dark 3N-photon signal would define a dark gene of N codons. The nice feature of the representation is that there is no need to organize the sensory receptors (say adhesion units) linearly at the level of the cell. The level of ordinary biomatter would be like RAM with ordering realized at the level of MB.

2. The naive picture is that if the dynamical gene realized in this manner has a dark counterpart at the level of flux tube accompanying DNA, gene expression could be initiated automatically as a feedback signal realized as a sequence of resonance peaks. Also RNA, proteins or MTs could be activated in an analogous manner.

   There would be a one-one correspondence between sensory inputs to MB and corresponding gene expressions and give a meaning for the genetic code. All sensory inputs to MB would be realized as N-genes in terms of generalized Josephson radiation which is frequency modulated and generates a sequence of resonance peaks inducing gene expression or RNA and protein activation.

3. The dynamical gene at MB need not correspond to an existing or expressible gene so that the response is not possible. This would give rise to an evolutionary pressure. Epigenesis controlled by MB could make the gene expressible. Also a suitable mutation for existing gene or emergence of new gene could produce the needed gene. Whether MB is able to induce this kind of mutations is an interesting question. Could a dark gene as a flux tube containing dark proton sequence representing the desired gene pair with ordinary DNA codons and give rise to a new gene?

   Or could MB "use scissors" to replace codon-anticodon pairs in an existing gene: this would mean reconnection of a closed flux tube pair containing the codon-anticodon pairs of the added gene fragment. Could a piece of dark DNA as a flux tube carrying the dark proton sequence pair with ordinary DNA codons and give rise to a new gene? Or could one add to an existing gene a piece represented as a dark DNA paired with the ordinary DNA. Most viruses have single stranded RNA genomes. Bacteriophages have double stranded DNA genomes. They are known to give rise to the modifications of the genome. Could these DNA modifications be induced by a reconnection of darkmagnetic flux tubes.

9.3.2   Universality of the genetic code and its higher dimensional representations

If genetic code at space-time surface is induced from a universal code assignable to the icosa-tetrahedral honeycomb of hyperbolic 3-space, representations of genetic code with dimensions $D = 0, 1, 2, 3$ are possible as induced representations. The codons associated with the cells of honeycombes projected to the space-time surface would define the induced codons [L35].

tRNA would be a 0-D representation and DNA, RNA, amino acids would be 1-D representations of the code. Also higher-dimensional representations are possible and could be associated with the basic biological structures.

1. I have proposed that cell membrane defines a 2-D representation of the genetic code [L35]. Also microtubuli could define a 2-D representation of genetic code. These 2-D representation could be dynamical and independent of genome and make genome dynamical. This would be a biological analog for AI able to write genes as program modules needed in a given situation.

2. Could a 3-D representation of genetic code be associated with the ECM and make it possible for MB to receive sensory input from ECM and control it? This layer of MB could also receive sensory information also from adhesive structures. The frequency range involved would be probably below EEG frequencies or at least below conscious frequencies since we do not experience the interior of body consciously and the time scale of dynamics is slow as compared to EEG scales.

   Hydrozyapatite molecules are present in bones forming a part of ECM. Fisher has proposed that the Posner molecules associated with hydroxyapatite molecules could have important

role in quantum biology [**?**]. This inspired the proposal that they provide a realization of genetic code [L6]. One cannot exclude the possibility that the code is 3-D. This would fit with the general idea that the genetic code serves as a universal code for communications and control.

9.3.3   Some TGD inspired numerology

If one takes the proposed general picture seriously, one must ask how the 13-bits codons assignable to talins and MTs could reduce to genetic codons. It is good to start with numerology or should one call it physics inspired poor man's number theory.

1. The number of protein domains in talin is 13. Also the number of tubulin dimers in 13-tubulin unit of MT/neurotubule appearing in cytoskeleton is 13. Could one think of communication between MTs and talins using 13 bit code? Or could the code using 13 bits be for some reason special? Could this code somehow reduce to the proposed universal 6-bit code defined by genetic code?

2. There are 4 protein domains consisting of 4 alpha helices and 9 domains with 5 alpha helices. This gives 61 alpha helices altogether. Numerologist might notice that 61 is the number of DNA codons with stop codons excluded. Could one assign to helices genetic codons and could these configurations labelled by 61 bits code for genes with length not longer than 61 units?

3. Numerologist might also notice that both $M_{13} = 2^{13} - 1$ and $M^{61} = 2^{61} - 1$ are Mersenne primes. If one has n bits and does not count the configuration with all bits 0 but assuming that at least single bit is always equal to 1, one has 2^{n-1} full bits.

   For M_{13} this corresponds to 12 full bits which corresponds to 2 genetic codons. To obtain 2 codons, single fixed talin should be unfolded and represent 1. Could this have interpretation in terms of a force threshold? One can argue that there is some minimal force unfolding some fixed talin. If the force is below the threshold, there is no need to communicate. Also in the case of MT the conformation of preferred tubulin, say the first or last one in 13-unit should always correspond to 1.

4. One cannot exclude the possibility that the responses of talin units correspond to two independent codons. This could be true also for13-bit units MTs.

   The alternative option is that both talins and 13-tubulin units of MT correspond to codon-anticodon pairs so that information content would reduce to that of single DNA codon. Half of the bits would serve as check bits. Also the purpose of the conjugate strand of DNA would be to serve as check codons.

   If this is the case, the adhesion unit would have only 2^6 different responses and would represent a genetic codon. The number of talins is few hundred that this would correspond to a DNA sequence of length of order 10^{-7} meters. In the case of MT 6 bits would be check bits.

5. The proposal would have far reaching consequences: the genetic code realized by MTs and talins would be dynamical rather than fixed and could represent a step to a higher evolutionary level.

6. The dynamics of the codon or of a pair of pair of independent codons assignable to the adhesion unit would mean change of the "sensory codon" possibly corresponding to a real codon assignable to it. The slow time variation of the gene assignable to the collection of adhesion units could define varying gene expression or some other activations (of say microtubuline).

These speculations encourage the question whether the codon-anticodon pairs possibly assignable to adhesion units integrate to sequences or perhaps even 2-D structures representing 2-D adhesion structures of DNA codon-anticodon pairs defining genes.

If these 2-D honeycomb structures at the level of MB decompose to piles of 1-D structures as microtubules do, they could even induce the expression of gene groups. Also 2-D gene expression

in terms of microtubules modifying the cytoskeleton can be considered. Note that the honeycomb structures are not needed at the level of ordinary biomatter.

9.3.4 A simple model for the adhesion units

In TGD framework magnetic body (MB) containing dark matter controls ordinary living matter. MB receives sensory input from organism in terms of dark Josephson radiation arriving from cell membranes acting as generalized Josephson juctions. Sensory information is coded by the modulation of membrane potential. For ordinary cells only small modulations of membrane potential would induce modulations of Josephson frequency. For neurons nerve pulse patterns introduce more drastic modulation.

1. The two states of the protein domains could correspond to different values of h_{eff}. The reduction of h_{eff} at the magnetic flux tube accompanying the protein would induce the shortening of the flux tube associated with the unfolded protein to the folded configuration.

2. Cohesion units would aserve as sources of sensory information about the net force acting on the cohesion unit and coded by 13 bits unless the bits are independent. For instance, different bits would correspond to different signals, say different frequencies of dark photons. If one takes the interpretation as a pair of codons seriously, the signal could consist of a dark 3-chord and its conjugate 3-chord sent to MB and defining at the MB a representation of gene to be possibly activated.

3. Josephson radiation as dark 3-photons from the part of the cell membrane considered would mediate the 13 bit signal defined coded to a local change of membrane potential with 2^{12} values defining 12 octaves if there is threshold corresponding to activation of a preferred talin. Note that the frequencies audible for humans are in the range 20 Hz- 20 kHz and correspond to 10 octaves.

4. MB would receive the sensory input and react by possibly sending control signal to DNA inducing gene expression or inducing activity of proteins or RNA. This means that talin molecules would not be active but MB receiving the sensory input from adhesion units.

   MB could also send control signal to microtubuli if MT contains a sequence of 13-tubulin units corresponding to the dynamical gene [L3] [I5] (https://en.wikipedia.org/wiki/Microtubule). This would reflect itself in the dynamics of MTs. This control loop would modify the force equilibrium by a modification of the shape of the cell.

5. MTs could represent an evolutionary step making the genome dynamical and independent of genes and extending ordinary genome as the microtubular response possible for eukariotes suggests. Also the long MTs inside axons conform with this interpretation.

6. MTs are highly dynamical. Their lengths are continually varying. According to "search-and-catch" model MTs inside cells are scanning their 3-D environment and whey the find a target attach to it and MT is stabilized. This conforms with general vision about U-shaped dynamical flux tubes serving as tentables and forming a reconnection with a similar U-tube of the target. Immune system would be rely on this mechanism at the fundamental level and allow the system to detect and catch invader molecules on basis of their cyclotron energy/frequency spectrum [K2, L38].

7. The general vision suggests that the feedback loop should involve also microfilaments and intermediate filaments. It would be interesting to see whether the structure of microfilaments and intermediate filaments could allow realization of the counterpart of genetic code. The basic signature are GTP and ATP molecules providing metabolic energy for motor action.

9.4 An application to memory and learning

Since the increase of synaptic strengths is believed to be behind the formation of memories as behaviors and habits, it is appropriate to discuss the notion of memory in TGD framework and consider connections with the model for the adhesion units at synaptic contacts.

The major issue with memory is potentiation (repeat of same memory which facilitatesmemory recall and learning) and amnesia, Alzheimer disease and memory when dreaming. There should be a compatible explanation for these phenomena.

In TGD one distinguishes between two kinds of memories. Episodal-/sensory memories and memories as associations/learned behaviors.

9.4.1   Memories as learned behaviors

Neuroscience explains learned behaviors in terms of strengthening of synaptic contacts and I believe that this is part of the story.

The formation of associations in conditioning is a highly emotional process and here the surprising finding [**?**] (see `http://tinyurl.com/ycqxyeqk`) few years ago (roughly) was helpful. The popular article " *Scientists Sucked a Memory Out of a Snail and Stuck It in Another Snail*" tells about the finding (see `http://tinyurl.com/y92w39gs`).

The RNA of a sea snail which had learned by (presumably painful) stimulus a behavior was scattered on the neuronal tissue of another sea snail in a Petri dish. The neuronal tissue learned the same behavior!

The TGD based explanation is following.

1. Emotions are realized already at the molecular level [L19] in terms of music of light - bioharmony [L2, L22, L32, L35]. The emotional stimulus at the MB of RNA induced learning by changing the allowed 3-chords of bioharmony. Also the sequences of 3-chords characterizing 3N-genes and other basic linear biomolecules changed. The resonant couplings to the basic biomolecules changed so that also chemical behavior changed.

2. The emotional state of the conditioned seanail RNA infected the RNAs and probably also DNAs and proteins of neurons and induced learning.

3. Synaptic strengths had to change and the molecular emotions as music of light would have induced this.

   If the idea about mechanical control of synaptic strengths by talin molecules by push and pull from ECM and cytoskeleton is correct, the molecular mood had to induce a strong force changing the talin conformations. Emotion would quite concretely correspond to a force!

   This would have induced a reaction at the level of microtubules with the mediary of MB as a response making the change permanent. Neurotubules of the cytoskeleton in dendrites and axons would be involved in realizing the learning as a permanent change.

9.4.2   Potentiation and two kinds of memories

The notion of potentiation applies to both kinds of memories.

1. The repetition of stimulus generating the learned behavior increases the synaptic strength. Perhapsby inducing a memory recall of the emotional experience at molecular level.

2. Potentiation for sensory memories creates an almost copy of sensory memory mental image at "geometric now": the re-experience and the more one has these almost copies in the geometric future of "geometric now", the higher the probability that the attempt to remember by sending dark photon signals to the future hits the memory mental image are successful. The latest memory recalls create memories mental images nearest to "geometric now" and the probability for memory recall is highest for them.

Why oldest sensory memories are those which survive when one begins to lose memories at old age?

1. There are a lot of almost copies about the oldest memories: does this mean that the memory recall has a higher probability to be successful?

2. One can also argue that the memory mental images of young age have also gone through a long sequenceof re-incarnations which have gradually increased the value of h_{eff}.

   Large h_{eff} means that the frequency f needed to produce a dark photon with energy $E = h_{eff}f$ in biophoton range is lower and therefore the period $T = 1/f$ is longer. Uncertainty Principle says that the time period over which memories are optimally recalled is of order$T = 1/f$.

9.4.3   Amnesia,Alzheimer, and why we forget dreams so fast

Amnesia might relate to the inability to recall sensory memories by sending signals with a correct frequency to the memory mental images. The energy of the dark photons is proportional to h_{eff} and if it is reduced in the recalling end as tends to happen in the absence of metabolic energy feed, the ability to recall memories is weakened or lost. For instance, alcoholism can lead to a loss of memory recall and this could be the reason.

Alzheimer means a loss of memories as behaviors and inability go generate new ones. In TGD framework [L11] the weakening of the synaptic connections would make the build up of connection between magnetic flux tubes associated with presynaptic dendrite and postsynaptic axon and the dark photon signal could not propagate because the connection is broken.

Also the propagation along axonal flux tubes could be impossible or highly attenuated if the value of h_{eff} for them is reduced. Also the energy for a given freqeuency would be reduced below the biophoton energy range.

Why do we forget dreams so fast? We do not remember anything about sleep without dreams. In ZEO this can be understood if sleep corresponds to "small death" for an appropriate layer of MB meaning re-incarnation with an opposite arrow of time. Dreams would correspond to states in which part of the brain is awake and possibly receives information from the sleeping part of the brain realized as a dream. Dream would be due to a communication of virtual sensory input from MB with opposite arrow of time to sensory organs.

This does not yet explain why we forget dreams so fast. As the memory image ages, it shifts to the future of "geometric now" in CD, and the needed frequency as inverse of the age decreases. Could it be that we cannot generate the frequencies of dark photons needed for the memory recall.

9.4.4   Memories change

Episodal memories are not carved in stone. They are modified in memory recalls. In TGD framework, the modification of (episodal) memory mental images is unavoidable. Memory mental images are living entities and evolve re-incarnation by re-incarnation. Memory recalls are basically analogous to quantum measurements of memory mental images induced BSFR and quantum measurement indeed changes the state of the system measured.

1. The sub-selves of self as mental images continue to live at sub-CDs which in the proposed model drift to the geometric future of CD increasing SSFR by SSFR. These sub-CDs experience BSFRs and evolve incarnation by incarnation. In general evolution happens and they become smarter and wiser. Memories are indeed said to grow sweeter in time.

2. Each memory recall must take the memory subself to a state in which it has arrow of time opposite to that of recaller so that the signal about the memory propagates to the geometric past to "geometric now" [the ball at center of CD at which future and past directed cones glued together].

   The BSFR for memory subself with the same arrow of time as recaller induces memory recall. Memory recall is a murderous process. If the memory recall occurs spontaneously, the murder is not not the recaller.

9.4.5   Confabulation

The phenomenon of confabulation relates most probably to episodal/sensory memories, not memories as behaviors and habits. Confabulation could be understood in the following manner. Memory mental images are just glimpses about what happened since only those aspects of the event which

receive the attention form memory mental images. Memory recaller builds a logical sounding story around these glimpses so that confabulation is unavoidable.

Even our sensory perception is fabrication of stories [L9]. Sensory organs are seats of primary sensory experience and there is feedback from MB and brain to sensory organs as virtual input. This feedback loop generates standardized mental images by pattern completions and recognition.

If the sensory input is meager the story can be non-realistic as I know as a person with a poor eye sight. REM dreams and hallucinations are an excellent example of this: in this case there is only virtual sensory input present.

10 Appendix: Tables of basic 3-chords for the icosahedral harmonies with symmetries

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

$(\mathbf{n_0, n_1, n_2})$	0-chords	1-chords	2-chords
(2, 12, 6)	$(Faug, Gaug)$	$(Cm, Dm, Em, F\sharp m, G\sharp m, B\flat m)$,	$(C9, D9, E9, F\sharp 9, G\sharp 9, B\flat 9)$.
		$(F6, G6, A6, B6, C\sharp 6, D\sharp 6)$.	

Table 2: Table gives various types of 3-chords for harmonies with Z_6 rotational symmetry. Note that half-octave shift is an exat symmetry. Note that $G^{aug} = CEG\sharp$, F^{aug} act as bridges between the groups related by half octave shift. The chords have been arranged so that they form orbits of Z_6. "Amino-acid chords" correspond to preferred chords at the orbits.

$(\mathbf{n_0, n_1, n_2})$	0-chords	1-chords	2-chords
(0, 16, 4)		$(D7, D6, G\sharp 7, G\sharp 6)$,	$(B\flat 9, B9, E9, F9)$.
		$(G4+, A9-, C\sharp 4+, D\sharp 9-)$,	
		$(Emaj7, Gmaj7, B\flat maj7, C\sharp maj7)$,	
		$(C9-, A9-, F\sharp 9-, D\sharp 9-)$.	
(4, 8, 8)	$(Cex3, Eex2, F\sharp ex3, B\flat ex2)$.	$(Dmaj7, E9-, A7, A6)$,	$(B\flat 9, F9, C9, G9)$.
		$(G\sharp maj7, B\flat 9-, D\sharp 7, D\sharp 6)$.	$(E9, B9, F\sharp 9, C\sharp 9)$.

Table 3: Table gives various types of 3-chords for the two harmonies with $Z_4 = Z_2^{rot} \times Z_2^{refl}$ symmetry. 4-plets represent the orbits. First cycle has no harmonic loners. Second cycle gives rise to bio-harmony (4, 8, 8) for which 0-quint chords are dissonant.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	0-chords	1-chords	2-chords
$(0, 16, 4)$		$(Em, B\flat m), (Cm, F\sharp m),$	$(D9, G\sharp 9),$
		$(G6, C\sharp 6), (A6, D\sharp 6),$	$(E9, B\flat 9).$
		$(D4+, G\sharp 4+), (B4+, F4+),$	
		$(Cmaj7, F\sharp maj7), (G6-, C\sharp 6-).$	
$(2, 12, 6)$	$(Aex4, D\sharp ex2).$	$(Am, D\sharp m), (G9-, C\sharp 9-),$	$(C9, F\sharp 9),$
		$(C4, F\sharp 4), (E4+, B\flat 4+),$	$(A9, D\sharp 9),$
		$(Dmaj7, G\sharp maj7),$	$(D9, G\sharp 9).$
		$(Bmaj7, Fmaj7).$	
$(4, 8, 8)$	$(Aex2, Hex8, D\sharp ex2, Fex8).$	$(D7, G\sharp 7), (Amaj7, D\sharp maj7),$	$(G9, C\sharp 9), (A9, D\sharp 9),$
		$(A4+, D\sharp 4+), (E7, B\flat 7).$	$(B9, F9), (E9, B\flat 9).$

Table 4: Table gives various types of 3-chords for harmonies with Z_2 rotation symmetry acting as half-octave shift. The doublets represent 2-chord orbits.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	0-chords	1-chords	2-chords
$(2, 12, 6)$	$(F\sharp ex3, Hex4),$	$(Am, D\sharp), (A6, D\sharp 7),$	$(C9, F9), (B9, F\sharp 9),$
		$(D7, B\flat 6), (G6-, Fmaj7),$	$(E9-, C\sharp 9).$
		$(D4+, B\flat 9-), (E9, G\sharp 4+),$	
$(2, 12, 6)$	$(Dex4, Hex4).$	$(F, Fm), (C6-, B\flat maj7),$	$(C9, D\sharp 9),$
		$(D7, G\sharp 6), (Gmaj7, D\sharp 6-).$	$(D\sharp 9, C\sharp 9),$
		$(C\sharp 4-, A4+), (E4+, F\sharp 6).$	$(E9, B9).$
$(4, 8, 8)$	$(Fex1, D\sharp ex3, G\sharp ex1, Aex2).$	$(E7, E6), (Amaj7, B9-),$	$(D9, B9), (C9, C\sharp 9),$
		$(G, C\sharp m), (D7, F\sharp 6).$	$(F9, G\sharp 9), (D\sharp 9, B\flat 9).$
$(2, 12, 6)$	$(Hex3, Eex7).$	$(D7, G\sharp 6), (G, D\sharp m),$	$(C9, D\sharp 9),$
		$(F, Fm), (C6-, B\flat maj7),$	$(D9, C\sharp 9),$
		$(A9-, C\sharp 4+), (E7, F\sharp 6).$	$(E9, B9).$
$(2, 12, 6)$	$(F\sharp ex2, Fex3).$	$(F, B\flat m), (C7, G\sharp 6),$	$(B\flat 9, D\sharp 9),$
		$(Amaj7, B9-), (E6, E7),$	$(C9, C\sharp 9),$
		$(G, C\sharp m), (D7, B6).$	$(D9, H9).$

Table 5: Table gives various types of 3-chords for harmonies with single reflection symmetry.

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