

Geometric Theory of Bio-Harmony

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Abstract

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

1. The model relies on the geometries of icosahedron and tetrahedron and representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 amino-acids (AAs).
2. One has three basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6 , Z_4 or Z_2 . For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle.
3. Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA. 4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint.
4. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA. Music expresses and creates emotions and the natural proposal is that these bio-harmonies correlate with moods that would appear already at molecular level. They could be realized in terms of dark photon triplets realized in terms of light and perhaps even music (living matter is full of piezo-electrets). In fact, also the emotions generated by other art forms could be realized using music of dark light.

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

1. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton’s cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied.
 - (a) There is a purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20?
 - (b) There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies.
2. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could AAs couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA? Could coding by the sum of frequencies appear in the coupling of tRNA with mRNA by codewords and coding by separate frequencies to the letterwise coupling of DNA and RNA nucleotides to DNA during replication and transcription?
3. What about tRNA. Could tRNA correspond to pairs of harmonies with 20+20+444 codons? What about single 20+4=24 codon representation as kind of pre-tRNA?
4. What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetric arguments fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible so that it would be possible to listen what DNA sequences sounds in given mood characterized by the harmony.
5. What disharmony could mean? A possible answer comes from 6 Hamiltonian cycles having no symmetries. These disharmonies could express “negative” emotions.

1 Introduction

The model for bio-harmony predicted vertebrate genetic code correctly has evolved to its recent form during 4 years. The recent progress in the understanding of the model motivated writing of a separate chapter summarizing the earlier results and adding the new results achieved during 2018.

Remark: In the sequel I will use the shorthand AA for amino-acids and shorthands DDNA, DRNA, DtRNA, DAA for the dark analogs of DNA, RNA, tRNA, and AA realizes as dark proton sequences with codon represented as dark proton triplet.

1.1 Some background

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

The article [L2] was meant to be a continuation to the mentioned article providing a proposal for a theory of harmony and detailed calculations. It however turned out that the proposed notion of bio-harmony was too restricted: all icosahedral Hamilton cycles with symmetries turned out to be possible rather than only the 3 cycles forced by the assumption that the polarity characteristics of the AAs correlate with the properties of the Hamiltonian cycle. This working hypothesis had to be given up. The fuel of the minirevolution was the observation the symmetries of the Hamiltonian cycles (Z_6, Z_4, Z_2) are nothing but the icosahedral symmetries needed to predict the basic numbers of the genetic code and its extension to include also 12st and 22nd AAs. Thus icosahedral Hamiltonian cycles predict genetic code without further assumptions.

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

1. 3-adicity and also 2-adicity are essential concepts allowing to understand the basic facts about harmony. The notion of harmony at the level of chords is suggested to reduce to the notion of closeness in the 3-adic metric using as distance the distance between notes measures as the minimal number of quints allowing to connect them along the Hamilton's cycle. In ideal case, harmonic progressions correspond to paths connecting vertex or edge neighbors of the triangular faces of icosahedron.
2. An extension of icosahedral harmony to tetra-icosahedral harmony was proposed as an extension of harmony allowing to solve some issues of icosahedral harmony relying on quint identified as rational frequency scaling by factor $3/2$.

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

Tetrahedral code is second member in the hierarchy of genetic codes [K4] inspired by the notion of Combinatorial Hierarchy $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$ giving the numbers $2, 4, 7, 64, 2^{126}, \dots$ as numbers of DNA codons. The fourth member would correspond to what I called "memetic code" allowing representation of codons as sequences of 21 DNAs. It is not known whether the Combinatorial Hierarchy of Mersenne primes continues as Hilbert conjectured.

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

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

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

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

5. The assumption that harmonic transitions between chords (DNA codons) minimize the distance between chords defined by quint-metric leads to highly non-trivial and testable predictions about both DNA sequences and AA sequences. Negentropy Maximization Principle (NMP) [K6] suggests that evolution favors the generation of harmony which should thus increase in the proposed sense for DNA sequences defining particular genes or other functional units of DNA during evolution. Large quint-distances between subsequent codons/chords would tend to be polished out under evolutionary pressures.
6. Could icosahedron, tetrahedron, and tetra-icosahedron have direct physical counterparts in living matter? For instance, water molecules form icosahedral clusters and the chathrates associated with synaptic contacts have icosahedral symmetries. Tetra-icosahedron has 13 vertices with the added vertex representing one note- say E- in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more than 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.
7. Music is language of emotions and peptides are molecules of emotion as Candace Pert [?] expressed it. Could bio-harmonies serve as direct correlates for emotions? What is bio-music? A natural TGD inspired guess is that sounds can be replaced with $h_{eff} = n \times h$ dark photons with low frequencies and having energies in the range of bio-photons (visible and UV range maximally effective biologically) as proposed on basis of some physical facts and theoretical ideas [K11]. The frequency spectrum of dark cyclotron photons along magnetic flux tubes would define bio-music as “music of dark light” and bio-harmonies would correlate with emotions and moods.

If one can find various icosahedral Hamilton’s cycles one can immediately deduce corresponding harmonies. This would require computer program and a considerable amount of analysis. My luck was that all this has been done. One can find material about icosahedral Hamilton’s cycles (see <http://tinyurl.com/pmghcwd>) in web, in particular the list of all 1024 Hamilton’s cycles with one edge fixed [A2, A4] (this has no relevance since only shape matters). If one identifies cycles with opposite internal orientations, there are only 512 cycles. If the cycle is identified as a representation of quint cycle giving representation of 12 note scale, one cannot make this identification since quint is mapped to fourth when orientation is reversed. The earlier article about icosahedral Hamiltonian cycles as representations of different notions of harmony is helpful [L5].

The tables listing the 20 3-chords associated with a given Hamilton’s cycle make it possible for anyone with needed computer facilities and music generator to test whether the proposed rules produce aesthetically appealing harmonies for the icosahedral Hamiltonian cycles. Biologist with

access to DNA sequences could experiment with DNA codons to see whether they are harmonious in the sense that the distance between subsequent chords assignable to DNA codons tend to be small in quint metric. Note that DNA decomposes to pieces corresponding to different Hamiltonian cycles (harmonies) so that the comparison is not quite straightforward.

This summarizes the original article about geometric model of harmony [L2] and contributions in online books [K13, K11]. This chapter contains besides this article also some new results and considerations related to music harmony. Most of them have emerged during 2018.

1.2 Questions emerged during 2018

The model of music harmony is separate from the model of genetic code based on dark proton triplets [L8] and one of the challenges has been to demonstrate that they are equivalent. One can raise several questions.

1. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton's cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied.
 - (a) There is purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20?
 - (b) There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies.
2. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could AAs couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA? Could coding by the sum of frequencies appear in the coupling of tRNA with mRNA by codewords and coding by separate frequencies to the letterwise coupling of DNA and RNA nucleotides to DNA during replication and transcription? Could the emergence of DNA be interpreted as an evolutionary step from a holistic picture using codons as basic units (dark codons cannot be decomposed to letters) to more analytic picture in which letters are treated separately?
3. As I developed the model of bio-harmony [L2] (see <http://tinyurl.com/yad4tqw1>) it did not occur to me that also the tRNA part of the dark code should have counterpart in the icosahedral model. Could tRNA correspond to pairs of harmonies with $20+20+4=44$ codons? What about single $20+4=24$ codon representation as kind of pre-tRNA? Could tRNA correspond to a union of 2 20-codon codes? Combining only 2 20-codon codes with 40 codons and tetrahedral code with 4 codons would give maximally 44-letter code and the upper bound for tRNAs is according to Wikipedia 45! Dark proton model predicts 40 DtRNAs suggesting that only the 40 icosahedral codons contribute to DtRNA code. The additional tRNAs could result from homonymy. The code sequences could be seen as a hierarchical sequence $3 \rightarrow 2 \rightarrow 1$ in this framework.

An important implication is that there are many realizations of DtRNA and tRNA harmony: (Z_6, Z_4) , (Z_6, Z_2) , (Z_4, Z_2) and Z_2 could be either $Z_{2,rot}$ or $Z_{2,refl}$. This could explain the homonymy of mRNA-tRNA pairing via difference in the chords in turn affecting biochemical counterparts. Note however that the chords for tRNA must be a subset of chords for mRNA so that RNA harmony determines tRNA harmony apart from the three choices (Z_6, Z_4) , (Z_6, Z_2) or (Z_4, Z_2) giving rise to 3 different contexts. If DAAs code by 3-chords the AAs then this choice does not affect AAs.

4. What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetry arguments fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible.

Hence it would be possible to listen what DNA sequences sounds in given mood characterized by the bio-harmony: the allowed 3-chords of harmonies with symmetries are given in [L2] and I can provide the basic Python modules allowing to transform DNA sequences for given harmony to audible form using Garage Band program.

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

Remark: I proposed the theory of bio-harmony in the article [L2]. I have discussed the model of bio-harmony also in the chapter “Quantum Model of Hearing” [K11] of book “TGD and EEG” and in the chapter “Three new physics realizations of the genetic code and the role of dark matter in bio-systems” [K13] of book “Genes and Memes”. The recent findings motivated writing a chapter including the previous results plus new results emerged during 2018.

2 What could be the basic principles of harmony?

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

2.1 Icosahedral harmonies

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

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

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

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

The basic classification is according to the number $n = 0, 1, 2$ of edges of cycle contained by them and the triplet $n = (n_0, n_1, n_2)$ for the numbers of faces of various kinds gives the first rough classification. 2-quint chords have common edge and thus two common notes with two 1-quint chords and are therefore natural intermediates in transitions between them. 0-quint chords are tonal loners having no edge neighbours turns out that they involve dissonances since they consists of three notes spanning length of 1 or 3/2 steps (say EFG , $EF\sharp G$ or $D\sharp EF$). Maximally symmetric harmony is an exception: 0-quint chords correspond to augmented chords of type $CEG\sharp$ with two major thirds.

The numbers of three different kinds of face neighbor pairs for the 12 edges of the path serve as an additional classification criterion in terms of the $p = (p_{1,1}, p_{1,2}, p_{2,2})$ for the numbers $p_{i,j}$ of different kind of edges. Note that the neighbor faces of an edge correspond to 3-chords, which

possess two common notes and are in this sense close to each other. These numbers characterize the most natural transitions between the chords of the harmony. A further criterion is the distribution of these neighbor pairs along the cycle.

2.2 Why fifths are near to each other harmonically?

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

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

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

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

1. By octave equivalence the scaling by power of two means nothing so that the scalings by $3/2$ are equivalent with scalings by 3 and the distance defined by 3-adic norm having values 3^k , where k is the number of fifths makes sense. The distance defined as fifths could be identified the absolute value of k along the fifth cycle in the direction in which the distance is shorter. If so, the maximal distance is 6 units.
2. 3-adic measure of distance seems to be rather realistic. Fifth corresponds to 1 unit distance. Half step corresponds to a distance of 5 units and 6 units defines the largest distance and corresponds to the tritonus interval which was forbidden by catholic church. Fourth (C-F) corresponds to 1- step in opposite direction and 11 steps in standard direction.
3. There is also a problem. Second (C-D) corresponds to 3 fifths but third (C-E) corresponds to 4 fifths and small third to 3 fifths in opposite direction. Major third would thus correspond to a longer harmonic distance than second. This is a genuine problem, whose solution might be provided by the extension of icosahedral scale to icosatetrahedral one bringing in one additional note which is very near to one of the icosahedral notes and is major or minor third of icosahedral note.
4. Could one use the number of icosahedral edges as distance between notes but not as a minimal distance along the Hamiltonian cycle but along a minimal edge path along icosahedron? The icosahedral measure of distance would be analogous to a distance between points of object along shortest route in space that it inhabits and depends on harmony characterized by the shape of icosahedral cycle. C and E (and also C and F \sharp !) could be close to each other in some harmony and distant from each other in some other harmony. Icosahedral geometry would become an active determinant of the harmony.

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

2.3 What could be the rules for building a harmony?

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

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

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

2. Could 2-quint chords act as bridges between two 1-quint chords? For instance, for the maximally symmetric harmony consisting of disjoint groups of chords related by half-octave scaling the augmented chords ($F^{aug} = FAC\sharp$ and G^{aug} mapped to each other both by half-octave scaling and reversal of orientation could serve as mediating bridges.
3. Could harmonic transitions take place only between neighboring faces of icosahedron (see <http://tinyurl.com/ns9aa>) or should it only tend to minimize the quint distance between subsequent chords (this distance vanishes if they have a common note)? For the 0-quint distance harmony, the harmonic movement could be seen as a path in dodecahedron which is dual of icosahedron. In the most general case the transition can take place to both wall and vertex neighbors, whose total number is $3+3=6$. In this geometric picture harmony and melody could be seen as duals of each other.

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

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

4. An interesting test for the idea would a computerized generation of random chord sequences satisfying at least one common vertex rule and finding whether they are aesthetically appealing. Incidence matrix (see Appendix) for the icosahedral (and tetra-icosahedral) triangles wholes element tells how many common vertices two chords have have allows computational construction of the allowed chord sequences as random sequences.
5. For most harmonies 0-quint chords involve dissonances induced by three nearby notes (such as $CC\sharp D$) and spanning large number of quints (maximally symmetric harmony has 2 0-quint chords, which do not have dissonances and second harmony with 2 reflection symmetries has no 0-quint chords). Also $maj7_-$, $sus4_+$, and 6_- 1-quint chords have half-note dissonances. Dissonances as such are however not un-sesthetical. For instance, Bach used them to create a deeply melacholic feeling.

2.4 More general notion of harmony

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

1. 0-quint rule is too restrictive already in chord based music. For instance, the downwards progression Am, G, F, E appearing in Spanish music and music forms like Passacaglia would have chords with 1-quint distance. Hence one must consider also a weaker notion of harmonic chord progression according to which this distance is minimized and below some maximum value k_{max} . One quint would define the smallest non-vanishing maximal distance. One can define incidence matrices for chords with n -quint distance. The incidence matrices with different values of k_{max} have disjoint sets of non-vanishing elements and the total incidence matrix is their sum.
2. Even this is not enough. The direction of step matters for scales (major-minor difference) and it seems to matter also for chord harmonies. The inverse E, F, G, Am of the above mentioned progression does not sound harmonic in the same Am key. The impression of achieving the goal/ending down to something dictated by fate is lost.

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

Also the number of n -quint steps between chords matters. The larger this number, the closer the chords are. Two 0-quint steps means that chords have two common notes, 1 0-quint step that they have single common note. The two 1-quint steps for downwards step $Am - G$ are between 3rd and 1st ($C \rightarrow G$) and 5th and 3rd ($E \rightarrow H$). For upwards 0-quint steps $E - H7$ 1-quint steps are between 5th and 5th ($H \rightarrow F\sharp$) and 1st and 1st ($E \rightarrow H$). For $H7 \rightarrow E$ the reversals of these steps occur. For $E7 \rightarrow Am$ one has 3 1-quint steps: (the reversals 1-quint steps $E \rightarrow A$ and $H \rightarrow E$ steps and 1 quint step $D \rightarrow A$. The last step seems to be the smallest one in a well-defined sense.

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

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

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

1. A conjecture inspired by the genetic code is that the codons defining the allowed melody notes associated with a given chord are in one-one correspondence with the triangles at the orbit of the triangle associated with the chord under the group Z_6, Z_4 , or Z_2 characterizing the chord as a counterpart of amino-acid. In table 3 the Z_6 orbits are represented as groups of 6 similar chords (2 for 1-quint chords and 1 for 2-quint chords). In table 4 for Z_4 chords the groups consist of 4 similar chords and in the tables 5 and 6 for Z_2 harmony the chord groups consist of 2 similar chords.
2. The first guess is that the union of the notes of these chords could define the chords, whose notes are compatible with chord in the time scale shorter than the duration of the chord. Note that same triangle can appear at orbits of several chords since the orbits of each group span entire icosahedron.

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

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

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

1. The simplest guess is that these groups are represented as subgroups of Z_{12} (also a subgroup of icosahedral group) representing quint cycle. Z_n generator would shift the basic note of the chord by $12/n$ - that is 2, 3, 6 quints.
2. Z_n maps chords of same type to chords of same type only if it is a *rotational* symmetry of the harmony. For instance, the action of Z_6 (see **Fig. ??**) on icosahedron allows doublet orbit consisting of $Xaug$ type chords, since Z_3 maps 2 0-quint triangles in the middle of the figure to themselves and reflection group Z_2 permutes them. 6-element orbits consist of either minor or major chords. More generally, the inspection of the cycles shows that the cyclic orbits of triangle under Z_n correspond to the orbits of corresponding subgroups of icosahedral group.
3. Z_2refl maps the shape of the chord to its mirror images and so that the character of the chord can vary along Z_4 orbits. The rules are $(M \leftrightarrow m)$, $(6 \leftrightarrow 7)$. For other chords the character is unaffected.
4. Any subgroup of icosahedral isometry group $A_5 \times Z_2^{refl}$ having 120 elements must map chords to chords (faces to faces). In particular any Z_n even if it is not a symmetry of a particular harmony. The character of the chord is not preserved and the number of quints can change. Whether these maps have interpretation in terms of music remains unclear.

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

1. All 11 Hamilton cycles are realized separately as DNA level harmonies. Amino-acid level harmonies would correspond to selection of three Hamiltonian cycles, one for each Z_n .
2. To get something one must give something away. Now one must give up the idea that (4, 8, 8) is special via the corresponding of n-quint property with polarity properties. This is a pity, since just taking this correspondence seriously led to the extension of the icosahedral cycles to tetra-icosahedral ones. Fortunately, the extension itself makes sense for all Hamiltonian cycles.

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

1. Z_2 would induce half-octave shift and map $C = (C, E, G)$ to $F\sharp m = F\sharp, B\flat, D\sharp$. The assignment of $F\sharp$ -tritonus - with C note sounds strange in the ears of harmonic conservatives.
2. Z_4 would map $C = (C, E, G)$ to $A = (A, C\sharp, E)$, $F\sharp = (F\sharp, B\flat, C\sharp)$ and $D\sharp = D\sharp = (D\sharp, G, B\flat)$. These would span 8 notes since $E, G, B\flat, C\sharp$, appear twice. Note that C, E, G, A are the notes assignable to the tetrahedron in the extension of the scale and pentatonic scale corresponds to C, D, E, G, A . Z^4 orbit does not contain the notes $DFG\sharp H$ but the orbit of G chord does so. The orbit of C chord plus $G7$ chord alone define the notes of C major key.
3. Z_6 would map C and E to the same "impressionistic" 6-note scale consisting of 6 whole notes. Together with the Z_6 image of G one obtains all 12 notes of the scale.

3 Harmony and biology

3.1 Could harmonic principles be realized in biology?

The basic idea behind icosahedral harmony is the connection with biology suggested by the fact that the number of icosahedral basic chords is 20 which is also the number of amino-acids. Actually there are two additional amino-acids and one ends up to an extension of genetic code by attaching to icosahedron a tetrahedron and thus adding one vertex more. The number of DNA codons increases from 60 for icosahedral code to 64 for the real code. The triangle along which icosahedral and tetrahedral amino-acids are attached together corresponds to punct coded by stopping codons.

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

1. The strictest rule stating that there must be common edge of Hamiltonian cycle between the amino-acids/DNAs cannot be satisfied since 0-quint amino-acids/DNA codons would be total loners and effectively eliminated from biology.
2. The weaker “common edge or vertex” rule could however make sense. A given codon in the group of 20 codons/amino-acid could be followed only by 3+3 different nearest neighbor similar codons/amino-acids. If the first amino-acid is fixed there would be only 6^N N-amino-acid sequences instead of 20^N sequences. This kind of symmetry would have been probably observed if exact but one can ask whether harmonic pairs could more probable than completely random pairs.
3. A more plausible formulation is obtained by restricting the rule to the level of DNA sequences and generalizing it so that it applies also to transitions between harmonies with different symmetries so that a transition between corresponding amino-acids is induces.
4. An even weaker formulations states that the transitions occur with highest probabilities between codons/amino-acids having shortest quint distance.

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

3.1.1 Icosahedral water clusters made from tetrahedra

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

Water molecules form icosahedral structures and - what is amazing to me - Plato regarded icosahedron as a symbol of water (<http://tinyurl.com/y7bo9omm4a3378c13bcad793a52213a325db7db0-30.html>)! The page “Water structure and science” of Martin Chaplin gives illustrations about the rather complex icosahedral structures. Icosahedral structures of size 3 nm can be formed from 20 14-molecule tetrahedral water molecule clusters containing 280 water molecules altogether. They can also consists of cyclic pentamers and tricyclo-decamers and also from bi-cyclo-octomers. The 20 tetrahedrons correspond to the faces of the icosahedron and tetra-icosahedron would be formed as tetrahedron is glued to the icosahedron along one of the faces.

The bioharmonies could manifest themselves already in the structure of water molecules. Second - more plausible - option is that they differ only at the level of the magnetic body of the biomolecule. Bio-harmony suggests that 3 radial magnetic flux tubes or flux tube pairs emerge from each water tetrahedron. Hamilton’s cycle could be realized as a flux tube connecting the vertices of the icosahedron and assigning the quint cycle to the cyclotron frequencies (magnetic field strengths).

This scenario raises several questions related to the pairings between ordinary DNA/amino-acids, their icosahedral representations, and their representations as dark proton sequences.

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

1. How dark proton sequences are realized? Could one regard them as icosahedral bound states of 20 dark protons? Or with a Hamiltonian cycle consisting of penta-quarks and representing dark nuclear string? Could the icosahedral representation as dark nucleus consisting of 20 dark protons and dodecahedral representation as dark nucleus consisting of 12 dark 5-proton states be dual ways to interpret the state or are they different states related duality. Equivalence of the two pictures would require that dark protons are color excited and in an entangled state.
2. Could dark proton sequences correspond to sequences of icosahedrons connected by flux tubes connecting the dark protons assignable to the dark proton states assignable to the faces of the icosahedrons? These dark nuclei would be definitely different from those possibly associated with the Hamiltonian cycle.
3. What about the tetrahedral part of the genetic code in relation to dark protons sequences? What dark proton states could tetrahedral codons and amino-acids correspond? Are they associated with water tetrahedrons representing the faces of the water icosahedron? Note the amusing numerological co-incidence that the vertices of tetrahedron have 3 quarks associated with them and those of icosahedron 5 and that the quint for icosahedral edge is replaced with third for tetrahedral edge.
4. Could the chords correspond to triplets of cyclotron frequencies for quarks associated with the three flux tubes emanating from the each face of the icosahedron? Could the breaking of the rotational symmetry from $SO(3)$ to $SO(2)$ - now actually $Z_3 \subset SO(2)$ - assumed to occur for dark proton states correspond to the reduction forced by the triangular geometry?
5. How DNA -amino-acid correspondence is represented at the level of dark DNA? The correspondence should be realized in terms of magnetic flux tube triplets connecting dark DNA and dark amino-acid and resonance condition would be essential. When the chords at the orbits of Z_n are of same type, different DNAs correspond to the same chord but with different key. When Z_2^{refl} is involved, the two chords at the orbit are not of same type (note the analogy with left and right-handed biomolecules). The only manner to circumvent the problem is to assume that the chord associated with amino-acids magnetic body is that of DNA. Information is not actually lost in translation, it is only transformed to different kind of information perhaps representing correlates of emotions.
6. Could the non-representability of one of the Z_6 codons as amino-acid have an analog?

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

1. Perhaps one should first try to identify the function of water icosahedrons. The first guess is that they serve as local bridges between dark DNA/amino-acid sequences and ordinary DNA/amino-acid sequences. This would suggest that dark proton of dark DNA forms a flux tube connection with the face of water icosahedron dictated by the state of the dark proton: this would take place by flux tube reconnection and cyclotron resonance. Water icosahedron in turn couples with the DNA/amino-acid like DNA conjugate codon with codon so that kind of double helix is formed.
2. What about the pairing of ordinary DNA/amino-acids and water icosahedrons? Water icosahedron has size of about 3 nm. The size of single DNA codon is about 1 nm. Single codon corresponds to a twist of $3\pi/5=36$ degrees, an angle closely related to Golden Mean. If the radius of the helix consisting of water icosahedrons is above some minimal radius which is easy to estimate from an equation for the helix. There are 10 DNAs per $L(151) = 10$ nm and they correspond to a total twist of $3 \times 2\pi$. Therefore the twist angle is $\Delta\Phi = \pi/5 = 36$ degrees for single codon and corresponds to a distance of $L(151)/10 = 1$ nm). From this one

has equation for DNA and icosahedron helices as $z = k\Phi$, $k = h/(6\pi)$, $h = L(151) = 10$ nm (radii are constant). Single codon corresponds to a distance $s = \sqrt{dz^2 + R^2d\phi^2}\Delta\Phi$ along the water icosahedron helix of radius R accompanying DNA helix. One must have $s \geq L = 3$ nm defining the size of water icosahedron in order to avoid overlap. $\Delta s \geq L = 3$ nm gives the condition $R \geq 10 \times \sqrt{2}/(3\pi)$ nm $\simeq 1.5$ nm.

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

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

1. Could Z_6 , Z_4 and Z_2 orbits associated with the Hamiltonian cycles be realized even in the structure of water icosahedrons? Could they be realized as structures formed by the water tetrahedra and correspond to three separate regions of these icosahedral structures? Could one assign to each of the three regions of icosahedron icosahedron such that the attached icosahedron decomposes to the orbits associated with that particular region? Could the hierarchy of the icosahedral symmetry breakings have a direct counterpart at the level of the icosahedral structures formed by water molecules? My intuitive feeling is that the answer to these questions is negative.
2. Could Hamiltonian cycles be realized only at the level of dark photons as quint cycles defined by closed flux tube giving rise to dark nucleus, that is in terms of 3-chords formed by dark photons propagating along flux tubes emanating from the icosahedron? If cyclotron frequencies of dark quarks are in question then the magnetic fields associated with the flux tubes would define the notes.
3. The breaking of Z_2^{refl} symmetry is of special interest since it could serve as a prebiotic analog of chiral selection and could relate to dark variant of weak physics with effectively massless weak bosons in nano-scales. This would require dark magnetic body. Half-octave scaling is second broken symmetry and would have also an analog in Z_2^{refl} variant of icosahedron. Note that 256 variants of the bio-harmony are predicted and could be realized for magnetic body naturally. The presence of electric fields at flux tubes is possible and if the electric and magnetic fields are non-orthogonal, U(1) instanton density is non-vanishing and induces parity breaking. Is this breaking associated with Z_2^{refl} only?

3.1.2 Clathrin molecules as icosahedral structures

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

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

the clathrin and molecule, by a resonant interaction by dark cyclotron photons, and by an h_{eff} reducing phase transition bringing the molecule to the face.

3.1.3 Microtubules as music instruments?

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

1. Tetra-icosahedron has 13 vertices with the added vertex representing one note- say E- in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more than 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.
2. The recent TGD inspired model of microtubules [L4], [K10] was inspired by the findings of the group of Bandyopadhyay (see <http://tinyurl.com/ze366ny>) [?], [?] relies on the general vision about bio-communications and control as being based on dark cyclotron photon radiation travelling along magnetic flux tubes.

These dark photons have a universal energy spectrum in the range of bio-photons (visible and UV) to which they transform as the value of $h_{eff} = n \times h$ reduces to its standard value. Frequencies would span a wide energy range but EEG frequencies would be of special importance since they would also couple to acoustic vibrations. The precise value of the energy scale of cyclotron photons would be determined by the strength of the magnetic field at flux tube.

3. Frequency modulation would be the general manner to code information in living matter: “whale’s song” would be a good metaphor for it. This is assumed in the model for cell membrane as generalized Josephson junction: the modulation would be now induced by the variations of generalized Josephson frequency by variations of the membrane potential. Also microtubules have been proposed to base their communications on frequency modulation.
4. The first possibility coming in mind is that the continually varying microtubule length codes for the frequency [L4]. The change of the frequency by say octave would however require quite fast and large variations of microtubule length. Neither does this realization conform with the idea that the state of single tubulin corresponds to frequency. Microtubule length could also code for the length of the music piece represented by the microtubule serving as a music instrument or musician at the bio-molecular level. It would also the number of microtubular units and thus the size of the orchestra consisting of 13-units.
5. Another possibility inspired by the proposal is that magnetic flux tubes form an analog of 3-D grid ideal for communication purposes using 12-note (or actually 13-note) system as a code equivalent with genetic code. Also microtubules would involve three kinds of flux tubes [L4] defining coordinate grid of cylindrical coordinates: longitudinal, radial and those which rotate along the microtubule. Radial flux tubes would be ideal for communication using 13-note system as a realization of genetic code.
6. 13-note system as cyclotron frequency spectrum for given value of h_{eff} would be determined by the spectrum of the magnetic field strengths going transversally through the microtubule and each tubulin would correspond to one particular note represented as magnetic field strength. The system would be highly analogous to the system formed by hair cells in cochlear. Note would indeed characterize single tubulin molecule rather than entire microtubule as required if one wants to code chords using the two tubulin conformations as a bit. Tubulin conformation would determine whether the tubulin serves as a sending/receiving antenna or not.
7. Melody in 12-note system can be interpreted as a discretized version of frequency modulation with frequency being piece-wise constant in time. Obviously the 13 bit sequences defined by

tubulin conformations code for the chords of rational 12-note scale involving a representation of one particular note (the third note of the Pythagorean scale) with two slightly different frequencies in order to avoid problems caused by the rational number ratios of frequencies. 13th bit could also serve as a kind of period. Also chords could be coded up to a chord with 13 notes so that microtubules would have quite a high representative power.

The is an objection against the model.

1. One could argue that a unit consisting of 13 tubulins allows only one octave to be represented. One can of course assume that the magnetic field strengths for subsequent units differ by octave. What makes this interesting is that microtubules allow two variants, called A and B. B type microtubules appear as 13-units since microtubular surface has a gap so that the helical symmetry is broken. For variant A, which is not found in vivo or in vitro, 13-units integrate to form longer helical units. This is assumed in Penrose-Hameroff model and the experimental absence of A type microtubules is one of the basic objections against Penrose-Hameroff hypothesis.
2. The TGD inspired proposal is that A type microtubules corresponds to a critical state having therefore an enhanced symmetry and long range correlations: criticality would explain their experimental absence. The experiments of the group of Bandyopadhyay support that the critical state is induced by a resonant excitation at specific AC frequencies [L4]. Long range correlations would mean enhance helical symmetry - that is fusion of several 13-units to form a longer helical structure. This structure would allow an interpretation as a structure with frequency spectrum of several octaves represented coherently in terms of magnetic field strength: the 10 octave span for hearing would mean the integration of 10 microtubule units meaning length scale of order micrometer assuming that tubulin size is of order 10 nm.
3. If the field strength for subsequent units differ by octave, one can argue that for variant B various octaves play their own music without knowing of each other and thus without coherence. In state A they would play together forming something analogous to orchestra or choir.

If the octave is same for all 13-units, the phase transition would involve octave scaling of the magnetic field strength at the flux tubes. The flux tube radius should suffer p-adic scaling by an integer number of half-octaves, which makes sense if one accepts p-adic length scale hypothesis. This kind of phase transition have been proposed as candidate for a basic step of energy metabolism since they can store or liberate cyclotron energy as metabolic energy.

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

To sum up, 13-note extension of 12-note system could be seen as a realization of the genetic code in terms of frequencies. The existence of kind of realization was obvious from the beginning and I proposed it in the model of microtubules as quantum antennas during the first years of TGD inspired theory of consciousness [K8]. Discovering the precise realization of the proposal has however required time.

3.2 Could biology help in the understanding of musical harmony?

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

1. The extension of the ideas about harmony to the case of isosatetrahedron is a non-trivial task. If one assumes that the extended Hamiltonian cycle is obtained by deforming tetrahedral Hamiltonian cycle according to the proposal made earlier, one ends up with a problem since the cycle makes a wedge while making a side track of two steps via the new vertex. The two steps must give one quint so that the new vertex must correspond to either minor or major

third of note where it started from (and ended to). This would add to the scale a chord of type CGD a chord of type CEG or CEbG (plus two other chords containing major or minor third. Depending on the orientation of the cycle one would obtain major or minor key. The remarkable feature of icosahedral harmonies is that they often lack a unique basic chord. Could it be that the addition of tetrahedron breaks the symmetry and fixes the key?

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

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

1. The proposed extension of the scale would break symmetry by bringing a third which is indeed nearest neighbor of the basic note plus two other notes, which are in corners of a *1-quint* triangle in the biological realization. Thus chord CEG and chord containing EG and third note would be introduced.
2. Using the general results one can readily find the possible extensions of harmony if one assumes that both major and parallel minor with same number of #s or bs are obtained. The chord chosen for extension must be CGA, which can be seen as part of C6 or Am7. If the added vertex corresponds to E one obtains $C = CEG$, $Am = CEA$, and the GEA which is part of C6/Am7 as also the lost chord. In amino-acid analog CGA would become “empty” amino-acid, punct, and would be replaced with GEA contained also in C6. One can perform this kind of realization for all 11 harmonies and/or their mirror images. The modification induces symmetry breaking and defines a key which is otherwise not obvious for the icosahedral harmonies. Also half-octave symmetry is broken.
3. One can perform the modification also for the inverted harmony. The transformation to reverted harmony $X \rightarrow Y$ corresponds to $X7 \leftrightarrow Y6$ and vice versa so that the presence of X7 type chords in harmony guarantees the existence of the required type extension in the reverted harmony. One can of course define extension also using X7 type chords. This would generate besides CEG two dissonant chords of type GEEb and CEEb.
4. In maximally symmetric harmony (2, 12, 6) with 6-fold rotation symmetry, there are as many as 6 ways to perform this modification so that any note of the 6-note scale spanning “impressionistic” octave can define the key. The key is either F, G, A or $Dm, E, F\sharp m$. The harmony contains however no X7 type chords and since the transition to the reverted harmony acts as $X6 \leftrightarrow Y7$, it does not allow a modification generating both major and parallel minor. There are also other harmonies possessing no X6 type chords such as (2, 12, 6) and bio-harmony (4, 8, 8) with 2-fold rotational symmetry so that the extension in the simplest form can be performed only for their reversals.
5. For the two harmonies with 4-fold reflection symmetry there are 2 ways to perform the modification and modified chords are related by half-octave shift. With the conventions of Table ?? the modification introduces key which is either A ($F\sharp m$) or $D\sharp$ (Cm) for both harmonies (second one is bio-harmony (4, 8, 8)).

3.3 About the interpretation of bioharmonies

1. *How ideas about harmony evolved?*

A brief summary about the evolution of the notion of bio-harmony is in order.

1. The first guess [L5] was that amino-acids could be understood as chords of icosahedral bioharmony characterized by 3-tuples (3, 10, 7), where the integers tell the numbers of icosahedral triangles with 0, 1, or 2 edges of the Hamiltonian cycle and identifiable as 3-chords with 0, 1, or 2 quints. The interpretation was that 3 0-quint chords correspond to 3 basic polar amino-acids, 10 1-quint chords to the 10 non-polar amino-acids, and 7 2-quint triangles to the 7 polar and acidic polar amino-acids. It turned out however that (3, 10, 7) does not appear as Hamiltonian cycle although it satisfies the necessary conditions.
2. I introduced also a model of genetic code motivated by the properties of the code table suggesting that 60 DNA codons are grouped into 3 groups of 20 codons. The idea that DNA codons coding for a given amino-acid form an orbit of a subgroup of icosahedral group with order which is not smaller than the number of these DNAs and has the aminoacid at it. Three subgroups Z_6 , Z_4 , and Z_2 would predict 3 amino-acids coded by 6 codons and two amino-acids coded by 1 codon, 5 amino-acids coded by 4 codons, and 10 amino-acids coded by 2 codons. The total number of codons would be $3 \times 6 + 2 + 4 \times 5 + 10 \times 2 = 20 + 20 + 20 = 60$ rather than 64. The number of doublets is 10 instead of 9. Could one Z_2 orbit corresponds to punct coded by two stopping codons? But what about the codon triplet associated with Ile? Something is clearly missing.

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

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

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

4. The geometric correlate for the fusion of the codes is gluing of tetrahedron to icosahedron along one face which corresponds to “empty” face identifiable as punct coded by stopping codons. The icosahedral Hamiltonian cycle (4, 8, 8), which exists as two variants, is extended to (4, 10, 8) with two new amino-acids.
5. The music analogy for the fusion of tetrahedron is symmetry breaking bringing in a definite key by introducing the major and minor chords as 1-quint chord (but with 2-edges since tetrahedral edges correspond to major and minor thirds).

2. Understanding the misunderstanding

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

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

orbit of the corresponding triangle can be totally dependent on the group structure emerging from the construction of the Hamiltonian cycles.

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

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

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

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

4. Harmonies are not for amino-acids but for DNAs coding them. One can however identify amino-acids as specific triangles the orbits and the chords associated with the amino-acids define much more restricted notion of harmony involving one representative of each basic type of chord. Perhaps the additional chords correspond to modulations of the harmony.
5. The rules of harmony generalize as such to transitions between DNA codons regarded as chords. If chords are near to each other with respect to the distance measured as quints, the transition between the chords respects harmony. One must think that DNA codons form a singular fiber space such that the union of fibers for type n gives the space of 20 amino-acids. The "gauge group" Z_n acting in the fiber is different in the 3 regions of the amino-acid space and the number of elements in the fiber is factor of n actually equal to n for $n \neq 6$ and having values 6 and 2 for $n = 6$. Each choice for the 3 Hamilton cycles of type Z_n , $n = 6, 4, 2$ defines a variant of this fiber space. The distance along the fiber isomorphic to the space of amino-acids is measured as minimal quint distance.

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

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

One can of course play with more stringent scenarios for the transitions between DNAs or RNAs). For instance, the assumption that transitions can occur between chords of same type, leads to contradiction since the *Xaug* chords of Z_6 harmony do not appear in any other harmony.

In any case, the quint-rule in its various forms is readily testable for DNA sequences.

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

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

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

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

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

1. The Z_6 symmetric 20-plet contains 3 6-plets and 1 doublet and the Z_2 symmetric code contains 10 doublets so that here is one 11 DNA doublets in the icosahedral code. "Ordinary" amino-acids have only 9 doublets. The interpretation is that the Z_6 doublet corresponds to ile and the additional ile is coded by tetrahedral codon. The second surplus doublet can be identified as 2 codons coding for punct, "punct". This gives $4+5+10=19$ amino-acid if "punct" is counted.
2. What is lacking is one ile, met, trp, plus Pyl and Sec. Also 4 DNA codons are needed. One of them must code ile, one met, one for punct, and one for trp. The tetrahedral codons would thus correspond to orbits of Z_1 . This is actually the only possible subgroup since for the choices $Z_n = 2, 3, 4$ the numbers of codons and amino-acids are not correct. This exhausts all DNA codons.
3. The only manner to proceed is to assume that icosahedral and tetrahedral codes can appear also as unfused versions. This would naturally occur for Z_2^{ref} for which all cycles contain X6 type chord but can occur also for Z_2^{rot} if the completion is done for the inverse harmony and then mapped to the harmony back. The icosahedral code would be as already described. The "free" tetrahedral codes would correspond to Z_1 and the faces coding punct in the two codes would code for Pyl and Sec. The fusion of the tetrahedral and icosahedral codes codes gives just the ordinary genetic code so that the proposal is consistent with the proposal that dark proton sequences realize genetic code [K5].
4. Note that geometrically this extension means only that the amino-acid sheet of the fiber space is extended by tetrahedral sheet.

The challenge is to construct the covering space of the icosahedron representing amino-acids.

1. The has as a local fiber the orbit under Z_n associated with the amino-acid defining base point. The space of amino-acids decomposes to disjoint regions corresponding to the 20+20-20 DNA codons. Z_n is the analog of gauge group and by symmetry breaking is different from three different regions of amino-acid space. There are $1 \times 2 \times 8 = 16$ variants of this space due to existence of several harmonies for given symmetries. There are actually only three different options for n given by $n = (0, 16, 4)$, $(2, 12, 6)$, and $(4, 8, 8)$.
2. The Z_n orbits of the three disjoint amino-acid regions (containing 3+1=4, 5, resp. 10 amino-acids) intersect each other. The challenge is to choose the representative amino-acids from the orbits of Z_n in such a way that the chosen amino-acids belong to the three disjoint regions. It remains to be proven that this is possible. One must also understand how uniquely this can be done.
3. One could think of choosing a set P_2 of 10 representatives from the 10 orbits of Z_2 related by 6-quint scaling along Hamiltonian cycle. The 3+1+5=9 amino-acids associated with Z_6 and Z_4 would belong to the mirror images $P(S)$ of this 10-element set. $P(S)$ decomposes into set P_6 of 3+1 triangles and set P_4 of 5 triangles and there are 2-element, 4-element and 6-element orbits connecting the elements of the sets P_2, P_4 , and P_6 .

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

1. The key observation is that the construction of the covering space - that is identifications of amino-acids at the orbits of the groups involved - depends only on whether the choice of Z_2 as Z_2^{rot} or Z_2^{refl} ! Thus the two codes (ordinary one and code with Pyl and Sec coded by stop codons) are distinguished by different DNA-amino-acid covering spaces. The details of the Hamiltonian cycle do not matter. Only the structures and mutual relationships of the groups $Z_6 = Z_3 \times Z_2^{refl}$, $Z_4 = Z_2^{rot} \times Z_2^{refl}$ and Z_2^{rot} and Z_2^{refl} matter. Furthermore, the actions of the groups Z_2^{rot} , Z_3 and Z_2^{refl} determine also the actions of Z_6 and Z_4 . Only Z_2^{rot} and Z_3 are non-commuting actions.
2. One can decompose amino-acids to 10 pairs of Z_2^{ref} orbits and visualize the 20 codons involved as two layers on top of each other such that two on top of each other correspond to the same 2-orbit - 2 boxes on top of each other. The choice of the two layers is not unique since one can permute the members of any vertical box pair.
3. By a suitable choice of the members of vertical box pairs one can arrange that Z_3 and Z_2^{rot} act along the two layers horizontally. Z_2^{rot} orbits divide each layer to 5 pairs of horizontal boxes. One can also permute the vertical pairs horizontally in such a way that the 5+5 Z_2^{rot} orbits correspond to neighboring horizontal boxes along upper and lower layer giving 2+2+2+2+2 decomposition. This still leaves the possibility to permute these 5+5 horizontal pairs defining 4-orbits of Z_4 horizontally with each other.

Simply by drawing one find that Z_3 orbits divide each layer to 3 triplets and 1 singlet and by a suitable choice Z_3 singlets correspond to the 10th box on the right for both layer. The Z_3 orbits and Z_2^{rot} orbits overlap in such a way that the middle Z_3 orbit contains entire Z_2^{rot} orbit.

4. It is clear how to choose amino-acids from the orbits.
 - (a) Consider first the $Z_2 = Z_2^{refl}$ case. The lower layer corresponds to the 10 Z_2^{refl} amino-acids (punct included) coded by 2 codons. One must choose from each Z_4 orbit consisting of a square of 4 boxes one upper box to represent Z_4 amino-acid (ala, val, gly, pro, thr). Each 4-unit contains one free upper box to which one can assign 1 Z_6 amino-acid. One cannot however put two amino-acids on 3-orbit. There are 3+1 Z_6 amino-acids and 5 boxes so that one box remains unused. This must be the case. The used box must belong to either second or third horizontal Z_2^{rot} 2-box: if it were filled, the middle Z_3 3-orbit would contain 2 Z_6 amino-acids and the fiber space-structure would fail. Contrary to the original intuition, the unfilled box is *not* at the 2-orbit of Z_6 containing as Ile but at the middle upper 3-orbit, which would contain 2 amino-acids if filled. It is associated with one of the 10 amino-acids coded by two codons and is same for both

4	6	4	6	4		4	6	4	6(2)
2	2	2	2	2	2	2	2	2	2
2	6	2	6	2		2	6	2	6(2)
4	2	4	2	4	2	4	2	4	2

Table 1: The representations of the associations of amino-acids to the orbits of Z_n , $n = 6, 4, 2$ for $Z_2 = Z_2^{refl}$ (upper two rows) and $Z_2 = Z_2^{rot}$ (lower two rows). The integer n in box tells that the amino-acid associated with that box corresponds to Z_n type amino-acid. “(2)” tells that the Z_6 orbit in question consists of 2 codons.

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

- (b) $Z_2 = Z_2^{rot}$ can be treated similarly. The upper row of boxes is filled in the same manner as in the previous case. The horizontal box pairs in the lower row contain one Z_2^{rot} box and one Z_4 box. The difference to the previous case is that Z_2 boxes are now shared by the both rows: in the previous case they belonged to the lower row.

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

Table 1 represent the two situations graphically.

3. *Music and physical correlates of emotions*

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

There are 11 candidates for the icosahedral harmony and its extensions. The candidates have either Z_6 (**Fig. ??**, Z_4 reflection symmetry (**Figs. ??, ??**), or Z_2 rotation symmetry (**Figs. ??, ??, ??**), and Z_2 reflection symmetry (**Figs. ??, ??, ??, ??, ??**). For the first case Z^2 reflection symmetry and for the second case Z_2 rotation symmetry are represented as as half-octave shift. Second reflection symmetry corresponds geometrically to reflection in horizontal direction. The extension assigns to them definite key and adds to 1-quint chords minor and major chords absent for the icosahedral bio-harmonies. The question is whether one of these harmonies is selected in biology or whether all three can appear and are perhaps realized at the level of magnetic bodies of amino-acids.

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

Could orientation reversal relate to time reversal, which in Zero Energy Ontology (ZEO) corresponds to state function at opposite boundary of causal diamond (CD)? This reversal would occur in volitional acts: the subsequent reduction would not affect the quantum state in positive energy but in TGD framework they affect the state at opposite boundary CD and in this manner give rise to the experience flow of time.

The simplest extension of the harmony in the proposed form requires that harmony possesses X_6 chord. It does not exist for the candidate with Z_2^{rot} symmetry but for its reversal 4 of them are present as images of $D7, E7$ and $G\sharp7, B\flat7$ which are chords of type X^6 . One can however map the harmony to its reversal, perform the completion for it, and perform the reversal back to the original harmony. The reversal depends on what note remains invariant in the reversal. One can require that it is the basic note of the chord to itself: with this condition one would obtain $Dm, Em, G\sharp m, Bbm$ and major keys $C\sharp, F, A, H$. 4 different harmonies would result. Without the restriction the number of harmonies is different and each has different emotional characteristics.

4. Religious myths, music, and biology

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

1. The hierarchy of symmetry breakings proceeding from Z_6 down to Z_2^{refl} brings strongly in mind evolution as loss of innocence. For Z_6 one as 4 orbits. One orbit contains 2 triangles (chords, DNA codons assignable to ile). The other orbits correspond to six codons assignable to amino-acids ser, arg, and leu. The chords at the orbits are major chords and 7-chords, and minor chords and 6-chords for the inverse of the harmony.

There are no dissonant chords in 0-quint sector: dissonances appear only for the remaining groups as 0-quint chords. This is musical representation of paradize. This harmony is based on 6-note scale for the basic notes of the chords and used by impressionistic composers. Amino-acids correspond to selections of preferred chord from each orbit and there are only four different chords: this sub-harmony is very simple. Life in paradize is simple!

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

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

Unfortunately, this identification is not consistent with the argument identifying the amino-acid chords at Z_n orbits (see table 1) the non-playable chord must belong to an intersection of 6-orbit and 4-orbit and is not completely unique without further assumptions. It belongs to a 2-orbit of Z_2^{refl} : if it is somehow special, it could belong to the 2-orbit assignable to punct. If the chords at the 2-orbit have basic notes differing by tritonus, the inspection of the Table 6 shows that it is possible to find a unique chord pair having this property for all 5 Z_2^{refl} cycles.

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

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

4. The banishing from the paradise takes place as Z_2^{refl} symmetric harmony replaces Z_2^{rot} harmony: half-octave shift is not a symmetry anymore, and one can tell between good and evil, and eventually church decides to deny tritonus as a symbol of evil! Paradise is left as icosahedral and tetrahedral code are fused to form the tetra-icosahedral code - the ordinary genetic code leading to the breaking of Z_2^{refl} symmetry.
5. In banishment punct ("empty" amino-acid) as a counterpart of chord shared by tetrahedron and icosahedron emerges and means stopping of the music piece altogether. Death of the sinner! For unfused codes this chord is playable as Sec/Pyl and the music piece is never-ending: life is eternal in paradise! No notion of time, no sin, no death! Amusingly, impressionist music with 6-note scale is music of "now", attempt to catch this moment.
6. Also the holy trinity finds an analog as $Z_6 - Z_4 - Z_2$ trinity of the bio-harmony. Holy Spirit, Father, Son: perhaps in this order. Even more, Z_2^{rot} can be associated with Son in Heaven and Z_2^{refl} with Son at Earth as ordinary mortal!

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

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

1. This requires specification of harmony by selecting one Hamiltonian cycle from the cycles belonging to the groups of cycles with Z_n , $n = 6, 4, 2$ symmetry and decomposing amino-acids to 3 groups correspondingly (those coded by 6, 4, and 2 codons). One must include tetrahedral codons and amino-acids.
2. The basic rule of harmony would be the minimization of quint distance between initial and final chords of the transition. One can consider probabilistic versions of this rule or pose strict form of the rules stating in the most stringent form that only transitions with vanishing quint distance (between neighboring triangles) are possible.
3. The transitions between different amino-acid regions would be governed by this rule. Also the transitions between different variants of the DNA-amino-acid space defined by different choices of the Hamilton cycles would be governed by the same rule
4. The most plausible looking model considers only transitions between DNA codons since DNA sequences induce amino-acid sequences.

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

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

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

The finding that behavioral patterns of planaria can be remembered also by the piece of split planaria without the brain is consistent with the idea that replication of magnetic body coding for behaviors is behind biochemical replication. That alleles of the same gene have different expression

could be understood if the bio-harmony assignable to gene carries additional information besides the biochemical information. An alternative explanation is that emotional memories associated with conditioning are realized at the level of the body of planaria.

These notions might also provide a fresh approach to epigenetics. Histone modification and DNA methylation are believed to induce kind of geometric locking preventing transcription. They could also affect the frequency assignable to DNA codon or some key unit so that the resonance condition making possible reconnection of U-shaped flux tubes allowing biomolecules to get in contact fails and transcription cannot proceed. Epigenetic inheritance could reduce to the inheritance of bio-harmony: the magnetic bodies of cells of offspring get in tune with those of parent. To how high degree magnetic body and bio-harmony are inherited? This becomes the key question.

1. Basic ideas related to magnetic body

Recall first some key ideas of TGD inspired quantum biology.

1. In TGD framework magnetic body extends the pair formed by organism and environment to a kind of holy trinity. Magnetic flux tubes and the realization of genetic code in terms of dark proton sequences has been the key hypothesis. The model for cold fusion [L6] suggests that also more general dark nuclei must be allowed. Dark neutron sequences could correspond to genes separated by dark protons. Dark weak interactions with large value of h_{eff} effectively massless below neuron size scale would play central role and induce large parity breaking effects (chiral selection).

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

2. Ontogeny could be seen as a kind of editing process for the text defined by the DNA. Control of control of... is involved so that situation is very complex. Who performs the editing? Does DNA edit itself and is the editing process defining evolution of genome coded by genome? Or is the editing performed by Darwinian selection at cell level (see <http://tinyurl.com/nd9a9ks>)? Or is the magnetic body the editor using genome also as its tool as TGD would suggest? What is important that in TGD framework self-organization in 4-D sense implied by Zero Energy Ontology replaces ordinary self organization leading to asymptotic spatial patterns and select spatiotemporal patterns as asymptotic behavioral patterns defining various biological functions. The role of magnetic body is central in this process.
3. Magnetic body contains cyclotron Bose-Einstein condensates and cyclotron frequencies determined by the strength of magnetic field would give for DNA and other biomolecules additional characteristics. In TGD based model for musical harmony DNA codons would correspond quite concretely to 3-chords but played using dark photons (also ordinary music represented as sounds could be transformed to dark photon music). If one accepts the icosahedral model of bio-harmonies predicting genetic code correctly, there would be 256 fundamental harmonies characterised by the allowed collection of 3-chords and they would add to the information carried by DNA molecules. I have constructed a program building random sequences of the allowed chords using the additional harmonic rule that two subsequent chords contain at least one common note and this music sounds rather harmonic (albeit boring in absence of any other elements!)
4. Could one distinguish between different states/phases of DNAs, mRNAs, tRNAs, and amino acids in terms of harmony? Could their functioning depend on the harmony? With the inspiration coming from the connection of emotions and musical harmonies I have proposed that the harmony associated with a gene or organ could correlate with something analogous to an emotional state or mood - maybe micro-mood or microemotion could be the proper notion. Could amino-acids be happy, hilarious, melancholic, sad, depressed? Could one distinguish between different phases of DNA, RNA, tRNA, aminoacid collections characterized by the

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

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

2. Problem

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

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

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

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

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

2. Could different automorphs correspond to different collections of chords physically just as global gauge transformations generate different physical situations? Isometries of groups G_i would therefore define physically different realizations of bio-harmonies such that for each of them only one of the DNA codons coding for given amino-acid could actually perform the coding. Ordinary genetic code with many-to-one correspondence would make sense in statistical sense only. If this is true, the cyclotron frequency 3-chord assignable to amino-acid depends on the DNA coding it and implies physical distinctions.
3. One can consider also a third alternative. DNA codon with same 3-chord as coding for amino-acid is in special role in that only it can resonate with the amino-acid! Could DNA codons codons correspond to same cyclotron frequency triplet (magnetic fields) but different value of h_{eff} so that one would have chord with respect to energy rather than frequency. Different values of h_{eff} for DNA codons coding for the same amino-acid would scale their cyclotron frequencies to the same amino-acid frequency while keeping cyclotron energies invariant? Cyclotron energy ratios for codons correspond to rational valued ratios $E_i/E_j = h_{eff}(i)/h_{eff}(j) = n(i)/n(j)$. Amino-acid would correspond to fixed h_{eff} and this creates a

problem: can DNA codon code for amino-acid with different value of h_{eff} . This option does not look attractive.

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

3. Questions about bio-harmony

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

1. It is not necessary to assign any interpretation on the harmony. Just the harmony could be enough if it is forced to be same for DNA, corresponding mRNA, tRNA, and aminoacids. One can however make questions. Is the harmony inherited invariant and could it distinguish between different personality types about which we learned in old books of psychology? Or could the harmonies correlate with our own moods?
2. Could differentiation selecting particular genes as expressed genes apply also to harmonies so that given gene would correspond only to a particular harmony and different copies of gene could correspond to different harmonies. Could this selection rely on the same mechanisms as ordinary differentiation realized in terms of epigenetic mechanisms and DNA editing? From the magnetic bodies of genes the harmony would be automatically transferred to the magnetic bodies of mRNA, tRNA and aminoacids since otherwise the transcription and translation do not work since magnetic bodies do not have common resonance frequencies and reconnection and resonant interaction is not possible.
3. Does given harmony characterize given gene or the entire cell? All basic biomolecules associated with a gene would naturally correspond to the same harmony. If the rRNAs associated with ribosomes are in harmony mutually cellular harmony seems to be the only option. If ribosomes have their own harmonies, only certain ribosomes can translate given gene. This would bring in additional control tool. The most plausible picture is that the situation depends on what happens in the self-organization process. Some organs/organisms are more harmonious, others not so harmonious. Harmony need not be given fixed to remain the same: magnetic body can have motor actions changing the cyclotron frequencies. Moods could reflect the character of harmony at gene level.
4. Does magnetic body control the differentiation by posing restrictions on gene expression or vice versa? The idea about magnetic body as intentional agent suggests that the first option is correct. There would be hierarchy of magnetic bodies with magnetic bodies at the higher level controlling bodies at the lower level. The value of Planck constant would label the hierarchy levels and also DNA codons would be characterized by "intelligence quotient" defined by h_{eff}/h . This would be nothing but the analog for the hierarchy of program modules and I have earlier considered the realization of this hierarchy [L7].
5. The selection of harmony could take place and be analogous to cell differentiation. This would be a self-organization process in which magnetic bodies of genes, cells, etc.. tune themselves to resonance with each other by modifying their magnetic fields by controlling their thickness (for monopoles flux the flux is invariant). Something analogous to the development of social skills. This could pose resonance as a constraint on processes like replication, transcription, reverse transcription, silencing, enhancing, editing, etc.... It might induce the differentiation at gene level.

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

4. *Can the notions of magnetic body and bio-harmony explain something that ordinary genetic cannot?*

It would be nice to identify some biological phenomenon difficult to understand in standard framework but having an elegant explanation in terms of magnetic body.

1. The notion of harmony could manifest itself at the level of genes as different expressions for the copies of same gene if they correspond to different notions of harmony. The copies of gene are known as alleles (see <http://tinyurl.com/bpee49t>). The alleles can indeed give rise to different phenotypic traits such as different pigmentation.
2. Morphogenesis provides examples of this kind of phenomena [?, ?, ?]. The first key idea is that DNA and cell replication is induced by the replication of magnetic bodies serving as information carriers [K10]. The second key idea is that in zero energy ontology (ZEO) magnetic body is 4-dimensional and represents behavioral patterns rather than only 3-dimensional patterns. For instance, memory as behavioral patterns can be inherited by the piece of planaria worm not containing the brain. The explanation could be that the magnetic body carries behavioral patterns replicated in the splitting of the worm.
3. Epigenetics (see <http://tinyurl.com/4xpwcm>) studies changes of gene expression not caused by the change of DNA itself. Epigenome (see <http://tinyurl.com/y9xkfb2u>) is the highly dynamic part of DNA controlling expression of the rather stable part of genome. One might regard stable part of genome as hardware and epigenome as topological quantum computer programs assignable to magnetic body and modifying gene expression epigenetically. Comment sign in computer code serves as a computer scientific metaphor for epigenetic control by repression.

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

1. The modification of transcription rate is the basic tool of epigenetic regulation. There are two basic mechanisms involved. Histone modification (see <http://tinyurl.com/y8ywse5v>) affects the histones of chromatin so that the transcription is repressed or activated. Histone modification takes place by several mechanisms. DNA methylation occurs for CpG pair and if it occurs for a promoter region it represses the transcription and serves as a kind of gene lock. The degree of methylation serves as a measure for the effectiveness of repression. I do not know whether the locking is absolute at the level of single gene or whether only the transcription rate is reduced. Two mechanisms are mentioned in the Wikipedia article (see <http://tinyurl.com/y9kwrwx>). Methylation can impede geometrically some step in the transcription. Methylated site can be also accompanied by proteins affecting histones in chromatin and in this manner impede transcription.
2. The notions of magnetic body and bio-harmony suggest an alternative - one might even hope fundamental - mechanism of repression. Methylation (histone modification) could affect some cyclotron frequency associated with DNA codon (histone). In the optimal situation for transcription the DNA and protein catalyzing the transcription or mRNA are in resonance. When cyclotron resonance condition is not exactly satisfied, the reconnection rate for the U-shaped flux tubes associated with the molecules involved in the process is reduced and also transcription is repressed.

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

3. The notions of epigenetic code (see <http://tinyurl.com/y8ztzza>) and histone code (see <http://tinyurl.com/y854w58p>) have been proposed. Epigenetic code would consist of histone modifications and additional modifications such as DNA methylation. The codeword of the epigenetic code could code for some larger unit than protein: say gene or entire cell. The hypothesis is that the chromatin-DNA interactions are induced by histone tail modifications (such as methylation, acetylation, ADP-ribosylation, ubiquitination, citrullination, and phosphorylation). There are 4 histones and the position of modification varies as well

as the modifier (the above modifications are not the only ones) so so that the number of modifications is very large.

The addition of bioharmonies to the genetic information could simplify the situation dramatically since the modifications could be seen as defining of of the 256 bio-harmonies with 64 chords each (this for fixed scale which varies if the value of magnetic field strength is varied: biophoton spectrum in visible is proposed to represent the range of values of magnetic field). The most plausible starting hypothesis is that given harmony characterizes the gene. Much simpler option would be that the harmony characterizes entire cell or even group of cells.

If the modification by kicking cyclotron frequency out of harmony is enough to repress transcription, almost endless number of bio-chemical ways to achieve would exist but the epigenetic code could be very simple at the basic level as TGD would predict. Each bio-harmony [L2] [K11] would provide a representation of genetic code in terms of 3-chords predicting correctly the DNA-amino-acid correspondence (there are actually two slightly differing codes explaining the presence of 21st and 22nd amino-acid and deviations from the standard code). The states of dark protons (or neutrons) are also proposed to realize genetic code [K7, K5]: it is an open question whether these codes imply each other as they should.

4. The understanding of transgenerational epigenetic inheritance (see <http://tinyurl.com/h6qg64c>) raises difficult challenges. One should understand how histone modification and DNA methylation are transferred to daughter cells in cellular division or inherited by the offspring. Transgenerational interaction of the genomes seems necessary. In TGD framework the interaction of magnetic bodies of via resonance mechanism could transfer the epigenetic programs to the offspring. Offspring could "learn" the epigenetic programs of the mother by tuning.
5. Gregory Carey (see <http://tinyurl.com/ydyznseq>) gives nice real life examples about the complexities of epigenesis identified quite generally as gene regulation (see <http://tinyurl.com/zb97cgs>). He compares the gene regulation involved with the handling of a stressful situation to "nightmarish Rube Goldberg mousetrap" and sees the process as extremely ineffective from engineering point of view. For instance, the hormones secreted to blood circulation are distributed to the entire body. The whole thing could be carried out in brain! He also wonders why evolution is so inefficient. All cells have same genome although most of the genes are silenced. Second strand of DNA is totally un-used and most of DNA consists of introns. His explanation is that evolution does not make long term plans but finds just a solution to a particular without thinking it from a wider perspective: "If it ain't broke, don't fix it".

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

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

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

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

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

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

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

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

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

Some background is needed to understand this rather technical summary.

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

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

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

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

It is now known that epigenetic changes in the gene expression can be inherited. The mechanisms are still poorly understood. What seems however clear the genome is more like a

slowly changing hardware and gene expression or whatever is behind it is the software and programs can change very rapidly by just adding or deleting comment signs in the code. A deeper understanding of this software is needed.

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

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

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

What was observed?

1. The transfer of RNA from soma cells to sperm cells was indeed found to occur. The transferred RNA can in turn induce epigenetic effects in germ cells known to be inherited by a mechanisms, which however remain poorly understood. Epigenetic mechanisms seem to be involved in the cases considered so that DNA is not changed, only its expression.
2. The transfer mechanism was identified. The transferred RNA is contained by exosomes analogous to synaptic vesicles transferring neurotransmitters from presynaptic to postsynaptic cell. Transfer of RNA takes place via fusion of the membranes just like transfer of neurotransmitters. Maybe genetic engineering using exosomes or analogous structures to transfer the needed material to cells has been tried.

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

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

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

3.3.2 Epigenesis, inherited memories and moods lasting over several generations

Nikolina Benedikovic had an interesting comment concerning multiverse interpretation. This motivated to write a summary about the connection between epigenesis, inherited memories interpreted as behaviors and moods lasting for several generations. Nikolina's comment was following.

“One can imagine an intelligent amoeba with a good memory. As time progresses, the amoeba is constantly splitting, each time the resulting amoebas having the same memories as the parent. Our amoeba hence does not have a life line, but a life tree.” - Hugu Everett

Nikolina: Dear Mr. Everett! Before we find out what the true interpretation of quantum mechanics is, we will have to answer this question; why the amoeba possesses this ”super power” of splitting and the electron and human being don’t.

I agree with Nikolina. The following is my comment about what is involved. I proceed by questions.

1. *What behaviors are?*

The behavior of amoeba has nothing to do with parallel universes of Everett. The behavior as such is however highly interesting and challenges standard theories of biology and perhaps also of physics. Memories seem to replicate.

1. What do we mean with memories now: do we mean behaviors, skills, conditionings? Or episodal, sensory memories. I think it is memories in the first sense of the word. Suppose that essentially conditionings are in question.

In this respect a lot of progress happened as it was discovered that RNA somehow represents the memories: taking RNA of conditioned sea snail and scattering it over the neurons fo second snail in lab induces the conditons of the snail to these neurons.

2. Epigenetic approach would suggest that the behaviours essentially the same but now one does not have any convincing model for the model of the epigenesis.

2. *What TGD inspired quantum biology and neuro-science can tell?*

There are two key questions that one must answer.

1. What replication is?

In TGD Universe we are 4-D entities - quantum states are superpositions of space-time surfaces obeying deterministic dynamics. This solves the problem of free will and basic problem of quantum measurement theory. The superposition of space-time surface would be analogous to superposition of deterministic computer programs, behaviours, or biological functions in classical sense. Free will would select the program [L11, ?, L16, L3] .

2. What memories as learned behaviours are? One can imagine several models, which need not exclude each other.

(a) For instance, could it be that the replicas of ameba have geometric past that is partially shared: the part of the past as amoeba before the replication?

(b) Second TGD explanation would be based on what conditionings are? They involve emotions in an essential manner. Emotions are induced and induce behaviors and conditionings involve long term moods. The mysterious epigenetic inheritance could be inheritance of moods affecting gene expression: moods could be inhereted and have time-span of several generations: this conforms with the first option.

3. *What moods are?*

Suppose that conditions are due to long term moods in turn correlating with behavior and at basic level with genetic expression. Consider a TGD based model for moods, second option.

1. Music - its harmony defined by allowed chords - represents emotions and generates them. The allowed 3-chords of bio-harmony, the set of which can vary, would define the mood.
2. Genes are associated with information. Codon contains 6 bits of information. Magnetic body with large $h_{eff} = nh_0$ is the boss, the ”wise guy”, controlling biological body and biochemistry so that genetic code must have primary representation at the level of flux tubes. Dark proton sequences at flux tubes interpreted as dark nuclei indeed represent codons as

3-proton units. The states of 3-proton units turn out to correspond to DNA, RNA, tRNA, amino-acids and vertebrate genetic code is predicted.

Chemical representation would be only a secondary representation only, mimicry, and often incomplete.

Dark proton sequences also realizing vertebrate genetic code would also have positive charge neutralizing the negative charge of nucleotides and make DNA stable. Pollack effect would generate the dark flux tube and this would require metabolic energy and in absence of it DNA would not be stable.

3. Dark proton sequences must also communicate by dark photons with large h_{eff} . The communications must rely on resonance, actually there must be resonance between similar 3-proton units, dark codons. Therefore 3-chords consisting 3 dark photons must represent the codons represented by 3 protons [L12]. Only identical codons have resonant coupling. This makes possible remote replication of DNA reported by HIV nobelist Montagnier [L1] (see <http://tinyurl.com/yygqen5g>).
4. Allowed 3-chords define the harmony and emotional state mood. In TGD representations of emotions in terms of bio-harmony would provide the representation of genetic codons defined by RNA as 3-chords of light, triplets of 3 dark photons. The icosatetrahedral model for harmony realizing bioharmony [L2, L19]. gives also rise to vertebrate genetic code: the 6-bit units defined by codons correspond to ordinary temporarily local intellect, and the harmony to the holistic emotional intellect.
5. RNA and DNA, tRNA, amino-acids would naturally be represented by light 3-chords in communications. Given codon would only tell its name by the chord and resonate with codon having same name. The codons would couple by chords via triple resonance. Same DNA sequences could be in different mood defined by bioharmony and its expression would depend on this: this would give rise to epigenetics. Epigenetic inheritance would be emotions lasting for several generations.
The bioharmony associated with RNA could represent the mood infecting also DNA and generating DNA expression giving rise to the behavior related to conditioning.
6. If this were the case then the inheritance of memories (in this sense could be inheritance of conditionings as long term moods. The replications of RNAs and DNAs and possible other biomolecules carrying the conditioning would give rise to replication of memories as behaviors induced by moods.
7. These moods can be very long term moods and extend over generations. This would fit with the model in which replicated amoebas have the 4-D magnetic body amoeba of the geometric past as part of their 4-D magnetic body.

To sum up, behaviors as conditionings could be caused by moods, which can last for several generations. This would bring in magnetic body as active agent. The representation genetic code in terms dark proton sequences and by 3-chords of dark photons would give a realization of both the "bitty" and emotional aspects of intelligence. Also the notions of 4-D brain and organism having temporal span of several generations as space-time surfaces would be essential for the understanding the inheritance of emotions. We should be very careful for what we do since also our children can feel themselves proud of or guilty for what we did.

3.3.3 E_8 symmetry, harmony, and genetic code

Bee gave in Facebook a link to an article about a connection between icosahedron and E_8 root system [?] (see <http://tinyurl.com/zotpm4b>). The article (I have seen an article about the same idea earlier but forgotten it!) is very interesting.

The article talks about a connection between icosahedron and E_8 root system (see <http://tinyurl.com/y7csb6uh>). Icosahedral group has 120 elements and its double covering $2 \times 120 = 240$ elements. Remarkably, E_8 root system has 240 roots. E_8 Lie algebra is 248 complex-dimensional contains also the 8 commuting generators of Cartan algebra besides roots: it is essential that the

fundamental representation of E_8 co-incides with its adjoint representation. The double covering group of icosahedral group acts as the Weyl group E_8 . A further crucial point is that the Clifford algebra in dimension $D = 3$ is 8-D.

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

1. *What I might have understood*

I try to explain what I have possibly understood.

1. The notion of root system is introduced. The negatives of roots are also roots but not other multiples. Root system is crystallographic if it allows a subset of roots (so called simple roots) such that all roots are expressible as combinations of these simple roots with coefficients having the same sign. Crystallographic root systems are special: they correspond to the fundamental weights of some Lie algebra. In this case the roots can be identified essentially as the quantum numbers of fundamental representations from which all other representations are obtained as tensor products. Root systems allow reflections as symmetries taking root system to itself. This symmetry group is known as Coxeter group and generalizes Weyl group. Both H_3 and H_4 are Coxeter groups but not Weyl groups.
2. 3-D root systems known as Platonic roots systems (A_3, B_3, H_3) assignable to the symmetries of tetrahedron, octahedron (or cube), and icosahedron (or dodecahedron) are constructed. The root systems consist of 3 suitably chosen unit vectors with square equal to 1 (square of reflection equals to one) and the Clifford algebra elements generated by them by standard Clifford algebra product. The resulting set has a structure of discrete group and is generated by reflections in hyper-planes defined by the roots just as Weyl group does. This group acts also on spinors and one obtains a double covering $SU(2)$ of rotation group $SO(3)$ and its discrete subgroups doubling the number of elements. Platonic symmetries correspond to the Coxeter groups for a "Platonic root system" generated by 3 unit vectors defining the basis of 3-D Clifford algebra. H_3 is not associated with any Lie algebra but A_3 and B_3 are.

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

3. The 3-D root systems (A_3, B_3, H_3) are shown to allow an extension to 4-D root systems known as (D_4, F_4, H_4) in terms of 3-D spinors. D_4 and F_4 are root systems of Lie algebras (see <http://tinyurl.com/y97dzqc2>). F_4 corresponds to non-simply-laced Lie group related to octonions. H_4 is not a root system of any Lie algebra.
4. The observation that the dimension of Clifford algebra of 3-D space is $2^3 = 8$ and thus allows embedding of at most 8-D root system must have inspired the idea that it might be possible to construct the root system of E_8 in 8-D Clifford algebra from 240 pinors of the double covering the 120 icosahedral reflections. Platonic solids would be behind all exceptional symmetry groups since E_6 and E_7 are subgroups of E_8 and the construction should give their root systems also as low-dimensional root systems.

2. *McKay correspondence*

The article explains also McKay correspondence stating that the finite subgroups of rotation group $SU(2)$ correspond to simply laced affine algebras assignable with ADE Lie groups.

1. One considers the irreducible representations of a finite subgroup of the rotation group. Let the number of non-trivial representations be m so that by counting also the trivial

representation one has $m + 1$ irreps altogether. In the Dynkin diagram of affine algebra of group with m -D Cartan algebra the trivial representation corresponds to the added node. One decomposes the tensor product of given irrep with the spin 2 representation into direct sum of irreps and constructs a diagram in which the node associated with the irrep is connected to those nodes for which corresponding representation appears in the direct sum. One can say that going between the connected nodes corresponds to forming a tensor product with the fundamental representation. It would be interesting to know what happens if one constructs analogous diagrams by considering finite subgroups of arbitrary Lie group and forming tensor products with the fundamental representation.

2. The surprising outcome is that the resulting diagram corresponds to a Dynkin diagram of affine (Kac-Moody) algebra of ADE group with Cartan algebra, whose dimension is m . Cartan algebra elements correspond to tensor powers of fundamental representation: can one build any physical picture from this? For $m = 6, 7, 8$ one obtains E_6 , E_7 , E_8 . The result of the article implies that these 3 Lie-groups correspond to basis of 3 3-D unit identified as units of Clifford algebra: could this identification have some concrete meaning as preferred non-orthogonal 3-basis?
3. McKay correspondence emerges also for inclusions of hyper-finite factors of type II_1 [K14] The integer m characterizing the index of inclusion corresponds to the dimensions of Cartan algebra for ADE type Lie group. The inclusions of hyperfinite factors (HFFs) are characterized by integer $m \geq 3$ giving the dimension of Cartan algebra of ADE Lie groups (there are also C, F and G type Lie groups). $m = 6, 7, 8$ corresponds to exceptional groups E_6 , E_7 , E_8 on one hand and to the discrete symmetry groups of tetrahedron, octahedron, icosahedron on the other hand acting as symmetries of corresponding 3-D non-crystallographic systems and not allowing interpretation as Weyl group of Lie group.

3. Connection with the TGD based model of harmony

These findings become really exciting from TGD point of view when one recalls that the model for bioharmony [K11] [L2] (see <http://tinyurl.com/yad4tqwl>) for 12-note harmonies central in classical music in general relies on icosahedral geometry. Bioharmonies would add something to the information content of the genetic code: DNA codons consisting of 3 letters A,T,C,G would correspond to 3-chords defining given harmony realized as dark photon 3-chords and maybe also in terms of ordinary audible 3-chords. This kind of harmonies would be roughly triplets of 3 basic harmonies and there would be 256 of them (the number depends on counting criteria). The harmonies could serve as correlates for moods and emotional states in very general sense: even biomolecules could have "moods". This new information should be seen in biology. For instance, different alleles of same gene are known to have different phenotypes: could they correspond to different harmonies? In epigenetics the harmonies could serve as a central notion and allow to realize the conjectured epigenetic code and histone code. Magnetic body and dark matter at them would be of course the essential additional element.

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

1. Given harmony would be defined by a particular representation of Pythagorean 12-note scale represented as self-non-intersecting path (Hamiltonian cycle) connecting the neighboring vertices of icosahedron and going through all 12 vertices. One assumes that neighboring vertices differ by one quint (frequency scaling by factor $3/2$): quint scale indeed gives full octave when one projects to the basic octave. One obtains several realizations (in the sense of not being related by isometry of icosahedron) of 12-note scale. These realizations are characterized by symmetry groups mapping the chords of harmony to chords of the same harmony. These symmetry groups are subgroups of the icosahedral group: Z_6 , Z_4 , and two variants of Z_2 (generated by rotation of π and by reflection) appear. Each Hamiltonian cycle defines a particular notion of harmony with allowed 3-chords identified by the 20 triangles of icosahedron.

2. Pythagoras is trying to whisper me an unpleasant message: the quint cycle does not quite close! This is true. Musicologists have been suffering for two millenia of this problem. One must introduce 13th note differing only slightly from some note in the quint cycle. At geometrical level one must introduce tetrahedron besides icosahedron - only four notes and four chords and gluing along one side to icosahedron gives only one note more. One can keep tetrahedron also as disjoint from icosahedron as it turns out: this would give 4-note harmony with 4 chords something much simpler than 12-note harmony.
3. The really astonishing discovery was that one can understand genetic code in this framework. First one takes three different types of 20-chord harmonies with group Z_6 , Z_4 , and Z_2 defined by Hamiltonian cycles: this can be done in many different manners (there are 256 of them). One has 20+20+20 chords and one finds that they correspond nicely to 20+20+20=60 DNA codons: DNA codons coding for a given amino-acid correspond to the orbit of the triangle assigned with the amino-acid under the symmetry group of harmony in question.

The problem is that there are 64 codons, not 60. The introduction of tetrahedron brings however 4 additional codons and gives 64 codons altogether. One can map the resulting 64 chord harmony to icosahedron with 20 triangles (aminoacids) and the degeneracies (number of DNA codons coding for given amino-acid in vertebrate code) come out correctly! Even the two additional troublesome amino-acids Pyl and Sec appearing in Nature and the presence of two variants of genetic code (relating to two kinds of Z_2 subgroups) can be understood.

4. What could the interpretation of the icosahedral symmetry?

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

1. A reasonable looking guess would be that it quite concretely corresponds to a symmetry of some biomolecule: both icosahedral or dodecahedral geometry give rise to icosahedral symmetry. There are a lot of biomolecules with icosahedral symmetry, such as clathrate molecules at the axonal ends and viruses. Note that dodecahedral scale has 20 notes - this might make sense for Eastern harmonies - and 12 chords and there is only single dodecahedral Hamiltonian path found already by Hamilton and thus only single harmony. Duality between East and West might exist if there is mapping of icosahedral notes and to dodecahedral 5-chords and dodecahedral notes to icosahedral 3-chords and different notions of harmony are mapped to different notions of melody - whatever the latter might mean!).
2. A more abstract approach tries to combine the above described pieces of wisdom together. The dynamical gauge group E_8 (or Kac-Moody group) emerging for $m=8$ inclusion of HFFs is closely related to the inclusions for the fractal hierarchy of isomorphic sub-algebras of super-symplectic subalgebra. $h_{eff}/h = n$ could label the sub-algebras: the conformal weights of sub-algebra are n -multiples of those of the entire algebra.

The integers n_i resp. n_f for included resp. including super conformal sub-algebra would be naturally related by $n_f = m \times n_i$. $m = 8$ would correspond to icosahedral inclusion and E_8 would be the dynamical gauge group characterizing dark gauge degrees of freedom. The inclusion hierarchy would allow to realize all ADE groups as dynamical gauge groups or more plausibly, as Kac-Moody type symmetry groups associated with dark matter and characterizing the degrees of freedom allowed by finite measurement resolution.

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

5. Experimental indications for dynamical E_8 symmetry

Lubos (see <http://tinyurl.com/htjp55h>) (thanks to Ulla for the link to the posting of Lubos) has written posting about experimental finding of E_8 symmetry emerging near the quantum critical

point of Ising chain at quantum criticality at zero temperature. Here is the abstract (see <http://tinyurl.com/zulzk9y>):

Quantum phase transitions take place between distinct phases of matter at zero temperature. Near the transition point, exotic quantum symmetries can emerge that govern the excitation spectrum of the system. A symmetry described by the E_8 Lie group with a spectrum of eight particles was long predicted to appear near the critical point of an Ising chain. We realize this system experimentally by using strong transverse magnetic fields to tune the quasi-one-dimensional Ising ferromagnet CoNb_2O_6 (cobalt niobate) through its critical point. Spin excitations are observed to change character from pairs of kinks in the ordered phase to spin-flips in the paramagnetic phase. Just below the critical field, the spin dynamics shows a fine structure with two sharp modes at low energies, in a ratio that approaches the golden mean predicted for the first two meson particles of the E_8 spectrum. Our results demonstrate the power of symmetry to describe complex quantum behaviors.

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

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

1. The large value of h_{eff} would be associated with dark magnetic body assignable to the magnetic fields accompanying the E_8 “mesons”. Zero temperature is not a prerequisite of quantum criticality in TGD framework.
2. One should clarify what quantum criticality exactly means in TGD framework. In positive energy ontology the notion of state becomes fuzzy at criticality. For instance, it is difficult to assign the above described “mesons” with either ferromagnetic or paramagnetic phase since they are most naturally associated with the phase change. Hence Zero Energy Ontology (ZEO) might show its power in the description of (quantum) critical phase transitions.

Quantum criticality could correspond to zero energy states for which the value of h_{eff} differs at the opposite boundaries of causal diamond (CD). Space-time surface between boundaries of CD would describe the transition classically. If so, then E_8 “mesons” would be genuinely 4-D objects - “transitons” - allowing proper description only in ZEO. This could apply quite generally to the excitations associated with quantum criticality. Living matter is key example of quantum criticality and here “transitons” could be seen as building bricks of behavioral patterns. Maybe it makes sense to speak even about Bose-Einstein condensates of “transitons”.

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

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

4 Icosahedral harmonies

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

4.1 About symmetries of the icosahedral harmonies

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

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

1. The first variant as $Z_3^{rot} \times Z_2^{refl}$ subgroup of icosahedral group as symmetries and its orbits correspond to 3 6-plets and 1 2-plets for which Z_3 leaves the triangle invariant. The counterparts for the orbits are 3 DNA 6-plets and one 2-plet.
2. The second variant has Z_4 symmetry generated by two commuting reflection as symmetries as is obvious from figures ??, ??: the reflections act on vertical and horizontal coordinates. The orbits are five 4-plets of chords. Vertical reflection induces half-octave shift and horizontal one permutes the note sequences $B\flat CDG\sharp F\sharp E$ and $D\sharp C\sharp HFGA$.
3. Z_2^{rot} or Z_2^{refl} acts as symmetries of the remaining 3+5 cycles. The covering space of 10 amino-acids involved defined by 20 DNA codons decomposes to 10 2-plets.

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

DNA codons have also almost exact Z_2 symmetry discussed in [K13, K1, ?].

1. For the last codon the reflection A-T, C-G is an almost symmetry broken only for special cases. This approximate symmetry could be understood as following from the fact that the number of DNAs coding given amino-adic is even in most cases. The exceptions are ile, met, trp coded by odd number of DNA codons. By mapping DNAs to binary sequences one can order the situation so that the 6: th binary digit is the almost-symmetry digit.
2. What is trivial is that RNA has chosen the third bi-digit to be the almost symmetry digit with the ordering UCAG of the nucleotides so that a genuine physical symmetry is in question. An interesting question is how this symmetry relates to the model of genetic code based on tetra-icosahedral orbits.

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

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

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

$$\begin{aligned}
CEG &\equiv C , & CD\sharp G &\equiv Cm , & CD\sharp F\sharp &\equiv C^o , & CEG\sharp &\equiv Caug , \\
CFG &\equiv C4 , & CF\sharp G &\equiv C4_+ , & CGG\sharp &\equiv C6_- , & CGA &\equiv C6 , \\
CGB\flat &\equiv C7 , & CGB &\equiv Cmaj7 , & CGC\sharp &\equiv C9_- , & CGD &\equiv C9 .
\end{aligned} \tag{4.1}$$

Table 2: Notation of chords inspired by popular music notations.

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

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

4.2 Summary of the basic results

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

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

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

Before continuing some terminology and notation is in order. Take C as the major key. Submediant or relative minor corresponds to Am , subdominant (sharp or flat) to F major (F) or Fminor (Fm), dominant to G . The notation for chords is such that quints correspond to subsequent notes in the chord. For 1-quint chords this means that first two notes define the quint. **Table 2** the notation inspired by the popular music notation. The basic different is that the third is in most cases excluded so that the emotional character of the chord is not fixed.

Besides these notions it is convenient to introduce additional notations for various dissonant chords appearing as 0-quint chords.

$$\begin{aligned}
CC\sharp D &\equiv Cex1 , & CC\sharp D\sharp &\equiv Cex2 , & CDD\sharp &\equiv Cex3 , & CDE &\equiv Cex4 , \\
CD\sharp E &\equiv Cex5 , & CC\sharp E &\equiv Cex6 , & CDF\sharp &\equiv Cex7 , & CDG\sharp &\equiv Cex8 .
\end{aligned} \tag{4.2}$$

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

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

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

- (a) The 8 2-quint chords consist of $BbFG \equiv Bb9, C9, F9, G9$ and their half-octave scalings. Clearly, the simple four-note scale appears here.
 - (b) Using the popular notion introduced earlier 1-quint chords consist of two 4-plets $Dmaj7, E9_-, A7, A6$ and $G\sharp maj7, Bb9_-, D\sharp7, D\sharp6$ related by half-octave shift. The harmony contains no “simple” major or minor chord and only the extension to tetrahedral harmony can provide them. The same is true for the second bio-harmony.
 - (c) The 4 0-quint chords are $Cex3 \equiv CDD\sharp$ and $Eex2 \equiv EFG$ and their half-octave scalings $F\sharp ex3 \equiv F\sharp G\sharp A$ and $Bbex2 \equiv BbBC\sharp G$.
4. There are 3 collections with Z_2 rotational symmetry with $48/2 = 24$ representatives in each. The triplets n are $(0, 16, 4)$ (see **Fig. ??**), $(2, 12, 6)$ (see **Fig. ??**), and $(4, 8, 8)$ (see **Fig. ??**). All these harmonies are symmetric with respect to half-octave shift (tritonus), which obviously corresponds to the Z_2 rotation. Tritonus would not have been tolerated by catholic church! This symmetry characterizes all 3 harmonies. Basic 3-chords do not contain pure minor and major chords. The reflection of the scale does not leave the collection of chords invariant but it is not clear whether this corresponds only to a change of scale, probably not. Consider the $(4, 8, 8)$ case (see **Fig. ??**).

- (a) The 8 2-quint chords appear as four-plet $H9, C\sharp9, D\sharp9, F9$ and its half octave shift (tritonus interval) acting as a symmetry of the harmony. 2-quint chords are always of type X^9 (note that the third is missing) but also 1-quint chord can be of form X^9 as explicit construction of chords demonstrates: I have denoted these 1-quint chords by symbol $X4$ (CDG is obviously equivalent with CDG).
- (b) Using the popular music notation introduced earlier, the 8 1-quint chords are $D7, Amaj7, A4_+, E7$ and their half-octave shifts $G\sharp7, D\sharp7, D\sharp4_+, Bb7$.

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

5. The four 0-quint chords appear in two types. $D\sharp ex2 \equiv D\sharp EF\sharp$ and its half-octave shift $Aex2 \equiv ABbC$ plus $Hex3 \equiv HC\sharp G$ and its half-octave shift $Fex3 \equiv FGC\sharp$. According to usual thinking these chords involve dissonances. This dissonance character is a rather general phenomenon for the harmonic loners and classical views about harmony would exclude them as asocial cases! In the case of maximally symmetric harmony the loners are diminished chords and thus not so dissonant. In some cases there are no 0-quint chords.

(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 3: Table gives various types of 3-chords for harmonies with Z_6 rotational symmetry. Note that half-octave shift is an exact symmetry. Note that $G^{aug} = CEG\sharp, F^{aug}$ 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.

(n_0, n_1, n_2)	0-chords	1-chords	2-chords
(0, 16, 4)		$(D7, D6, G\sharp 7, G\sharp 6),$	$(B\flat 9, B9, E9, F9).$
		$(G4+, A9-, C\sharp 4+, D\sharp 9-),$	
		$(Emaj7, Gmaj7, Bbmaj7, C\sharp maj7),$	
		$(C9-, A9-, F\sharp 9-, D\sharp 9-).$	
(4, 8, 8)	$(Cex3, Eex2, F\sharp ex3, B\flat ex2).$	$(Dmaj7, E9-, A7, A6),$	$(B\flat 9, F9, C9, G9).$
		$(G\sharp maj7, B\flat 9-, D\sharp 7, D\sharp 6).$	$(E9, B9, F\sharp 9, C\sharp 9).$

Table 4: Table gives various types of 3-chords for the two harmonies with $Z_4 = Z_2^{rot} \times Z_2^{refl}$ symmetry. 4-plets represent the orbits. First cycle has no harmonic loners. Second cycle gives rise to bio-harmony (4, 8, 8) for which 0-quint chords are dissonant. Both cycles have Z_2 rotation symmetry acting as a vertical reflection symmetry in figures and realized also as half-octave shift so that 4-plets contains chords and their half-octave shifts. The genuine reflection symmetry acts as a horizontal reflection symmetry in figures. The cycles correspond to figures ??, ??

There are 5 collections with Z_2 reflection symmetry having 24 representatives in each (see **Figs. ??, ??, ??, ??, ??**). The integer triplets n are (2, 12, 6), (2, 12, 6), (4, 10, 6), (2, 12, 6), (2, 12, 6). Bio-harmony has representative also in this class (see **Fig. ??**). The half-octave scaling symmetry is broken for these harmonies. I have not found simple characterization for the symmetry which corresponds to reflection in the direction of x-axis since it changes the interval structure of the chords.

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

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

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

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

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

(n_0, n_1, n_2)	0-chords	1-chords	2-chords
(0, 16, 4)		$(Em, Bbm), (Cm, F\sharp m),$ $(G6, C\sharp6), (A6, D\sharp6),$ $(D4+, G\sharp4+), (B4+, F4+),$ $(Cmaj7, F\sharp maj7), (G6-, C\sharp6-).$	$(D9, G\sharp9),$ $(E9, Bb9).$
(2, 12, 6)	$(Aex4, D\sharp ex2).$	$(Am, D\sharp m), (G9-, C\sharp9-),$ $(C4, F\sharp4), (E4+, Bb4+),$ $(Dmaj7, G\sharp maj7),$ $(Bmaj7, Fmaj7).$	$(C9, F\sharp9),$ $(A9, D\sharp9),$ $(D9, G\sharp9).$
(4, 8, 8)	$(Aex2, Hex8, D\sharp ex2, Fex8).$	$(D7, G\sharp7), (Amaj7, D\sharp maj7),$ $(A4+, D\sharp4+), (E7, Bb7).$	$(G9, C\sharp9), (A9, D\sharp9),$ $(B9, F9), (E9, Bb9).$

Table 5: Table gives various types of 3-chords for harmonies with Z_2 rotation symmetry acting as half-octave shift. The doublets represent 2-chord orbits. The cycles correspond to figures ??, ??, and ??.

(n_0, n_1, n_2)	0-chords	1-chords	2-chords
(2, 12, 6)	$(F\sharp ex3, Hex4),$	$(Am, D\sharp), (A6, D\sharp7),$ $(D7, Bb6), (G6-, Fmaj7),$ $(D4+, Bb9-), (E9-, G\sharp4+),$	$(C9, F9), (B9, F\sharp9),$ $(E9, C\sharp9).$
(2, 12, 6)	$(Dex4, Hex4).$	$(F, Fm), (C6-, Bbmaj7),$ $(D7, G\sharp6), (Gmaj7, D\sharp6-).$ $(C\sharp4-, A4+), (E4+, F\sharp6).$	$(C9, D\sharp9),$ $(D\sharp9, C\sharp9),$ $(E9, B9).$
(4, 8, 8)	$(Fex1, D\sharp ex3, G\sharp ex1, Aex2).$	$(E7, E6), (Amaj7, B9-),$ $(G, C\sharp m), (D7, F\sharp6).$	$(D9, B9), (C9, C\sharp9),$ $(F9, G\sharp9), (D\sharp9, Bb9).$
(2, 12, 6)	$(Hex3, Eex7).$	$(D7, G\sharp6), (G, D\sharp m),$ $(F, Fm), (C6-, Bbmaj7),$ $(A9-, C\sharp4+), (E7, F\sharp6).$	$(C9, D\sharp9),$ $(D9, C\sharp9),$ $(E9, B9).$
(2, 12, 6)	$(F\sharp ex2, Fex3).$	$(F, Bbm), (C7, G\sharp6),$ $(Amaj7, B9-), (E6, E7),$ $(G, C\sharp m), (D7, B6).$	$(Bb9, D\sharp9),$ $(C9, C\sharp9),$ $(D9, H9).$

Table 6: Table gives various types of 3-chords for harmonies with single reflection symmetry. The cycles correspond to figures ??, ??, ??, ??, ??.

5 New results related to the notion of bio-harmony

This section contains some new results related to music harmony. During 2018 some new results related to the model of bio-harmony emerged. In the sequel they are collected together.

Remark :In the sequel I will use the shorthand AA for amino-acids and shorthands DDNA, DRNA, DtRNA, DAA for the dark analogs of DNA, RNA, tRNA, and AA realizes as dark proton sequences with codon represented as dark proton triplet.

5.1 Summary of the background

For some years ago I developed a model of music harmony [L2] (see <http://tinyurl.com/yad4tqw1>), which should define map of dark codons to 3-chords represented as dark photon triplets and defining allowed 3-chords of music harmony (music of light and perhaps also of sound). The Appendix provides the tables describing the details of the harmonies.

1. The model relies on the geometries of icosahedron and tetrahedron and representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron [A5, A2, A4, A1, A3]. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 AAs.

Single step of Hamiltonian cycle connecting vertices of a face of icosahedron (triangle) is assume to correspond to a scaling of the frequency by factor $3/2$. This leads to a problem since 12 scalings of this kind does not quite given 7 octaves which reduced octave equivalence to the basic octave would give 12-note scale. The solution is to add single note slightly differing from 7 octaves and represented as vertex P of a tetrahedron glued to icosahedron along face. The Hamilton cycles are deformed so that they begin and end from this vertex. This also gives the missing 4 DNA codons realized as 3-chords and also defines unique ground note for the scales.

2. One obtains 3 basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6 , Z_4 or Z_2 . For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle.

Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA.

4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint. The model predicts a highly unique and realistic model for numbers of DNA codons coding for a given AA. The model in its original form predicts two codes and also explains the fact that there are two additional AAs Pyl and Sec that appear as end-products.

3. AAs correspond to single 20-codon code, DNA and RNA to a union of 3 20-codon codes with symmetries Z_6 , Z_4 or Z_2 : here Z_2 would correspond to $Z_{2,rot}$ or $Z_{2,refl}$ and this would give to two two different codes.
4. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA.

Music expresses and creates emotions and the natural proposal is that these bio-harmonies correlate with moods that would appear already at molecular level. They could be realized in terms of dark photon triplets realized in terms of light and perhaps even music (living matter is full of piezo-electrets). In fact, also the emotions generated by other art forms could be realized using music of dark light. [L15]. Dark photons in various wavelength ranges and correspond to various values of h_{eff} would correspond to various sensory qualia and are represented at pineal gland (“third eye”) as imagined sensory percepts [L10]. They can be

transformed to real sensory percepts at sensory organs by using DMT molecules as bridges allowing the propagation of dark photons (or the bio-photons resulting in their energy conserving transformation to ordinary photons) to sensory organs, where they generate genuine sensory experience identified as dream, psychedelic experience, hallucination, etc...

The model of music harmony is separate from the model of genetic code based on dark proton triplets [L8] and one of the challenges has been to demonstrate that they are equivalent. One can raise several questions.

1. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton's cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied.
 - (a) There is purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20.
 - (b) There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies.
2. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could AAs couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA?
3. As I developed the model of bio-harmony [L2] (see <http://tinyurl.com/yad4tqw1>) it did not occur to me that also the tRNA part of the dark code should have counterpart in the icosahedral model. Could tRNA correspond to pairs of harmonies with $20+20+4=44$ codons? What about single $20+4=24$ codon representation as kind of pre-tRNA? Could tRNA correspond to a union of 2 20-codon codes? Combining only 2 20-codon codes with 40 codons and tetrahedral code with 4 codons would give maximally 44-letter code and the upper bound for tRNAs is according to Wikipedia 45! Dark proton model predicts 40 DtRNAs suggesting that only the 40 icosahedral codons contribute to DtRNA code. The additional tRNAs could result from homonymy. The code sequences could be seen as a hierarchical sequence $3 \rightarrow 2 \rightarrow 1$ in this framework.

An important implication is that there are many realizations of DtRNA and tRNA harmony: (Z_6, Z_4) , (Z_6, Z_2) , (Z_4, Z_2) and Z_2 could be either $Z_{2,rot}$ or $Z_{2,refl}$. This could explain the homonymy of mRNA-tRNA pairing via difference in the chords in turn affecting biochemical counterparts. Note however that the chords for tRNA must be a subset of chords for mRNA so that RNA harmony determines tRNA harmony apart from the three choices (Z_6, Z_4) , (Z_6, Z_2) or (Z_4, Z_2) giving rise to 3 different contexts. If DAAs code by 3-chords the AAs then this choice does not affect AAs.

4. What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetry arguments fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible so that it would be possible to listen what DNA sequences sounds in given mood characterized by the harmony.
5. What disharmony could mean? A possible answer comes from 6 Hamiltonian cycles having no symmetries. These disharmonies could express "negative" emotions.

5.2 Some questions about the realization of the bio-harmony

In the sequel by I will proceed by posing questions related to the relationship between the 3 representations of genetic code [K13] in terms of bio-molecules, their dark analogs represented as sequences dark proton triplets, and as 3-3-chords of bio-harmony.

5.2.1 What conditions pairings pose on the frequency triplets?

The realization of DDNA-DtRNA and DDNA-DAA pairings in terms of frequencies must involve a loss of information since the correspondence is many-to-one.

1. For DNA-mRNA pairing information is not lost and the pairing must be of form $(f_1, f_2, f_3) \rightarrow (f_1, f_2, f_3)$. Note that the frequencies cannot be associated with the letters. It is however possible to consider the assignment of (f_1, f_2) to the first letter pair XY as a whole and f_3 to the third letter Z.
2. For DDNA-DAA and DmRNA-DAA pairing the natural hypothesis is $(f_1, f_2, f_3) \rightarrow f_1 + f_2 + f_3$. AA couples to the sum of the frequencies of the triplet. The simplest possibility is that the $f_1 + f_2 + f_3$ is same for all codons codin for given AA. One might say that AA sequence defines melody and mRNA sequence the accompaniment. If the sums for codons coding given AA are different they must couple resonantly to it. If there are several harmonies the sum must same for all realizable 3-harmonies or all chords of 3-chord harmonies coding for same AA couple to it resonantly. Since one has linear 1-D structures one might ask whether frequency differences coming as multiples of lattice frequencies are allowed. Second natural possibility is octave equivalence. mRNA-AA pairing would take place directly rather than with the mediation of of tRNA.
3. In the case of DmRNA-DtRNA pairing one one does not lose so much information since the number of dark DNAs is 40 (as also the 3-chords if tetrahedron does not contribute). One must remember that tRNAs are pairs of RNA like codons - call them RNA_t , and AAs. Therefore there pairing involves also the pairing mRNA-AA give by $(f_1, f_2, f_3) \rightarrow f_1 + f_2 + f_3$ and guaranteeing that the code is realized by this pairing alone irrespective of mRNA- RNA_t pairing. At chemical level the first to mRNA codons pair with tRNA anticodons according to the standard rules. Could RNA_t have completely passive role in carrying the AA? This cannot be the case since the last two letters of RNA_t couple in standard manner to the first two letters of mRNA.

Remark: tRNA is analogous to melody + accompaniment using one of the 3 possible 2-harmonies for a given 3-harmony.

Suppose that mRNA- RNA_t pairing corresponds to 3 possible choices of 2-harmonies as sub-harmonies of 3-harmony. This would suggest these different sub-harmonies define maps $(f_1, f_2, f_3) \rightarrow (f_1, f_2, f_3)$ such that RNA_t pairs only with two sub-harmonies. For each choice RNA_t would correspond effectively to 40 sub-codons of the entire code (forgetting the tetrahedral part giving 4 additional codons). The three different realizations of the projection would give rise to the homonymy. Also the AA-trNA coupling would come out correctly.

DAAs would be different in the sense that they couple only to the sum of the frequencies. This is in accordance with bio-harmony in which AAs correspond to orbits of 3-chords for DNA under isometries rather than single 20-chord harmony. The coupling to the sum of frequencies is in accordance with the quantal interpretation as 3-dark-photon state whose energy is $E = h_{eff}(f_1 + f_2 + f_3)$ and couples to AA chemically via the transition to ordinary photons with the same energy.

This leaves some questions.

1. Could one consider the possibility that the chords of one of the 20-chord harmonies corresponds to AAs? There would be 3 basic types of AAs. This does not look plausible and the association of AAs with the orbits of 20-note chords is more natural and fits nicely with $f = f_{XYZ}$ picture.
2. It would be nice to assign notes to the individual letters of codons. This is not possible since codons with 2 or 3 identical letters would reduce to 2-chords or 1-chords. It is also impossible to assign frequencies with letters at dark level since letter decomposition does not exist. Thus the 3-chord has resonant interaction with the entire codon.
3. The symmetries of the genetic code however suggest that it might make sense to treat the first two letters XY of the codon as a single unit and the third letter as separate single unit.

Could one assign to XY a 2-chord not reducible to frequencies for the letters X and Y , and to letter Z its own frequency. The frequencies of A, G, T, C as third letter must be different. Four 32 codons of standard code the AA would not be sensitive to the frequency of Z : this is possible if these frequencies are resonance frequencies of the same AA. For the remaining 32 codons the AA would not distinguish between frequencies of T and C *resp.* A and G so that the two frequencies would be both resonance frequencies of the corresponding AA.

5.2.2 Probabilistic estimates for single 20-chord harmony

One can make first some naïve probabilistic estimates about single 20-chord harmony.

1. Given 20-chord harmony makes $20/220 = 1/11 \simeq 9$ per cent about all possible 3-chords. Three 20 chord harmonies would make $3 \times 9 = 27$ per cent about all possible 3-chords if there are no common chords so that the optimistic expectation might make sense. Of course, one cannot exclude the possibility that there are also triplets of 20-codon codes which gives smaller number of codons.
2. The total number of chords with different notes is $12 \times 11 \times /3! = 220$. Bio-harmony has 64 chords corresponding to faces of icosahedron: this is about $64/220$ making 29 per cent of all possible 3-chords with different notes. Given bio-harmony thus throws out roughly $2/3$ of all possible codons. This should be easy to test. For instance, does given gene correspond to a fixed bioharmony? Or does even entire genome do so. If bio-harmony is realized for non-nuclear genomes, it must satisfy rather strong constraints.
3. Given 20-chord harmony corresponds to 12 edges. Each edge is shared by two adjacent triangles. If all 20 triangles would contain just single face, there would be 24 triangles altogether. Therefore there must be triangles containing two subsequent edges of the cycle. Each triangle of this kind reduces the number of 24 neighbours by 2 units. Hence it seems that one must have at least 2 triangles with 2 edges at the cycle (two quints in the 3-chord).
If there are more than 2 triangles of this kind, there must be triangles having no edges along the path. Each vertex of icosahedron is shared by 5 triangles and there are 5 edges starting from it.
4. The notion of Hamilton cycle generalizes to any graph and magnetic flux tube networks define such graphs as tensor networks. Why only icosahedron? Could one consider the possibility that any tensor network is characterized by harmonies characterize by Hamiltonian cycles and that one could assign some kind of codes with the combinations of these cycles? In the general case symmetries would be absent so that the notion of code in the proposed sense would fail: one could not identified codons as points at orbits of symmetry group. Rather, one can imagine that the notion of code could be defined quite generally in terms of orbits as AAs and points at them as DNAs coding them. For regular polygons in any dimension the symmetries are present and one could define the notion of code and also fuse the codes.
For arbitrary tensor network the faces need not be symmetry related and one can also have faces that can be interpreted as higher-dimensional polytopes.
One can also ask whether the icosahedron is realized physically. Icosahedral geometry is indeed very common in biology. Could the fusion of icosahedral and tetrahedral geometries have some concrete realization at molecular level?

5.2.3 Is the maximal number of codons for the fusion of 3 20-codon codes possible?

It has not earlier occurred to me to wonder whether the chords associated with the 3-different icosahedral harmonies giving 20 codons each correspond to $20+20+20=60$ different chords as assumed. Could there be common 3-chords? This question could be answered by studying the Hamiltonian cycles at icosahedron.

Remark: Perhaps more important constraint than absence of common chords is the chemical realizability of the codes. If same mRNAs and DNAs realized different bio-harmonies then they must be able to respond resonantly to several 3-chords.

One can make naïve probability estimates for a pair of codes to allow the maximal number of 60 codons. It seems natural to assume that the isometries of icosahedron (or their subgroup) can be applied separately and only the isometries acting on both in similar manner are symmetries. The situation would be the same as in the case of many-particle system: only the translations acting on all particles simultaneously remain symmetries and relative translations cease to be symmetries.

With this assumption the icosahedral group gives a large number of code pairs. For the fusion of 3 20-codon codes giving DNA/RNA the number is even higher. By choosing suitably the relative isometries it might be possible to obtain the maximal number of 60 different codons for the icosahedral genetic code. On the other hand, by a suitably choice of relative isometries one might have undesired common 3-chords. In any case, the earlier estimate 256 for the number of bio-harmonies [L2] suggested to correlate with “emotional” states of the basic biomolecules is expected to change.

Before going to estimates one must consider some delicacies related to the notion of 12-note scale as Hamiltonian cycle.

1. One can regard the cycles as purely geometric objects without orientation or assign to them orientation. For two different orientations the scales would run in opposite directions as scalings by $3/2$ along single edge of the cycle. If two codes have common edge, the scaling must be same along it. If the orientation of the second cycle is changed, the common edge ceases to be common.
2. The basic note of the 12-note scale at cycle can be chosen arbitrarily: this corresponds to the choice of the key in music (one could of course argue that the key does not make sense in 12-note scale if one has tempered scale with notes comes as powers of $2^{1/2}$ scaling of ground note rather than Pythagorean scale with rational ratios of notes).

The fusion of tetrahedron to icosahedron selects one particular triangular face and brings in one additional vertex outside the icosahedron, call it P . It would be natural to assign the ground note as P . The isometries not affecting P would correspond to those of icosahedron leaving the common face invariant and isometries of tetrahedron leaving P un-affected and continuable to icosahedral isometries. One would have subgroup of icosahedral group as allowed isometries acting on the cycles to be fused.

3. If one assigns note sequences to the cycle by quint rule, cycles C_1 and C_2 can have common triangle in geometric sense but if the distances of the vertices A, B, C of the triangles from P measured as the number of edges of cycle portion connecting them are not same along C_1 and C_2 , the triangles correspond to different chords and are thus orthogonal in the proposed description as many-fermion states.
4. To sum up, the states associated with triangles would be characterize by the position of triangle (20 values), by the notes of the triangle characterized by the distances from P , and the number 0, 1, 2 of the edges belonging to the cycle and should make easier to find ortogonal basis.

Again one can make probabilistic estimates: cycles are treated as purely geometric entities without orientation and without assignment of notes to the triangles.

1. Given cycles C_1 and C_2 what is the probability that they have at least one common edge as purely geometric entities without the sequence of notes? There are 30 edges so that given edge is shared with probability $1/30$. If the edges of cycles were chosen randomly (certainly not true), the probability of having a common edge for two cycles would be $P(1) = 12/30$. The assumption of note sequence reduces this probability dramatically.
2. By the above estimate each cycle contains at least two triangles with 2 edges at the cycle with minimal angle between them. One can call these these edge pairs V-corners. Assume that for cycle C_1 one has V-corner ABC at vertex A, call it $V_{1,A}$. What is the probability that one one of the V-corners of C_2 is located at A co-incides with ABC. The probability of V-corner of C_2 to locate at A is $1/12$ and the probability that the edge of C_2 from B is BC is $1/4$ so that the probability of having common V-corner is $1/48$. If C_2 contains n V-edges the probability is naïvely $n/48$.

This estimate takes into account only geometry. The situation changes if one assumes that the cycles are oriented. In this case one can have common V-corner if the local orientations of C_1 and C_2 are opposite at the V-corner. If one assumes that the external vertex P of the tetrahedron defines the ground note then the number of edges connecting P to A defining distance $d(P, A)$ must be same for C_1 and C_2 .

- Given C_1 and C_2 (and vertices A with same distance $d(P, A)$) it might be possible to perform suitable isometry for C_2 that there is common V-corner. Therefore not all possible combinations of three code types allowing relative isometries need not maximal number of 3-chords.

Remark: An interesting question is whether these can be allowed meaning that some codons are missing in the chemical realization of the dark codons in terms of ordinary DNA codons. Also the 1-1 pairing between dark DNA and dark RNA would not be 1-1 if mediated by 3-chord resonance and one would have homonymy. This suggests that only codes without common chords can be allowed.

- What about chords having 1 edge at cycle for two cycles C_1 and C_2 ? Let the edge be AB . As found, the naïve probability for this is $P(1) = 12/30$. Both cycles must go through the third vertex C of the triangular face. The subsequent notes along cycle differ by a quint that is scaling of the frequency by factor $3/2$. Notes are same if the numbers of the needed quints are same for C_1 and C_2 . For C_1 the number $n_B > 1$ of quints is known. In the approximation that possible portions of C_1 represent n -step non-self-intersecting random walks from B to C , one must estimate the number of all non-self-intersecting n -step-paths from B to C and find what is the number of the paths leading to C . One can go from A to C with n_A steps and similar estimate applies.
- The third possibility is that the one has 3 common vertices A, B, C forming a triangular face such that neither cycle contains any of its edges.

The cautious conclusion is that it is plausible that one can find 3 cycles having no common chords if one allows relative rotations of the cycles and that this condition is necessary for realizing the absence of homonymies at dark level. The automatic orthogonality of the Hamiltonian cycles cannot be excluded but would allow also codes with codons containing more than 3 letters so that one could have kind of super-DNA. Whether they can be realized chemically depends on whether there are biomolecules resonating with the the n frequency triplets involved. Octave equivalence for frequencies might give hopes about chemical realization of several harmonies. Therefore the evolution might be seen as gradual emergence of molecules able to pair with DDNA and one can even imagine artificial evolution by tailoring the frequencies involved (maybe cyclotron frequencies).

5.2.4 How the symmetries of the model of harmony could relate to those of the genetic code?

Genetic code has surprisingly strong symmetries. I have discussed a possible interpretation of these symmetries using analogies with particle physics and considered also a mechanism explaining their emergence earlier [K1, ?]. The proposal was that 3-letter code emerged as a fusion of 2-letter code with 16 codons and 1-letter coded with 4 codons. In the recent framework, a more natural option is that the third codon of 3-letter code was originally passive and became active via symmetry breaking distinguishing first between UC and AG pairs and later between U and C *resp.* A and G. Note that for the standard code the breaking is minimal and caused by odd number of Start and Stop codons.

- For vertebrate code one half of codons has very high symmetry in the sense that the two first letters dictate the AA for 32 cases. Exception is UUU, which codes for Phe or Leu for some modifications of the standard code. $UUU \rightarrow$ Leu means breaking of maximal symmetry.
- There is also a second symmetry, which I have referred to as isospin symmetry. It is only slightly broken. For general codons XYU and XYC code for same AA as also XYA and ad XYG. For the standard code this symmetry is broken only in columns containing initiation codon or stop. The Start codon AUG codes also for met. UGA and UGG code for Stop and

Trp. For the remaining codons one has slightly broken “isospin symmetry”. The breaking of isospin symmetry is minimal for vertebrate code. The modifications of the code tend to break the isospin symmetry and even the maximal symmetry of 32 codons. This must be important.

If the model of genetic code based on music harmony [L2] is correct, the symmetries for the model of music harmony must relate to those of genetic code.

1. How the symmetries of the genetic code relate to the symmetries of icosahedron (60-element group) and tetrahedron (permutation group S_4 with 24 elements) in the model of bio-harmony? Icosahedral symmetry group has 60 elements and has sub-groups $Z_2, Z_4, Z_5, Z_6 = Z_2Z_3$. Note that there are two Z_2 :s having rotation by π and reflection as generators.

The gluing of tetrahedron to icosahedron along single face reduces its group of symmetries to S_3 leaving the point P not belonging to icosahedron invariant. S_3 has as subgroups reflection group $Z_{2,refl}$ and Z_4 consisting of rotations.

2. What is the counterpart for maximal symmetry in icosahedral and tetrahedral groups? Do the 3-chords for codon XYZ decompose to two-chord characterizing XY and a note characterizing Z= A,U,C,G, which can depend on XY. The symmetry relating UC pair and AC pair could correspond to $Z_{2,refl}$ reflection symmetry, which is shared by icosahedral and tetrahedral groups. For 32 icosahedral codons the action of $Z_{2,refl} \times Z_{2,rot}$ would be trivial so that AA would not depend on the third letter at all. For most of the remaining codons the action of the symmetry group on icosahedral codons would reduce to $Z_{2,rot}$ permuting the third letters U and C *resp.* A and G. At the level of frequencies the sums of frequencies for codons coding for the same AA could be same modulo octave equivalence.

The addition of tetrahedron brings in 4 tetrahedral codons with one of them shared with icosahedron. Icosahedral $Z_{2,rot}$ does not make sense for these codons. Intriguingly, there are 4 codons in vertebrate code which break isospin symmetry AUA and AUG coding for I and Met/start and UGA and UGG coding for Stop and Trp. If these codons correspond to the tetrahedral codons which cannot have $Z_{2,rot}$ as isospin symmetry, the breaking of $Z_{2,rot}$ would follow from the breaking of symmetry induced by the attachment of tetrahedron to icosahedron.

5.2.5 What is the origin of 12-note scale?

One fundamental question is why dark photon realization of genetic code should involve 12-note scale as icosahedral model requires.

Remark: The gluing of tetrahedral codons gives 4 additional codons but if tetrahedron is glued to icosahedron along one of its faces, the additional vertex gives only one additional note, which should be very near to the 12:th one. This could relate to the basic problem observed already by Pythagoras that 12-note Pythagorean scale with rational valued frequency ratios does not quite close.

A popular article in Spacedaily with title “*Scientists crack how primordial life on Earth might have replicated itself*” (see <http://tinyurl.com/y92ng5vd>) led to a possible answer to the above question. The research paper [?] is titled “*Ribozyme-catalysed RNA synthesis using triplet building blocks*” and published in eLife (see <http://tinyurl.com/ya5qyjfn>).

It is possible to replicate unfolded RNA strands in Lab by using enzymes known as ribozymes, which are RNA counterparts of enzymes, which are amino-acidic sequences. In the presence of folding the replication is however impossible. Since ribozymes are in general folded, they cannot thus catalyze their own replication in this manner. The researchers however discovered that the replication using RNA triplets - genetic codons - as basic unit can be carried out in laboratory even for the folded RNA strands and with rather low error rate. Also the ribozyme involved can thus replicate in codon-wise manner. For units longer than 3 nucleotides the replication becomes prone to errors.

These findings are highly interesting in TGD framework. In TGD the chemical realization of genetic code is not fundamental. Rather, dark matter level would provide the fundamental realizations of analogs of DNA, RNA, tRNA, and amino-acids as dark proton sequences giving rise

to dark nuclei at magnetic flux tubes [L12] (see <http://tinyurl.com/yalny39x>). Also ordinary nuclei correspond in TGD Universe to sequences of protons and neutrons forming string like entities assignable to magnetic flux tubes.

The basic unit representing DNA, RNA and tRNA codon and amino-acid would consist of 3 entangled dark protons. The essential aspect is that by entanglement the dark codons do not decompose to products of letters. This is like words of some languages, which do not allow decomposition to letters. This representation is holistic. As we learn to read and write, we learn the more analytic western view about words as letter sequences. Could the same hold true in evolution so that RNA triplets would have come first as entities pairing with dark RNA codons from from dark proton triplets as a whole? Later DNA codons would have emerged and paired with dark DNA codons. Now the coupling would have been letter by letter in DNA replication and transcription to mRNA.

It is intriguing that tRNA consists of RNA triplets combined from amino-acids and analogs of mRNA triplets! The translation of mRNA to amino-acids having no 3-letter decomposition alone forces the holistic view but one can ask whether something deeper is involved. This might be the case. I have been wondering whether during RNA era RNA replicated using a prebiotic form of translational machinery, which replicated mRNA rather than translated RNA to protein formed from amino-acids (AAs) with AA serving as a catalyst.

1. During RNA era amino-acids associated with pre-tRNA molecules would served as catalysts for replication of RNA codons. The linguistic mode would have been “holistic” during RNA era in accordance with the findings of the above experiments. RNA codon would have been the basic unit.
2. This would have led to a smaller number of RNAs since RNA and RNA like molecules in tRNA are not in 1-1 correspondence. A more realistic option could have been replication of subset of RNA molecules appearing in tRNA in this manner.
3. Then a great evolutionary leap leading from RNA era to DNA era would have occurred. AA catalyzed replication of RNA would have transformed to a translation of RNA to proteins and the roles of RNA and AA in tRNA would have changed. [Perhaps the increase of h_{eff} in some relevant structure as quantum criticality was reached led to the revolution]
4. At this step also (subset of) DNA and its transcription to (a subset of) mRNA corresponding to tRNA had to emerge to produce mRNA in transcription. In the recent biology DNA replicates and is transcribed nucleotide by nucleotide rather than using codon as a unit so that helicases and DNA and RNA polymerases catalyzing replication and transcription should have emerged at this step. The ability of DNA to unwind with the help of helicase enzyme helping DNA to unwind is essential for the transcription and translation of DNA. Therefore helicase must have emerged together with the “analytic linguistic mode” as an analog of written language (DNA) decomposing codons to triplets of letters. This would be a crucial step in evolution comparable to the emergence of written language based on letters. Also the counterpart of RNA polymerase and separate RNA nucleotides for transcription should have emerged if not already present.

An alternative option would involve “tDNA” as the analog of tRNA and the emergence of helicase and polymerases later as the transition from holistic to analytic mode took place.

The minimal picture would be emergence of a subset of DNA codons corresponding to RNAs associated with pre-tRNA and the emergence of the analogs of helicase and DNA and RNA polymerases as the roles of amino-acid and RNA codon in tRNA were changed.

5. How DNA could have emerged from RNA? The chemical change would have been essentially the replacement of ribose with de-oxiribose to get DNA from RNA and $U \rightarrow T$. Single O-H in ribose was replaced with H. O forms hydrogen bonds with water and this had to change the hydrogen bonding characteristics of RNA.

If the change of $h_{eff} = n \times h_0$ was involved, could it have led to stabilization of DNA? Did cell membrane emerge and allow to achieve this? I have proposed [L12] (see <http://tinyurl.com/yalny39x>) that the emergence of cell membrane meant the emergence of new representation of dark genetic code based on dark nuclei with larger value of h_{eff} .

Remark: One has $h = 6 \times h_0$ in the most plausible scenario [L9, L14] (see <http://tinyurl.com/goruuzm> and <http://tinyurl.com/y9jxyjns>).

One can of course ask whether something simpler could be imagined by utilizing the potential provided by dark variants of bio-molecules present already from beginning and providing both genes and metabolism simultaneously.

1. Viruses are probable predecessors of cellular life. So called positive sense single stranded RNA (ssRNA) associated with viruses can form temporarily double strands and in this state replicate just like DNA (see <http://tinyurl.com/yc5f8b3t>). The resulting single stranded RNA can in turn be translated to proteins by using ribosomal machinery. RNA replication takes place in so called viral replication complexes associated with internal cell membranes, and is catalyzed by proteins produced by both virus and host cell.

Could ribozyme molecules have catalyzed RNA replication during RNA era? For this option AA translation would have emerged later and the storage of genetic information to DNA only after that. There is however the question about the emergence of AAs and of course, DNA and RNA. Which selected just them from enormous variety of options.

2. Lipid membranes are formed by self-organization process from lipids and emerge spontaneously without the help of genetic machinery. It would be surprising if prebiotic life would not have utilized this possibility. This idea leads to the notion of lipid life as a predecessor of RNA life. In this scenario metabolism would have preceded genes (see <http://tinyurl.com/y7ehv8cq> and <http://tinyurl.com/y8n1tb9e>). The basic objection against both genes-first and metabolism-first options is that they need each other!
3. In TGD framework the dark variants of DNA, RNA, AA, and tRNA would provide the analogs of genes and all basic biomolecules. They would also provide a mechanism of metabolism in which energy feed by (say) solar radiation creates so called exclusion zones (EZs) of Pollack [?] in water bounded by a hydrophilic substance. EZs are negatively charged regions of water giving rise to a potential gradient (analog of battery) storing chemically the energy provided by sunlight and the formation of these regions gives rise to dark nuclei at magnetic flux tubes with scaled down binding energy.

When the p-adic length scale of these dark nuclei is liberated binding energy is liberated as metabolic energy so that metabolic energy feed giving basically rise to states with non-standard value $h_{eff}/h = n$ of Planck constant is possible. For instance, processes like protein folding and muscle contraction could correspond to this kind of reduction of h_{eff} liberating energy and also a transformation of dark protons to ordinary protons and disappearance of EZs.

The cell interiors are negatively charged and this is presumably true for the interiors of lipid membranes in general and they would therefore correspond to EZs with part of protons at magnetic flux tubes as dark nuclei representing dark variants of basic biomolecules. Already this could have made possible metabolism, the chemical storage of metabolic energy to a potential gradient over the lipid membrane, and also the storing of the genetic information to dark variants of biomolecules at the magnetic flux tubes formed in Pollack effect.

4. In TGD framework biochemistry would have gradually learned to mimic dark variants of basic processes as a kind of shadow dynamics. Lipid membranes could have formed spontaneously in water already during prebiotic phase when only dark variants of DNA, RNA, AAs and tRNA, water, and lipids and some simple bio-molecules could have been present. The dark variants of replication, transcription and translation would have been present from the beginning and would still provide the templates for these processes at the level of biochemistry.

Dark-dark pairing would rely on resonant frequency pairing by dark photons and dark-ordinary pairing to resonant energy pairing involving transformation of dark photon to ordinary photon. The direct pairing of basic biomolecules with their dark variants by resonance mechanism could have led to their selection explaining the puzzle of why so few biomolecules survived.

This is in contrast with the usual view in which the emergence of proteins would have required the emergence of translation machinery in turn requiring enzymes as catalyzers so that one ends up with hen-or-egg question: which came first, the translation machinery or proteins. In RNA life option similar problem emerges since RNA replication must be catalyzed by ribozymes.

5. Gradually DNA, RNA, tRNA, and AA would have emerged by pairing with their dark variants by resonance mechanism. The presence of lipid membranes could have been crucial in catalyzing this pairing. Later ribozymes could have catalyzed RNA replication by the above mentioned mechanism during RNA era: note however that the process could be only a shadow of much simpler replication for dark DNA. One can even imagine membrane RNAs as analogs of membrane proteins serving as receptors giving rise to ionic channels. Note however that in TGD framework membrane proteins could have emerged very early via their pairing with dark AA associated with the membrane. These membrane proteins and their RNA counterparts could have evolved into transcription and translation machineries.

DNA molecules would have emerged through pairing with dark DNA molecules. The difference between deoxy-ribose and ribose would correspond to the difference between dark RNA and dark DNA manifesting as different cyclotron frequencies and energies making possible the resonant pairing for frequencies and energies. Proteins would have emerged as those proteins able to pair resonantly with dark variants of amino-acid sequences without any pre-existing translational machinery. It is difficult to say in which order the basic biomolecules would have emerged. They could have emerged even simultaneously by resonant pairing with their dark variants.

The communication between dark ordinary variants of biomolecules involves resonance mechanism and would also involve genetic code represented as 3-chords, music of light, and it is interesting to see whether this model provides additional insights.

1. The proposal is that 3-chords assignable to nucleotides as music of light with allowed 64 chords defining what I have called bio-harmony is essential for the resonance [L15, L17, L14](see <http://tinyurl.com/ydhxen4g>, <http://tinyurl.com/yd5t82gq>, and <http://tinyurl.com/y9jxyjns>). The 3 frequencies must be identical in the resonance: this is like turning 3 knobs in radio. This 3-fold resonance would correspond to the analytic mode. The second mode could be holistic in the sense that it would involve only the sum only the sum of the 3 frequencies modulo octave equivalence assigning a melody to a sequence of 3-chords.
2. The proposal is that amino-acids having no triplet decomposition are holistic and couple to the sum of 3 frequencies assignable to tRNA and mRNA in this manner. Also the RNAs in tRNA could couple to mRNA in this manner. One could perhaps say that tRNA, mRNA and amino-acids codons sing whereas DNA provides the accompaniment proceeding as 3-chords. The couplings of DNA nucleotides to RNA nucleotides would rely on the frequencies assignable to nucleotides.
3. If the sum of any 3 frequencies associated with mRNA codons is not the same except when the codons code for the same amino-acids, the representation of 3-chords with the sum of the notes is faithful. The frequencies to DNA and RNA nucleotides cannot be however independent of codons since the codons differing only by a permutation of letters would correspond to the same frequency and therefore code for the same amino-acid. Hence the information about the entire codon would be needed also in transcription and translation and could be provided either by dark DNA strand associated with DNA strand or by the interactions between the nucleotides of the DNA codon.
4. The DNA codon itself would know that it is associated with dark codon and the frequencies assignable to nucleotides could be determined by the dark DNA codon. It would be enough that the frequency of the letter depends on its position in the codon so that there would be 3 frequencies for every letter: 12 frequencies altogether.

What puts bells ringing is that this the number of notes in 12-note scale for which the model of bio-harmony [L2, L15] (see <http://tinyurl.com/yad4tqwl> and <http://tinyurl.com/yad4tqwl>).

com/ydhxen4g) based on the fusion of icosahedral (12 vertices and 20 triangular faces) and tetrahedral geometries by gluing icosahedron and tetrahedron along one face, provides a model as Hamiltonian cycle and produces genetic code as a by-product. Different Hamiltonian cycles define different harmonies identified as correlates for molecular moods.

Does each DNA nucleotide respond to 3 different frequencies coding for its position in the codon and do the 4 nucleotides give rise to the 12 notes of 12-note scale? There are many choices for the triplets but a good guess is that the intervals between the notes of triplet are same and that fourth note added to the triplet would be the first one to realize octave equivalence. This gives uniquely $CEG\sharp$, $C\sharp FA, DF\sharp B\flat$, and $DG\sharp B$ as the triplets assignable to the nucleotides. The emergence of 12-note scale in this manner would be a new element in the model of bio-harmony.

There are $4! = 24$ options for the correspondence between $\{A, T, C, G\}$ as the first letter and $\{C, C\sharp, D, D\sharp\}$. One can reduce this number by a simple argument.

- (a) Letters and their conjugates form pyrimidine-purine pairs T, A and C, G . The square of conjugation is identity transformation. The replacement of note with note defining at distance of half-octave satisfies this condition (half-octave - tritonus - was a cursed interval in ancient music and the sound of ambulance realizes it). Conjugation could correspond to a transformation of 3-chords defined as

$$CEG\sharp \leftrightarrow DF\sharp B\flat, \quad C\sharp FA \leftrightarrow D\sharp GB.$$

- (b) One could have

$$\begin{aligned} \{T, C\} \leftrightarrow \{CEG\sharp, C\sharp FA\}, \quad \{A, G\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\}, \\ \text{or} \\ \{T, C\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\}, \quad \{A, G\} \leftrightarrow \{CEG\sharp, C\sharp FA\}. \end{aligned}$$

- (c) One can permute T and C and A and G in these correspondences. This leaves 8 alternative options. Fixing the order of the image of (T, C) to say $(C, C\sharp)$ fixes the order of the image of (A, G) to $(D, D\sharp)$ by the half-octave conjugation. This leaves 4 choices. Given the bio-harmony and having chosen one of these 4 options one could therefore check what given DNA sequence sounds as a sequence of 3-chords [L2].

That the position the frequency associated with the nucleotide depends on its position in the codon would also reflect the biochemistry of the codon and this kind of dependence would be natural. In particular, different frequencies associated with the first and third codon would reflect the parity breaking defining orientation for DNA.

5.2.6 What disharmony could mean?

Harmonies - also those, which are sad (consider only passions of Bach) - are usually thought of as something beautiful. Could negative emotions really correspond to any bio-harmonies characterized by symmetries. In a discussion with Sini Kunnas I realized that also the notion of disharmony could make sense. There are indeed 6 Hamiltonian cycles without any symmetries [A2, A3, A1]. I neglected them in the model of harmony because they would represent which one might call disharmony. Could one of the contributing 3 Hamiltonian cycles in bio-harmony correspond to this kind of dis-harmony and bring in 20 3-chords without any symmetries? If so the relationship between geometry and aesthetics would become very concrete. The alternative view would be that there are several harmonies realized simultaneously and this creates disharmony.

The faces of the icosahedron belonging to the orbits of the symmetries of the harmony correspond to DNA codons coding for the same AA assignable to the orbit. The fact that there are no symmetries for these 6 bio-disharmonies, suggests one-to-one correspondence between DNA and AAs if also stop codon corresponds to ordinary AA.

5.2.7 How to concretely realize emotions as music of light?

Music expresses emotions and also create higher level emotions. As all art, it also induces experience of beauty. Since $h_{eff}/h = n$ [?, K9] serves as a kind of IQ in the evolutionary hierarchy, there are good reasons to expect that the emotions/feelings induced by music and other art forms are assignable to MB.

The dynamics of MB involves oscillations characterized by frequencies and in EEG frequencies are of key importance for the part of MB outside biological body. The communications from cell membrane to MB involve modulation of EEG frequencies identified as generalized Josephson frequencies by nerve pulse patterns [K12] and would define a coding of sensory data to higher level emotions. The control signals from MB via DNA inducing gene expression would use dark photons at cyclotron frequencies to control BB. How to realize the music of genes represented as sequences of 3-chords of dark light as a communication tool between dark and ordinary DNA/RNA and possibly even dark and ordinary variants of tRNA and amino-acids?

1. Communication between ordinary and dark matter levels must be possible. This is guaranteed if the transition energy spectra at different levels of $h_{eff}/h = n$ hierarchy contain common transition energies so that a resonant interaction by exchange of dark photons becomes possible. This condition is extremely demanding and could explain why basic bio-molecules are selected amongst numerous alternatives [L12] - this is indeed one of the hen-egg problems of pre-biotic evolution.
2. A hypothesis worth of studying is that the cyclotron transition energies of both ordinary DNA and RNA nucleotides and their dark variants represented as dark proton sequences are same [L12]. Cyclotron transition energies should cover several octaves and the natural proposal is that magnetic field strength associated with the flux tube codes for the notes. In music experience roughly 10 octaves are needed corresponding to the range of audible sounds.
3. The cyclotron frequencies of DNA nucleotides A, T, C, G are very nearly the same and near 1 Hz for $B = B_{end} = .2$ Gauss since their masses do not differ much. Since the nucleotides are negatively charged, also the cyclotron energies for codons and codon sequences are around 1 Hz. $h_{eff} = h_{gr}$ hypothesis states that the cyclotron energies of DNA are in the energy range of bio-photons in visible and UV [K9, K2, K3] [L14].

There should be correspondences between a) the 64 ordinary DNA codons and allowed 3-chords and b) 64 dark variants of DNA codons and allowed 3-chords. These correspondences fix that between ordinary and dark codons. One would have triality.

1. To realize music of genes one the value of B must have values in a range of several octaves. The magnetic field strengths B associated with the flux tubes accompanying DNA strand should have a spectrum given by 12-note scale. Both 64 dark DNA codons and $4^3 = 64$ ordinary DNA codons should correspond to $20 + 20 + 20 + 4 = 64$ allowed 3-chords formed from the notes of 12-note scale.
2. Dark codons correspond to entangled states of 3 dark protons. The positions of dark protons are different so that ermutations of the positions of dark protons are involved. The invariance of 3-chord under permutations of notes would correspond to fermionic statistics. These permutations are lifted to braidings if dark protons are connected by flux tubes to some other system, for instance ordinary DNA.

If the dark protons are ordered linearly along flux tube, it would seem that these these positions correspond to those of ordinary code letters. This does not make sense. If the letters of codon are connected to the dark protons by flux tubes, the permutations of dark codons induce braiding of the flux tubes but do not affect the order of the letters of the ordinary codon. Braiding would become an essential part of the correspondence between ordinary and dark codons.

3. One should understand the correspondence of dark codons with the allowed 3-chords of a given harmony and also with the ordinary DNA codons. Bio-harmony is defined as a

composite of 3 harmonies with 20 allowed 3-chords and having symmetries Z_6 , Z_4 , and Z_2 and of tetrahedral harmony with 4 chords. Tetrahedron can be regarded as disjoint object or attached to DNA, and this gives two variants of code.

How could these the icoso-tetra-hedral Hamilton cycles relate to the physical realization of dark proton triplets? Each icosahedral cycle should give rise to 20 dark proton triplets. Why the icosahedral geometry with Hamiltonian cycle should make itself manifest in the quantum physics of dark proton triplet?

4. Could icosahedral geometry quite concretely correspond to a tensor network? The vertices of the icosahedron would be connected by a sequence of flux tubes connecting nearest neighbors to form a Hamiltonian cycle. Dark proton triplets would quite concretely be localized at the triangular faces of the icosahedron.

Braided triplet of flux tubes would emerge from the vertices of an icosahedral triangle defining 3-chord and would connect it to the nucleotides of the corresponding ordinary DNA codon. Magnetic field strengths at these flux tubes would correspond to the notes of 12-note scale as defined by the Hamiltonian cycle in question. The permutations of the dark proton states at the vertices of the triangle would induce braidings of the flux tube triplet actually defining minimal braid in topological quantum computation (sic!) The braiding accompanying the states of 3 dark protons would make the correspondence with ordinary ordered DNA codons possible.

Note that each dark proton triplet could be also connected (without braiding) to its conjugate dark proton triplet by a triplet of flux tubes so that one would obtain closed flux loops and one could speak of knots instead of braids.

Remark: Braiding brings strongly in mind the many TGD inspired proposals for DNA as topological quantum computer [K1, K13]: maybe DNA as topological quantum computer could be (also?) realized in this manner.

What physical objects could the 20 vertices of icosahedron correspond to? Hydrogen bonded water clusters give rise to both tetrahedral and icosahedral structures. Could one associate dark proton triplets to the dark parts of these structures? Could one try to experimentally identify possible sequence of icosahedral water molecule clusters with vertices connected by hydrogen bonds associated with the DNA sequence? If the hydrogen bonds correspond to flux loops as suggested, they can be rather long (proportional to $h_{eff}/h = n$) so that even distant water molecules can become hydrogen bonds and one could have a fractal hierarchy of icosahedra.

5. Resonance condition suggests that at the level of ordinary DNA double strand the cyclotron energies of dark protons associated with the hydrogen bonds connecting DNA nucleotides correspond to those of flux tube triplets connecting ordinary and dark DNA codons. The magnetic field strengths associated with the dark flux tubes accompanying hydrogen bonds would correspond to those associated with the triangles of icosahedral triangle. This would make possible communication between the two dark sectors by dark-photon triplets as music of genes.

This leaves unanswered questions.

1. Why the $20+20+20=60$ 3-chords from 3 harmonies with different icosahedral symmetries (Z_6, Z_4, Z_2) and 4 chords from tetrahedral harmony would combine to form single bio-harmony with 64 chords? This requires the presence of 3 Hamiltonian cycles with different symmetries. Why all three different symmetry types for DNA and RNA? Could the 20 amino-acids correspond to single symmetry type? Could tRNA codons correspond to two symmetry types?
2. How the 3-chords of dark photons could be played? 3-chord should be a collective effect affecting both dark and ordinary codon by inducing emission of 3-photon state like - like playing a chord by string instrument. The notes of the light chord need not emerge simultaneously but as arpeggios. Could there be a pulse travelling along the Hamiltonian cycle and picking all the cyclotron notes at the vertices containing dark proton and sending a cyclotron

signal along flux tubes to ordinary DNA codon. This pulse would travel along dark DNA and play the music defined by dark DNA sequence.

5.3 Can one imagine a modification of bio-harmony?

The model for how one can understand how 12-note scale can represent 64 genetic codons has the basic property that each note belongs to 16 chords. The reason is that there are 3 disjoint sets of notes and given 3-chord is obtained by taking 1 note from each set. For bio-harmony obtained as union of 3 icosahedral harmonies and tetrahedral harmony note typically belongs to 15 chords. The representation in terms of frequencies requires 16 chords per note.

If one wants consistency one must somehow modify the model of icosahedral harmony. The necessity to introduce tetrahedron for one of the 3 fused harmonies is indeed an ugly looking feature of the model. The question is whether one of the harmonies could be replaced with some other harmony with 12 notes and 24 chords. If this would work one would have 64 chords equal to the number of genetic codons and $5+5+6 = 16$ chords per note. The addition of tetrahedron would not be needed.

One can imagine toric variants of icosahedral harmonies realized in terms of Hamiltonian cycles and one indeed obtains a toric harmony with 12 notes and 24 3-chords. Bio-harmony could correspond to the fusion of 2 icosahedral harmonies with 20 chords and toric harmony with 24 chords having therefore 64 chords. Whether the predictions for the numbers of codons coding for given amino-acids come out correctly for some choices of Hamiltonian cycles is still unclear. This would require an explicit construction of toric Hamiltonian cycles.

5.3.1 Previous results

Before discussing the possible role of toric harmonies some previous results will be summarized.

1. *Icosahedral bio-harmonies*

The model of bio-harmony [L2, L18] starts from a model for music harmony as a Hamiltonian cycle at icosahedron having 12 vertices identified as 12 notes and 20 triangular faces defining the allowed chords of the harmony. The identification is determined by a Hamiltonian cycle going once through each vertex of icosahedron and consisting of edges of the icosahedral tessellation of sphere (analog of lattice): each edge corresponds to quint that is scaling of the frequency of the note by factor $3/2$ (or by factor $2^{7/12}$ in well-tempered scale). This identification assigns to each triangle of the icosahedron a 3-chord. The 20 faces of icosahedron define therefore the allowed 3-chords of the harmony. There exists quite a large number of icosahedral Hamiltonian cycles and thus harmonies.

The fact that the number of chords is 20 - the number of amino-acids - leads to the question whether one might somehow understand genetic code and 64 DNA codons in this framework. By combining 3 icosahedral harmonies with different symmetry groups identified as subgroups of the icosahedral group, one obtains harmonies with 60 3-chords.

The DNA codons coding for given amino-acid are identified as triangles (3-chords) at the orbit of triangle representing the amino-acid under the symmetry group of the Hamiltonian cycle. The predictions for the numbers of DNAs coding given amino-acid are highly suggestive for the vertebrate genetic code.

By gluing to the icosahedron tetrahedron along common face one obtains 4 more codons and two slightly different codes are the outcome. Also the 2 amino-acids Pyl and Sec can be understood. One can also regard the tetrahedral 4 chord harmony as additional harmony so that one would have fusion of four harmonies. One can of course criticize the addition of tetrahedron as a dirty trick to get genetic code.

The explicit study of the chords of bio-harmony however shows that the chords do not contain the 3-chords of the standard harmonies familiar from classical music (say major and minor scale and corresponding chords). Garage band experimentation with random sequences of chords requiring conservability that two subsequent chords have at least one common note however shows that these harmonies are - at least to my opinion - aesthetically feasible although somewhat boring.

2. *Explanation for the number 12 of notes of 12-note scale*

One also ends up to an argument explaining the number 12 for the notes of the 12-note scale [L18]. There is also second representation of genetic code provided by dark proton triplets. The dark proton triplets representing dark genetic codons are in one-one correspondence with ordinary DNA codons. Also amino-acids, RNA and tRNA have analogs as states of 3 dark protons. The number of tRNAs is predicted to be 40.

The dark codons represent entangled states of protons and one cannot decompose them into a product state. The only manner to assign to the 3-chord representing the triplet ordinary DNA codon such that each letter in $\{A, T, C, G\}$ corresponds to a frequency is to assume that the frequency depends on the position of the letter in the codon. One has altogether $3 \times 4 = 12$ frequencies corresponding to 3 positions for given letter selected from four letters.

Without additional conditions any decomposition of 12 notes of the scale to 3 disjoint groups of 4 notes is possible and possible chords are obtained by choosing one note from each group. The most symmetric choice assigns to the 4 letters the notes $\{C, C\#, D, D\#\}$ in the first position, $\{E, F, F\#, G\}$ in the second position, and $\{G\#, A, B\flat, B\}$ in the third position. The codons of type XXX would correspond to $CEG\#$ or its transpose. One can transpose this proposal and there are 4 non-equivalent transposes, which could be seen as analogs of music keys.

Remark: $CEG\#$ between C-major and A-minor very often finishes finnish tango: something neither sad nor glad!

One can look what kind of chords one obtains.

1. Chords containing notes associated with the same position in codon are not possible.
2. Given note belongs to 6 chords. In the icosahedral harmony with 20 chords given note belongs to 5 chords (there are 5 triangles containing given vertex). Therefore the harmony in question cannot be equivalent with 20-chord icosahedral harmony. Neither can the bio-harmony with 64 chords satisfy the condition that given note is contained by 6 3-chords.
3. First and second notes of the chords are separated by at least major third as also those second and third notes. The chords satisfy however octave equivalence so that the distance between the first and third notes can be smaller - even half step - and one finds that one can get the basic chords A-minor scale: Am, Dm, E7, and also G and F. Also the basic chords of F-major scale can be represented. Also the transposes of these scales by 2 whole steps can be represented so that one obtains $A_m, C\#_m, F_m$ and corresponding major scales. These harmonies could allow the harmonies of classical and popular music.

These observations encourage to ask whether a representation of the new harmonies as Hamiltonian cycles of some tessellation could exist. The tessellation should be such that 6 triangles meet at given vertex. Triangular tessellation of torus having interpretation in terms of a planar parallelogram (or perhaps more general planar region) with edges at the boundary suitable identified to obtain torus topology seems to be the natural option. Clearly this region would correspond to a planar lattice with periodic boundary conditions.

5.3.2 Is it possible to have toric harmonies?

The basic question is whether one can have a representation of the new candidate for harmonies in terms of a tessellation of torus having $V = 12$ vertices and $F = 20$ triangular faces. The reading of the article "Equivelar maps on the torus" [A6] (see <http://tinyurl.com/ya6g9kwe>) discussing toric tessellations makes clear that this is impossible. One however have $(V, F) = (12, 24)$ (see <http://tinyurl.com/y7xfromc>). A rather promising realization of the genetic code in terms of bio-harmony would be as a fusion of two icosahedral harmonies and toric harmony with $(V, F) = (12, 24)$. This in principle allows also to have 24 3-chords which can realize classical harmony (major/minor scale).

1. The local properties of the tessellations for any topology are characterized by a pair (m, n) of positive integers. m is the number of edges meeting in given vertex (valence) and n is the number of edges and vertices for the face. Now one has $(m, n) = (6, 3)$. The dual of this tessellation is hexagonal tessellation $(m, n) = (3, 6)$ obtained by defining vertices as centers of the triangles so that faces become vertices and vice versa.

2. The rule $V - E + F = 2(1 - g) - h$, where V , E and F are the numbers of vertices, edges, and faces, relates $V - E - F$ to the topology of the graph, which in the recent case is triangular tessellation. g is the genus of the surface at which the triangulation is im eded and h is the number of holes in it. In case of torus one would have $E = V + F$ giving in the recent case $E = 36$ for $(V, F) = (12, 24)$ (see <http://tinyurl.com/y7xfomc>) whereas in the icosahedral case one has $E = 32$.
3. This kind of tessellations are obtained by applying periodic boundary conditions to triangular lattices in plane defining parallelogram. The intuitive expectation is that this lattices can be labelled by two integers (m, n) characterizing the lengths of the sides of the parallelogram plus angle between two sides: this angle defines the conformal equivalence class of torus. One can also introduce two unit vectors e_1 and e_2 characterizing the conformal equivalence class of torus.

Second naïve expectation is that $m \times n \times \sin(\theta)$ represents the area of the parallelogram. $\sin(\theta)$ equals to the length of the exterior product $|e_1 \times e_2| = \sin(\theta)$ representing twice the area of the triangle so that there would be $2m \times n$ triangular faces. The division of the planar lattice by group generated by $pe_1 + qe_2$ defines boundary conditions. Besides this the rotation group Z_6 acts as analog for the symmetries of a unit cell in lattice. This naïve expectation need not of course be strictly correct.

4. As noticed, it is not possible to have triangular toric tessellations with $(V, E, F) = (12, 30, 20)$. Torus however has a triangular tessellation with $(V, E, F) = (12, 36, 24)$. An illustration of the tessellation can be found at <http://tinyurl.com/y7xfomc>. It allows to count visually the numbers V, E, F , and the identifications of the boundary edges and vertices. With good visual imagination one might even try to guess what Hamiltonian cycles look like.

The triangular tessellations and their hexagonal duals are characterized partially by a pair of integers (a, b) and (b, a) . a and b must both even or odd (see <http://tinyurl.com/y7xfomc>). The number of faces is $F = (a^2 + 3b^2)/2$. For $(a, b) = (6, 2)$ one indeed has $V = 12$ and $F = 24$. From the article [A6] (see <http://tinyurl.com/ya6g9kwe>) one learns that the number of triangles satisfies $F = 2V$ for $p = q$ at least. If $F = 2V$ holds true more generally one has $V = (a^2 + 3b^2)/4$, giving a tight constraints on a and b .

Remark: The conventions for the labelling of torus tessellation vary. The above convention based on integers (a, b) used in the illustrations at <http://tinyurl.com/y7xfomc> is different from the convention based on integer pair (p, q) used in [A6]. In this notation torus tessellation with $(V, F) = (12, 24)$ corresponds to $(p, q) = (2, 2)$ instead of $(a, b) = (6, 2)$. This requires $(a, b) = (3p, q)$. With these conventions one has $V = p^2 + q^2 + pq$.

1. *The number of triangles in the 12-vertex tessellation is 24: curse or blessing?*

One could see as a problem that one has $F = 24 > 20$? Or is this a problem?

1. By fusing two icosahedral harmonies and one toric harmony one would obtain a harmony with $20+20+24 = 64$ chords, the number of DNA codons! One would replace the fusion of 3 icosahedral harmonies and tetrahedral harmony with a fusion of 2 icosahedral harmonies and toric harmony. Icosahedral symmetry with toric symmetry associated with the third harmony would be replaced with a smaller toric symmetry. Note however that the attachment of tetrahedron to a fixed icosahedral face also breaks icosahedral symmetry.

This raises questions. Could the presence of the toric harmony somehow relate to the almost exact $U \leftrightarrow C$ and $A \leftrightarrow G$ symmetries of the third letter of codons. This does not of course mean that one could associated the toric harmony with the third letter. Note that in the ico-tetra model the three harmonies are assumed to have no common chords. Same non-trivial assumption is needed also now in order to obtain 64 codons.

2. What about the number of amino-acids: could it be 24 corresponding ordinary aminoacids, stopping sign plus 3 additional exotic amino-acids. The 20 icosahedral triangles can corresponds to amino-acids but not to stopping sign. Could it be that one of the additional

codons in 24 corresponds to stopping sign and two exotic amino-acids Pyl and Sec appearing in biosystems explained by the icosahedral model in terms of a variant of the genetic code. There indeed exists even third exotic amino-acid! N-formylmethionine (see <http://tinyurl.com/jsphvgt>) but is usually regarded as as a form of methionine rather than as a separate proteinogenic amino-acid.

3. Recall that the problem related to the icoso-tetrahedral harmony is that it does not contains the chords of what might be called classical harmonies (the chords assignable to major and minor scales). If 24 chords of bio-harmony correspond to toric harmony, one could obtain these chords if the chords in question are chords obtainable by the proposed construction.

But is this construction consistent with the representation of 64 chords by taking to each chord one note from 3 disjoint groups of 4 notes in which each note belongs to 16 chords. The maximum number of chords that note can belong to would be $5+5+6=16$ as desired. If there are no common chords between the 3 harmonies the conditions is satisfied. Using for instance 3 toric representations the number would be $6+6+6=18$ and would require dropping some chords.

4. The earlier model for tRNA as fusion of two icosahedral codes predicting $20+20=40$ tRNA codons. Now tRNAs as fusion of two harmonies allows two basic options depending on whether both harmonies are icosahedral or whether second harmony is toric. These options would give $20+20=40$ or $20+24=44$ tRNAs. Wikipedia tells that maximum number is 41. Some sources however tell that there are 20-40 different tRNAs in bacterial cells and as many as 50-100 in plant and animal cells.

2. A more detailed model for toric harmonies

One can consider also more detailed model for toric harmonies.

1. The above discussed representation in terms of frequencies assigned with nucleotides depending on their position requires the decomposition of the notes to 3 disjoint groups of 4 notes. This means decomposition of 12 vertices of Hamiltonian cycle to 4 disjoint groups such that within given group the distances between the members of group are larger than one unit so that they cannot belong to same triangle. There are $Bin(12, 4) \times Bin(8, 4)$ decomposition to 3 disjoint groups of for vertices, where $Bin(n, k) = n!/(n-k)!k!$ is binomial coefficient.
2. Once the Hamiltonian cycle has been fixed and is one assumes that single step along cycle corresponds to quint, one knows what the notes associated with each vertex is and given the note of the 12-note scale one knows the number $0 \leq n < 12$ of quint steps needed to obtain it. For instance, for the proposed grouping $\{C, C\#, D, D\#\}$ and its two transposes by 2 hole steps one can assign 4 integers to each group. The condition is that within each group the notes labelled by the integers have minimum distance of 2 units between themselves.
3. One could try to understand the situation in terms of the symmetries of the system.
 - (a) Could the triplet $\{C, E, G\#\}$ and its four translates be interpreted as Z_3 orbits. Could suitable chosen members from 4 disjoint quartets quite general form Z_3 orbits.
Remark: Particle physicists notes the analogy with 4 color triplets formed by u and d quarks having spin 1/2. Z_4 would correspond to spin and color spin and Z_3 to color.
 - (b) Z_4 acts as symmetries of the tessellation considered and these symmetries respect distances so that their action on a quartet with members having mutual distances larger than unit creates new such quartet. Could the triplet $\{C, E, G\#\}$ and its four translates by an n -multiple of half note, $n = 0, 1, 2, 3$ correspond to an orbit Z_4 ?
 Could the groups of 4 notes quite generally correspond to the orbits of Z_4 ? This can be true only if the action of non-trivial Z_4 elements relates only vertices with distance larger than one unit.
4. The group of isometries of the toric triangulation acts as symmetries. $Z_{24} = Z_6 \times Z_4$ is a good candidate for this group. Z_6 corresponds to the rotations of around given point of

triangulation and should leave the tessellation invariant. The orbit of given triangle defining the set of DNA codons coding the amino-acid represented by the orbit would correspond to orbit of subgroups of Z_{24} . Only orbits containing orbits containing 1, 2, 3, 4 or 6 triangles are allowed by the degeneracies of the genetic code. These numbers would correspond to degeneracies that is the numbers of codons coding for given amino-acid. All these numbers appear as degeneracies.

3. What one can say about toric Hamiltonian cycles?

First some basic notions are in order. The graph is said to be equivelar if it is a triangulation of a surface meaning that it has 6 edges emanating from each vertex and each face has 3 vertices and 3 edges [A6]. Equivelarity is equivalent with the following conditions;

1. Every vertex is 6-valent.
2. The edge graph is 6-connected.
3. The graph has vertex transitive automorphism group.
4. The graph can be obtained as a quotient of the universal covering tessellation (3,6) by a sublattice (subgroup of translation group). 6-connectedness means that one can decompose the tessellation into two disconnected pieces by removing 6 or more vertices
5. Edge graph is n -connected if the elimination of $k < n$ vertices leaves it connected. It is known that every 5-connected triangulation of torus is Hamiltonian [A7] (see <http://tinyurl.com/y7cartk2>). Therefore also 6-connected $(6, 3)_{p=2, q=2}$ tessellation has Hamiltonian cycles.
6. The Hamiltonian cycles for the dual tessellation are not in any sense duals of those for the tessellation. For instance, in the case of dodecahedron there is unique Hamiltonian cycle and for icosahedron has large number of cycles. Also in the case of $(6, 3)$ tessellations the duals have different Hamilton cycles. In fact, the problem of constructing the Hamiltonian cycles is NP complete.

Can one say anything about the number of Hamiltonian cycles?

1. For dodecahedron only 3 edges emanates from a given vertex and there is only one Hamiltonian cycle. For icosahedron 5 edges emanate from given vertex and the number of cycles is rather large. Hence the valence and also closely related notion of n -connectedness are essential for the existence of Hamilton's cycles. For instance, for a graph consisting of two connected graphs connected by single edge, there exist no Hamilton's cycles. For toric triangulations one has as many as 6 edges from given vertex and this favors the formation of a large number of Hamiltonian cycles.
2. Curves on torus are labelled by winding numbers (M, N) telling the homology equivalence class of the cycle. M and N can be any integers. Curve winds M (N) times around the circle defining the first (second) equivalence homology equivalence class. Also Hamiltonian cycles are characterized by their homology equivalence class, that is pair (M, N) of integers. Since there are only $V = 12$ points, the numbers (M, N) are finite. By periodic boundary conditions means that the translations by multiples of $2e_1 + 2e_2$ do not affect the tessellation (one can see what this means geometrically from the illustration at <http://tinyurl.com/y7xfrcmc>). Does this mean that (M, N) belongs to $Z_2 \times Z_2$ so that one would have 4 homologically non-equivalent paths.

Are all four homology classes realized as Hamiltonian cycles? Does given homology class contain several representatives or only single one in which case one would have 20 non-equivalent Hamiltonian cycles?

It turned out that there exist programs coding for an algorithm for finding whether given graph (much more general than tessellation) has Hamiltonian cycles. Having told to Jebin Larosh about the problem, he sent within five minutes a link to a Java algorithm allowing to show whether a given graph is Hamiltonian (see <http://tinyurl.com/y7y9tr5t>): sincere thanks to Jebin! By a suitable modification this algorithm find all Hamiltonian cycles.

1. The number N_H of Hamiltonian cycles is expected to be rather large for a torus triangulation with 12 vertices and 24 triangles and it is indeed so: $N_H = 27816!$ The image of the tessellation and the numbering of its vertices are described in figure below (see **Fig. 1**). Incide matrix A characterizes the graph: if vertices i and j are connected by edge, one has $A_{ij} = A_{ji} = 1$, otherwise $A_{ij} = A_{ji} = 0$ and is used as data in the algorithm finding the Hamiltonian cycles.

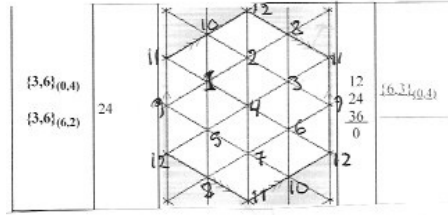


Figure 1: The number of the vertices of $(V, F) = 12, 24$ torus tessellation allowing path $(0, 1, 2, 3, 4, 6, 5, 8, 10, 7, 11, 9, 0)$ as one particular Hamiltonian cycle.

The cycles related by the isometries of torus tessellation are however equivalent. The guess is that the group of isometries is $G = Z_{2,refl} \times (Z_{4,tr} \times Z_{n,rot})$. $Z_{n,rot}$ is a subgroup of local $Z_{6,rot}$. A priori $n \in \{1, 2, 3, 6\}$ is allowed.

On basis of [A6] I have understood that one has $n = 3$ but that one can express the local action of $Z_{6,rot}$ as the action of the semidirect product $Z_{2,refl} \times Z_{3,rot}$ at a point of tessellation (see <http://tinyurl.com/ya6g9kwe>). The identity of the global actions $Z_{2,refl} \times Z_{3,rot}$ and $Z_{6,rot}$ does not look feasible to me. Therefore $G = Z_{2,refl} \times (Z_{4,tr} \times Z_{3,rot})$ with order $ord(G) = 24$ will be assumed in the following (note that for icosahedral tessellation one has $ord(G) = 120$ so that there is symmetry breaking).

Z_4 would have as generators the translations e_1 and e_2 defining the conformal equivalence class of torus. The multiples of $2(e_1 + e_2)$ would leave the tessellation invariant. If these arguments are correct, the number of isometry equivalence classes of cycles would satisfy $N_{H,I} \geq N_H/24 = 1159$.

2. The actual number is obtained as sum of cycles characterized by groups $H \subset Z_{12}$ leaving the cycle invariant and one can write $N_{H,I} = \sum_H (ord(H)/ord(G))N_0(H)$, where $N_0(H)$ is the number of cycles invariant under H .

What can one say about the symmetry group H for the cycle?

1. Suppose that the isometry group G leaving the tessellation invariant decomposes into semi-direct product $G = Z_{2,refl} \times (Z_{4,tr} \times Z_{3,rot})$, where $Z_{3,rot}$ leaves invariant the starting point of the cycle. The group H decomposes into a semi-direct product $H = Z_{2,refl} \times (Z_{m,tr} \times Z_{3,rot})$ as subgroup of $G = Z_{2,refl} \times (Z_{4,tr} \times Z_{3,rot})$.
2. $Z_{n,rot}$ associated with the starting point of cycle must leave the cycle invariant at each point. Applied to the starting point, the action of H , if non-trivial - that is $Z_{3,rot}$, must transform the outgoing edge to incoming edge. This is not possible since Z_3 has no idempotent elements so that one can have only $n = 1$. This gives $H = Z_{2,refl} \times (Z_{m,tr}$. $m = 1, 2$ and $m = 4$ are possible.
3. Should one require that the action of H leaves invariant the starting point defining the scale associated with the harmony? If this is the case, then only the group $H = Z_{2,refl}$ would remain and invariance under Z_{refl} would mean invariance under reflection with respect to the axis defined by e_1 or e_2 . The orbit of triangle under $Z_{2,refl}$ would consist of 2 triangles always and one would obtain 12 codon doublets instead of 10 as in the case of icosahedral code.

If this argument is correct, the possible symmetry groups H would be Z_0 and $Z_{2,refl}$. For icosahedral code both Z_{rot} and $Z_{2,refl}$ occur but $Z_{2,refl}$ does not occur as a non-trivial factor of H in this case.

The almost exact $U \leftrightarrow C$ and $A \leftrightarrow G$ symmetry of the genetic code would naturally correspond to $Z_{2,refl}$ symmetry. Therefore the predictions need not change from those of the icosahedral model except that the 4 additional codons emerge more naturally. The predictions would be also essentially unique.

4. If H is trivial Z_1 , the cycle would have no symmetries and the orbits of triangles would contain only one triangle and the correspondence between DNA codons and amino-acids would be one-to-one. One would speak of disharmony. Icosahedral Hamiltonian cycles can also be of this kind. If they are realized in the genetic code, the almost exact $U \leftrightarrow C$ and $A \leftrightarrow G$ symmetry is lost and the degeneracies of codons assignable to 20+20 icosahedral codons increase by one unit so that one obtains for instance degeneracy 7 instead of 6 not realized in Nature.

What can one say about the character of toric harmonies on basis of this picture.

1. It has been already found that the proposal involving three disjoint quartets of subsequent notes can reproduce the basic chords of basic major and minor harmonies. The challenge is to prove that it can be assigned to some Hamiltonian cycle(s). The proposal is that the quartets are obtained by Z_{rot}^3 symmetry from each other and that the notes of each quartet are obtained by $Z_{4,tr}$ symmetry.
2. A key observation is that classical harmonies involve chords containing 1 quint but not 2 or no quints at all. The number of chords in torus harmonies is $24 = 2 \times 12$ and twice the number of notes. The number of intervals in turn is 36, 3 times the number of the notes. This allows a situation in which each triangle contains one edge of the Hamiltonian cycle so that all 3-chords indeed have exactly one quint.
3. By the above argument harmony possesses Z_2 symmetry or no symmetry at all and one has 12 codon doublets. For these harmonies each edge of cycle is shared by two neighboring triangles containing the same quint. A possible identification is as major and minor chords with same quint. The changing of the direction of the scale and the reflection with respect to the edges the Hamiltonian cycle would transforms major chords and minor chords along it to each other and change the mood from glad to sad and vice versa.

The proposed harmony indeed contains classical chords with one quint per chord and for $F, A, C\sharp$ both minor and major chords are possible. There are 4 transposes of this harmony.

4. Also Hamiltonian cycles for which n triangles contain two edges of Hamiltonian path (CGD type chords) and n triangles contain no edges. This situation is less symmetric and could correspond to a situation without any symmetry at all.
5. One can ask whether the classical harmonies corresponds to 24 codons assignable to the toric harmony and to the 24 amino-acids being thus realizable using only amino-acids. If so, the two icosahedral harmonies would represent kind of non-classical exotics.

5.3.3 Appendix: Some facts about toric tessellations

Genus $g = 1$ (torus) is unique in that it allows infinite number of tessellations as analogs of planar lattices with periodic boundary conditions. $g = 0$ allows only Platonic solids as tessellations and $g > 1$ allows very few tessellations. The article [A6] gives a nice review about toric tessellations.

1. Toric tessellations correspond to tessellations of plane by periodic boundary conditions. Torus tessellation allows a universal covering identifiable as counterpart of infinite lattice in plane. There are infinite number of coverings of given tessellation labelled by two integers (m, n) since the homology group of torus is $Z \times Z$. The tessellation is obtained by dividing $Z \times Z$ by its normal subgroup. Also the rotation group Z_6 acts as group leaving the tessellation invariant and correspond to the rotation leaving invariant the lattice cell consisting of 6 vertices around given vertex.

2. The tessellation is called decomposable if there is a k -sheeted covering map (map corresponds to a collection of charts) characterized by the subgroup of the isometries of the covering of the tessellation which corresponds to a sub-tessellation. This subgroup is characterized by a pair (p, q) of integers being generated by the translation $pe_1 + qe_2$ and $2\pi/6$ rotation. The unit vectors can be chosen to be $e_1 = (1, 0)$ and $e_2 = (1, \sqrt{3})/2$ for triangular tessellation (presumably this tessellation is regular tessellation with the conformal equivalence class of torus fixed by the angle between e_1 and e_2). Line reflection transforms $(3, 6)_{p,q}$ to $(3, 6)_{q,p}$ (see Fig 1 of <http://tinyurl.com/ya6g9kwe>). The tessellation is invariant under reflections - regular - if $pq(p - q) = 0$. The peculiar looking form of the conditions follows from the identity $(3, 6)_{q,p} = (3, 6)_{p+q, -q}$ (also $p = 0$ or $q = 0$ is possible) Note that the tessellation $(3, 6)_{2,2}$ is invariant under reflection and thus non-chiral.
3. The number V of vertices of the triangular tessellation is given by $V = p^2 + q^2 + pq$. The regular tessellation $(p, q) = (2, 2)$ has 12 vertices and is the interesting one in the recent case. It is the smallest regular tessellation. For given (p, q) one can have several non-equivalent pairs (p, q) defining combinatorially non-equivalent tessellations. My interpretation is that they correspond to different conformal equivalence classes for torus: the intuitive expectation is that this should not affect the topology of tessellation nor Hamiltonian cycles. For $(6, 3)_{p,q} = (6, 3)_{2,2}$ with s ($V = 12, F = 24$) there are $1+6 = 7$ combinatorially non-equivalent tessellations: one non-chiral and 6 chiral ones.

Quite generally, the tessellations with V vertices with $V \bmod 4 = 0$ (as in the case of $V = 12$) allow one map (chart consisting of faces) with isotropy group of order 2 and 6 maps with isotropy group of order 4. These variants are labelled by an $SL(2, Z)$ matrix $(a, b; 0, c)$ with determinant equal to $V = ac$. For $V = 12$ one has decompositions $12 = 1 \times 12, 12 = 2 \times 6, 12 = 3 \times 4$. $-c < b < a - c$ is unique modulo a . In the recent case one has $ac = 12$ allowing $(a, c) \in \{(1, 12), (2, 6), (3, 4)\}$ and pairs obtained by permuting a and c . These matrices need not define combinatorially different tessellations since modular transformations generate equivalent matrices.

5.4 Icosa-tetrahedral and icoso-dodecahedral bioharmonies as candidates for genetic code

Both the icoso-tetrahedral [L2] and icoso-dodecahedral harmony to be discussed below can be considered as candidates for bio-harmony as also the harmony involving fusion of 2 icosahedral harmonies and toric harmony [L13]. The basic reason is that the third harmony corresponds to doublets. One cannot exclude the possibility of several equivalent representations of the code.

5.4.1 Icosa-tetrahedral harmony

Icosahedral harmonies can be characterized by a subgroup of icosahedral isometries A_5 having 60 elements. If reflections are included the isometry group, one has $A_5 \times Z_2$ with 120 elements. The group of symmetries is Z_6, Z_4 , or Z_2 . There are two choices for Z_2 and the interpretation has been that Z_2 correspond to either reflection or rotation by π . A_5 however allows also $Z_2 \times Z_2$ as subgroup. AAs correspond to orbits of the symmetry group and DNA codons coding for the AA correspond to triangles (3-chords) at the orbit. In purely icosahedral model one obtains $20+20+20$ codons. A fusion with tetrahedral harmony gives 64 codons.

1. Z_6 gives rise to 3 AAs coded by 6 codons each (leu, se, arg) and 2 AAs coded by 2 codons: the choice of the doublet would require additional conditions. One option is ile doublet.
2. Depending on whether one includes reflection or not, one can have either $Z_4 \subset A_5$ ($60 = 4 \times 15$) or $Z_4 = Z_{2,rot} \times Z_2 \subset A_5 \times Z_2$. I have assumed that $Z_4 = Z_{2,rot} \times Z_2$ but the recent argument suggests the first option. This does not have any implications for the earlier model. Icosahedral Z_4 gives rise to 5 AAs coded by 4 codons each ($5 \times 4 = 20$). This leaves 11 AAs and 3 "empty" AA formally coded by stop codons.
3. Icosahedral Z_2 gives rise to 10 doublets. These 4-plets would correspond to (phe, tyr, his, gln, asn, lys, asp, glu, cys, stop-doublet) This leaves (stop, trp) doublet and (ile, met) doublet with broken Z_2 symmetry.

The fusion with tetrahedral code with 4- codons and 4 AAs should explain these 4 AAs. Tetrahedral isometries form group S_3 and reduce to group Z_3 for tetrahedral cycle.

- (a) One could argue that ile-triplet and met correspond to 3-element orbits with 1-element orbit. (stop, trp) would be formed by Z_2 symmetry breaking from trp doublet and there is no obvious mechanism for this.
- (b) If one tetrahedral face is fixed as a face shared with icosahedron, the symmetry group of tetrahedral cycle reduces to Z_1 . This would give 4 singlets identifiable as (ile, met) and (stop, trp) symmetry broken doubles. Since ile appears also in doublet, tetrahedral 1-orbit and icosahedral 2-orbit must have a common doubled triangle identifiable as the common face of icosahedron and tetrahedron. The doubling of the common triangle replaces ile-doublet with ile-triplet. This option looks rather reasonable.

5.4.2 Dodecahedral harmony

Dodecahedral harmony correspond to the unique Hamilton cycle at dodecahedron. Dodecahedral harmony as 20 notes and 12 5-chords. If one assumes that the octave divides to 20 notes, this brings in mind “eastern” view about harmony.

The obvious objection against dodecahedral harmony is that dodecahedral faces are pentagons so that dodecahedral chords would be 5- rather than 3-chords so that the correspondence between chords and DNA codons would be lost. The situation changes if 3 notes - 3-chord - determine the 5-chord completely and one can assign a unique 3-chord to each pentagon. This is indeed the case!

1. 3-edges meet in every dodecahedral vertex (this makes the dodecahedral cycle unique apart from rotations) and each edge pair in the vertex belongs to same pentagon (in the case of icosahedron there are 5 edges per vertex so that this is not true). Therefore each pentagon must contain at least 2 edges of Hamilton’s cycle.

The cycle must visit all vertices of pentagon, and the visit to the vertex means that the cycle shares at least one edge with pentagon. Since all vertices of the pentagon must be visited, there are two options. For option a) given pentagon shares with the cycle disjoint 2-edge with 3 vertices and 1-edge with two vertices. For option b) the pentagon shares with the cycle 4-edge with 5 vertices.

2. The numbers n_a of pentagons with 4-edges and $n_b = 12 - n_a$ 2-edge+ 1-edge (making 3 edges) can be deduced easily. Cycle has 20 edges. Pentagon of type a) shares 3 edges with the cycle and the edge is shared by 2 pentagons. This gives $3n_a/2$ edges. Pentagon of type b) shares 4 edges with the cycle. This gives $2n_b = 2(12 - n_a)$ edges. The total number of edges is $3n_a/2 + 2n_b = 20$, which gives $n_a = 8$ and $n_b = 4$. Dodecahedral Hamilton’s cycle can be found from web (see <http://tinyurl.com/y5woajcb>). The structure is as deduced here.

For case a) the 3-chords correspond naturally to the 3 vertices of the 2-edge shared with the cycle. Therefore it is possible to assign unique 3-chords to the dodecahedral harmony and to obtain connection with codons in this case. One however obtains also 12 2-chords: could they have some genetic counterpart?

What about 5-chords for pentagons of type b)? Hamiltonian cycle can be oriented and this induces orientation of the pentagons. One can say that the first vertex in the 4-edge is the vertex at which cycle arrives to the pentagon and identify the 3-chord as the first three vertices. It turns out that for the replacement of quint cycle this is not actually necessary.

5.4.3 Is icosadodecahedral harmony consistent with the genetic code?

One must check whether icosadodecahedral harmony is consistent with the degeneracies of the genetic code.

1. A fusion of 2 icosahedral harmonies and 2 copies of dodecahedral harmony would be in question. As in the case of icosahedral harmony already discussed, the two icosahedral harmonies would have symmetry groups Z_6 and Z_4 and give the codons coding for 3 6-plets and 1 doublet+ 5 4-plets + two copies of dodecahedral harmony.

- Can the model predict correctly the numbers of codons coding for AAs? It is known that dodecahedral Hamilton cycle divides dodecahedron to two congruent pieces related by Z_2 symmetry (see <http://tinyurl.com/yy6pcogt>). Also the Hamiltonian cycle defining the common boundary has Z_2 symmetry. A good guess is that these Z_2 's corresponds to reflection symmetry and rotation by π but I am not able to exclude $Z_4 \subset G_0$, where G_0 consists of 60 orientation preserving isometries. In this case some orbits - presumably all 3 of them - could contain 4 pentagons. This is not consistent with the condition that one has doublets and singlets.

If the second symmetry corresponds to reflection, it can be excluded by simply assuming that reflections change the orientation of the cycle.

- Rotation by π has two fixed points corresponding to opposite poles so that one has 5 2-orbits and 2 1-orbits giving 12 triangles for each copy. Two copies of dodecahedral harmony would give $5+5=10$ doublets and $2+2=4$ singlets. A possible interpretation would be as (ile,met) and (stop,trp).

Consider now objections against dodecahedral harmony.

- Why two copies of dodecahedral code? What distinguishes between them? If imirror symmetry leaves the cycle invariant apart from orientation the copies could be mirror images and consist of same faces. The second option is that they related by a rotation?
- The number of dodecahedral AAs is 24 rather than 20. Could the additional 4 AAs as orbits have interpretation as AAs in some sense. Could the "empty" AAs coded by stop codons be counted as AAs exceptional in some sense. In TGD framework one can consider the possibility that although AA is "empty", there is analog of AA as physical signature for the end of protein telling what stopping codon it corresponds. The magnetic body of protein is a good candidate.

Genetic code has several slightly differing variants. Could the 2 additional exotic AAs Pyl and Sec correspond in some situations to the additional AAs?

- Essential for the bio-harmony as a fusion of harmonies is that one can select from each orbit single face as a representative of the AA it codes - kind of gauge choice is in question - and that the orbits corresponding to different AAs can be chosen to be disjoint. Otherwise codons belonging to the orbits of different Hamilton cycles can code for the same AA if the AA can be chosen to be in intersection. If not, the same codon can code for 2 different AAs - this can indeed occur in reality [L17]!

The condition that orbits of different cycles do not intersect seems quite stringent but has not been proven. But what if it is actually broken? Indeed, in the case of icosahedral harmony with Z_1 symmetry tetrahedron and icosahedron could have common a doubled face the breaking of this condition would geometrically explain why ile belongs to both icosahedral and tetrahedral orbit.

Ile is the problem also in the case if icoso-dodecahedral harmony. Dodecahedral singlet codes for ile as also icosahedral doublet. Could one talk about doubling of ile face so that it corresponds to a pair of triangle and pentagon (in 1-1 correspondence with triangle as chord).

- The two copies of the dodecahedral code should correspond to 5 doublets and 2 singlets each. One expects that together they give rise to $10+2+10+2=24$ faces. Do they? Mirror symmetry and rotation by π act as symmetries of the cycle so that neither can map the two cycles to each other. Dodecahedral (equivalently icosahedral) rotations give rise to new equivalent cycles. The action on pentagons corresponds to the action on vertices of icosahedron so that it easy to understand what happens.

Each symmetry corresponds to a rotation around some axis and has opposite icosahedral vertices at this axis as fixed points. Hence any two cycles obtained in this manner have 2 common pentagons. This means reduction $24 \rightarrow 22$ unless one interprets the situation in terms doubled faces? Could the disappearing doublet correspond to stop-doublet? What about the remaining stop of the vertebrate code pairing with trp? Why does second singlet correspond to empty AA and not something else such as exotic AA.

C	G	D	A	E	H	F+	C+	G+	D+	B-	F
C	F	B \flat	D+	G+	C+	F+	H	E	A	D	G

Table 7: Inversion of the scale leaving C (and also $F\sharp$) invariant.

M, 0	m, 0	sus4, 0	aug, 0	4, 0	9, 0	4+, 0	9-, 0	6-, 0	maj7, 0
m, 11	M, 11	sus, 0	aug, 0	4, 0	9, 10	9-, 11	4+, 11	maj7, 11	6-, 11
6, 0	7, 0	ex1, 0	ex2, 0	ex3, 0	ex4, 0	ex5, 0	ex6, 0	ex7, 0	ex8, 0
7, 11	6, 11	ex1, 10	ex3, 3	ex2, 3	ex4, 8	ex6, 8	ex5, 80	ex8, 6	ex7, 6

Table 8: Table gives the transformation of inversion leaving C invariant on the basic chords having C as basic note.

- There is also further problem. Suppose that an intersection of orbits takes place at single triangle. Suppose that one cannot choose this triangle to be “AA” triangle for both orbits. In this case it is not clear to which AA the codon codes. This kind of phenomenon actually takes place in some cases and is known as homonymy [L17]. It is associated with the deviations of the code from the vertebrate code and involves exotic AAs Pyl and Sec. Codons can serve as a stop codon or code for an exotic AA.

Clearly, the notion of bio-harmony involves many unclear aspects but my strong feeling is that there is very beautiful mathematics involved.

6 Appendix

6.1 Chord tables for some harmonies and their inverses

The formula for inversion of the harmonic keeping note X as fixed can be represented as a product of translation taking X to C , inversion keeping C fixed, and translation taking C back to X . The inversion maps the chord having C as basic note to its mirror image so that the order of notes can change and basic note can change. For instance, the major chord $CM = CEG$ goes to minor chord $CG\sharp F = Fm$ so that $k = 0$ goes to $k \equiv \Delta k_{inv} = 11$. This delicacy must be taken into account. If X remains fixed inversion is just the transformation

$$k \rightarrow k_{inv} = (2 \times k(X) - \Delta k_{inv}) \text{ mod } 12 . \quad (6.1)$$

Table 7 gives the inversion of the scale leaving C (and also $F\sharp$) invariant: The inversion for the types of the chords does not depend on the basic note as is clear from the distance preserving character of the inversion. **Table 8** gives the inversion of for the types of the chords leaving C fixed. The elements of the rows give the type of the chord and the number of quints k corresponding to it. For chords having C as basic note one has $k = 0$. It is easy to deduce the transformation formula in more general case from the table.

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

6.2 Calculation of incidence matrices

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

ro6	iro6	re41	ire41	re42	ire42	ro21	iro21
F.aug	F.aug	D.7	A.6	C.ex3	A.ex2	E.m	F.M
G.aug	D+.aug	D.6	A.7	E.ex2	F.ex3	B-.m	B.M
C.m	F.M	G+.7	D+.6	F+.ex3	D+.ex2	C.m	A.M
D.m	D+.M	G+.6	D+.7	B-.ex2	B.ex3	F+.m	D+.M
E.m	C+.M	G.4+	E.9-	D.maj7	B.6-	G.6	D.7
F+.m	B.M	A.9-	D.4+	E.9-	A.4+	C+.6	G+.7
G+.m	A.M	C+.4+	B-.9-	A.7	E.6	A.6	C.7
B-.m	G.M	D+.9-	G+.4+	A.6	E.7	D+.6	F+.7
F.6	C.7	E.maj7	G.6-	G+.maj7	F.6-	D.4+	G.9-
G.6	B-.7	G.maj7	E.6-	B-.9-	D+.4+	G+.4+	C+.9-
A.6	G+.7	B-.maj7	C+.6-	D+.7	B-.6	B.4+	B-.9-
B.6	F+.7	C+.maj7	B-.6-	D+.6	B-.7	F.4+	E.9-
C+.6	E.7	C.9-	B.4+	F.9	D+.9	C.maj7	A.6-
D+.6	D.7	A.9-	D.4+	C.9	G+.9	F+.maj7	D+.6-
C.9	C.9	F+.9-	F.4+	G.9	C+.9	G.6-	D.maj7
D.9	B-.9	D+.9-	G+.4+	E.9	E.9	C+.6-	G+.maj7
E.9	G+.9	B.9	G.9	B.9	A.9	D.9	D.9
F+.9	F+.9	E.9	D.9	F+.9	D.9	G+.9	G+.9
G+.9	E.9	F.9	C+.9	C+.9	G.9	E.9	C.9
B-.9	D.9	B-.9	G+.9	B-.9	B-.9	B-.9	F+.9

Table 9: Pairs “X” and “iX” of columns give the chords of the bio-harmonies and their inversions depicted in figures ??, ??, ??, ??.

ro22	iro22	ro23	iro23	re21	ir21	re22	ir22
A.ex4	G.ex4	A.ex2	B-.ex3	F+.ex3	D+.ex2	D.ex4	E.ex4
D+.ex2	C.ex3	H.ex8	B-.ex7	H.ex4	B-.ex4	H.ex4	F+.ex4
A.m	B-.M	D+.ex2	E.ex3	A.m	E.M	F.M	E.m
D+.m	E.M	F.ex8	F.ex7	D+.M	B-.m	F.m	E.M
G.9-	C.4+	D.7	A.6	A.6	E.7	C.6-	A.maj7
C+.9-	F+.4+	G+.7	D+.6	D+.7	B-.6	B-.maj7	B.6-
C.4	C.4	A.maj7	D.6-	D.7	B.6	C.9-	A.4+
F+.4	F+.4	D+.maj7	G+.6-	B-.6	D+.7	D.7	G.6
E.4+	D+.9-	A.4+	D.9-	G.6-	F+.maj7	G+.6	C+.7
B-.4+	A.9-	D+.4+	G+.9-	F.maj7	G+.6-	G.maj7	D.6-
D.maj7	F.6-	E.7	G.6	D.4+	B.9-	D+.6-	F+.maj7
G+.maj7	B.6-	B-.7	C+.6	B-.9-	D+.4+	C+.4	C+.4
B.maj7	G+.6-	B-.9	G+.9	G+.4+	F.9-	A.4+	C.9-
F.maj7	D.6-	G.9	B.9	E.9-	A.4+	E.4+	F.9-
C.9	D.9	C+.9	F.9	C.9	G+.9	F+.6	D+.7
F+.9	G+.9	A.9	A.9	F.9	D+.9	D+.9	C+.9
A.9	F.9	B.9	G.9	B.9	A.9	C+.9	D+.9
D+.9	B.9	F.9	C+.9	F+.9	D.9	E.9	C.9
D.9	C.9	E.9	D.9	E.9	E.9	B.9	F.9
G+.9	F+.9	D+.9	D+.9	C+.9	G.9	D+.9	C+.9

Table 10: Pairs “X” and “iX” of columns give the chords of the bio-harmonies and their inversions depicted in figures ??, ??, ??, ??.

re23	ire23	re24	ire24	re25	ire25		
F.ex1	F.ex1	H.ex3	G.ex2	F+.ex2	F.ex3		
D+.ex3	G+.ex2	E.ex7	F+.ex8	F.ex3	F+.ex2		
G+.ex1	D.ex1	D.7	A.6	F.M	B-.m		
A.ex2	D.ex3	G+.6	D+.7	B-.m	F.M		
E.7	B.6	G-.M	B.m	C.7	D+.6		
E.6	B.7	D+.m	G+.M	G+.6	G.7		
A.maj7	F+.6-	F.M	F+.m	A.maj7	F+.6-		
B.9-	E.4+	F.m	F+.M	B.9-	E.4+		
G.M	G+.m	C.6-	B.maj7	E.6	B.7		
C+.m	D.M	B-.maj7	C+.6-	E.7	B.6		
D.7	C+.6	A.9-	D.4+	G.M	G+.m		
F+.6	A.7	C+.4+	B-.9-	C+.m	D.M		
B-.9	C.9	E.7	G.6	D.7	C+.6		
D.9	G+.9	F+.6	F.7	B.6	E.7		
B.9	B.9	C.9	F+.9	D+.9	G.9		
C.9	B-.9	D+.9	D+.9	C.9	B-.9		
F.9	F.9	D.9	E.9	C+.9	A.9		
G+.9	D.9	C+.9	F.9	B-.9	C.9		
D+.9	G.9	E.9	D.9	D.9	G+.9		
C+.9	A.9	B.9	G.9	H.9	B-.9		

Table 11: Pairs “X” and “iX” of columns give the chords of the bio-harmonies and their inversions depicted in figures ??, ??, ??.

- Incidence matrices can be computed by using expressions of chords as sets of three notes (possible in Python) and just counting the number of common notes defining the value of the element of the incidence matrix. The quint distance between the chords vanishes if they have common notes. More general incidence matrices would correspond to a larger quint distance.
- In the case of genetic code and amino-acids one Hamilton cycle from each class labelled by Z_n , $n \in \{6, 4, 2\}$ is involved.
 - There are $N = 1 \times 3 \times 8 = 24$ cycle combinations if one does not allow the inverse harmonies. Allowing them gives $N = 8 \times 24$ combinations. If transitions between all representations are possible, there are $M = N^2$ 20×20 -dimensional incidence matrices to be calculated for the icosahedral restriction of the code. Incidence matrices are symmetric so that only $D(D+1)/2 = 20(20+1)/2 = 210$ independent matrix elements need to be calculated for given 20×20 -D incidence matrix.
 - Equivalently, one can calculate the incidence matrix for a space with $N \times 20$ points which is Cartesian product of N amino-acid spaces with 20 points. N has values 24 and 8×24 . Remarkably, the magic number 24 of also stringy mathematics appears.
 - If the transitions can be restricted to single triplet of cycles, one must calculate 6 20×20 -dimensional incidence matrices. This situation could be realistic for portions of the genetic code if the transitions between different cycle triplets are analogous to phase transitions. The number of incidence matrices (one can also use single 60×60 incidence matrix) is still reasonably small and can be documented in written form. In a model for random chord sequences one must specify the probabilities for the transitions between chords with different n for Z_n . Simplest starting point assumption is that the probabilities are identical.
- For the extended genetic code the most natural assumption is that the extension of the code to icoso-tetrahedral code take places place only in Z_2 sector meaning the extension of amino-acid space by 4 amino-acids and the increase of the number of DNA codons from 60 to 64. There are two kinds of transitions between icosahedral and tetrahedral codons. Tetrahedral codon can correspond to a codon, which is outside the icosahedron having at least one common vertex with the icosahedral codon: this allows 3+3 transitions. Tetrahedral codon can correspond also to punct. Unless the codon/amino-acid contains at least one of

these notes, it cannot precede stopping codon. These chords extend the harmony by the counterparts of CM and Am and punct corresponds to $C6 = CGA$.

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

6.3 Simulation of harmonic DNA sequence

The following sequence represents a random harmonic sequence based on zero quint distance between neighboring chords (at least one common note). The harmony is combination 3 harmonies ??, ??, and ?? extended by adding chords Bb , Gm and $G7$ and associated $Bb6$ representing stopping codon and punct in tetra- icosahedral code and Sec or Pyl in their unfused variants. These three harmonies correspond to groups of 20, 20, and 24 DNA codons at orbits of Z_6 , Z_4 , and Z_2 which is now taken to be Z_2^{refl} . To deduce DNA sequence one must assume detailed correspondence between the codons at the orbits and corresponding chords.

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

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

6.4 Illustrations of icosahedral Hamiltonian cycles with symmetries

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

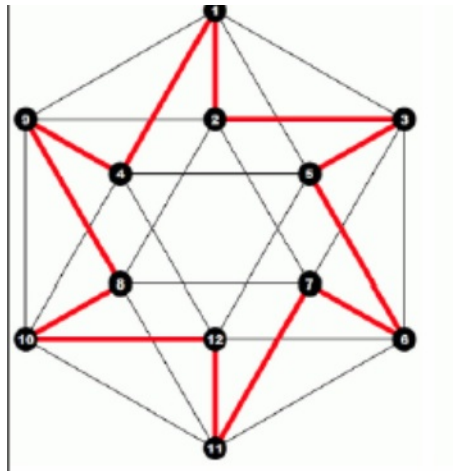


Figure 2: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 6-fold rotation symmetry acting shifts generated by a shift of 2 quints.

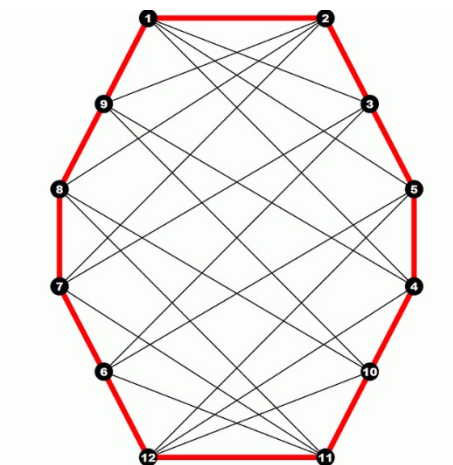


Figure 3: $(n_0, n_1, n_2) = (0, 16, 4)$ Hamiltonian cycle with 4 reflection symmetries generated by reflections in vertical and horizontal directions.

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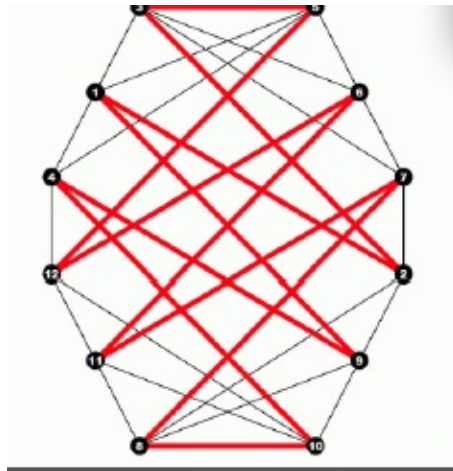


Figure 4: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 4 reflection symmetries.

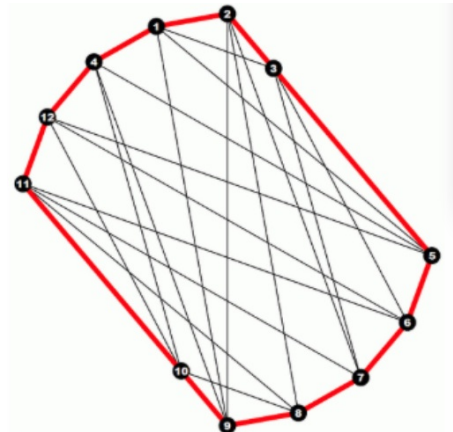


Figure 5: $(n_0, n_1, n_2) = (0, 16, 4)$ Hamiltonian cycle with 2-fold rotational symmetry realized as 6-*quint* shift along the cycle.

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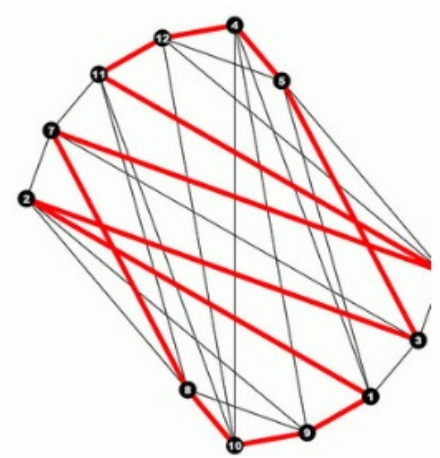


Figure 6: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold rotation symmetry.

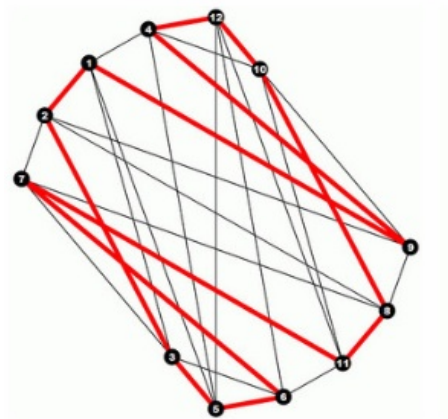


Figure 7: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold rotation symmetry.

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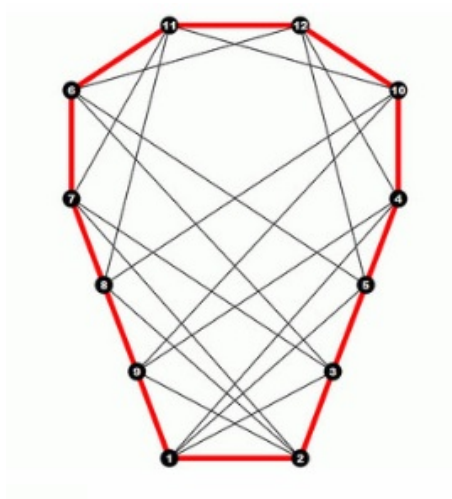


Figure 8: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry realized as horizontal reflection

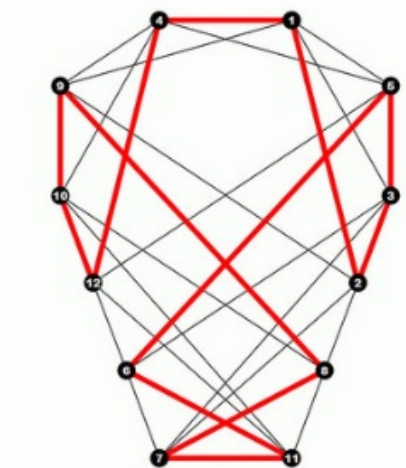


Figure 9: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

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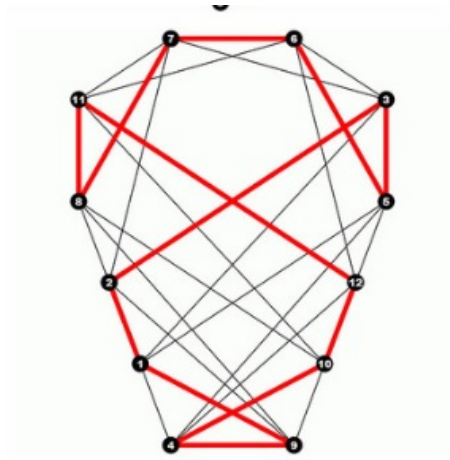


Figure 10: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold reflection symmetry.

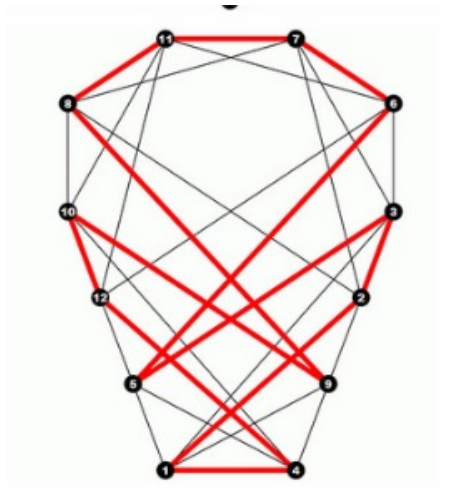


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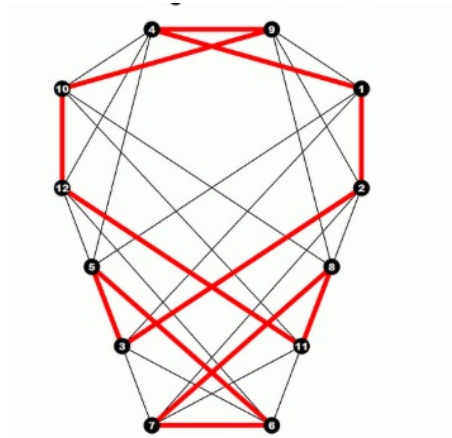


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