About the Correspondence of Dark Nuclear Genetic Code and Ordinary Genetic Code

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Abstract

The basic problem in the understanding of the prebiotic evolution is how DNA, RNA, amino-acids and tRNA and perhaps even cell membrane and microtubules . The individual nucleotides and amino-acids emerge without the help of enzymes or ribozymes but the mystery is how their polymers emerged. If the dark variants of these molecules served as templates for their generation one avoids this hen-and-egg problem. The problem how just the biomolecules were picked up from a huge variety of candidates allowed by chemistry could be solved by the resonance condition making possible metabolic energy transfer between biomolecules and dark nuclei.

Simple scaling argument shows that the assumption that ordinary genetic code corresponds to $h_{eff}/h = n = 2^{18}$ and therefore to the p-adic length scale $L(141) \simeq .3$ nm corresponding to the distance between DNA and RNA bases predicts that the scale of dark nuclear excitation energies is .5 eV, the nominal value of metabolic energy quantum. This extends and modifies the vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compre it to PAH world hypothesis.

p-Adic length scale hypothesis and thermodynamical considerations lead to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures. Thermal constraints allow cell membrane of thickness about 5 nm as a realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. Metabolic energy quantum is predicted to be .04 eV, which corresponds to membrane potential. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is below the thermal energy for photons but the notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum.

Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is .02 eV slightly below thermal energy at room temperature: this could relate to the inherent instability of microtubules. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

1 Introduction

The idea about the realization of genetic code in terms of dark proton sequences giving rise to dark nuclei is one of the key ideas of TGD inspired quantum biology [L5]. This vision was inspired by the totally unexpected observation that the states of three dark protons (or quarks) can be classified to 4 classes in which the number of states are same as those of DNA, RNA, tRNA, and amino-acids. Even more, it is possible to identify genetic code as a natural correspondence between the dark counterparts of DNA/RNA codons and dark amino-acids and the numbers of DNAs/RNAs coding given amino-acid are same as in the vertebrate code [L5]. What is new is that the dark codons do not reduce to ordered products of letters.

During years I have considered several alternatives for the representations of genetic code. For instance, one can consider the possibility that the letters of the genetic code correspond to the four spin-isospin states of nucleon or quark or for spin states of electron pair. Ordering of the letters as states is required and this is problematic from the point of view of tensor product unless the ordering reflects spatial ordering for the positions of particles representing the letters. One representation in terms of 3-chords formed by 3-photon states formed from dark photons emerges from the model of music harmony [L1]. By octave equivalence the ordering of the notes is not needed.

1.1 Insights

The above observations inspire several speculative insights.

1. The emergence of dark nuclei identified as dark proton sequences would relate to Pollack's effect in which irradiation of water generates in presence of gel phase bounding the water

what Pollack calls exclusion zones (EZs). EZs are negatively charged and water has effective stoichiometry $H_{1.5}O$. EZs deserve their name: somehow they manage to get rid of various impurities: this might be very important if EZs serve as regions carrying biologically important information. The protons of water molecules must go somewhere and the proposal is that they go to the magnetic body of some system consisting of flux tubes. The flux tubes contain the dark protons as sequences identifiable as dark nuclei.

2. Since nuclear physics precedes chemistry, one can argue that prebiotic life is based on these dark biomolecules serving as a template for ordinary biomolecules. To some degree biochemistry would be shadow dynamics and dark dynamics would be extremely simple as compared to the biochemistry induced by it. In particular, DNA replication, transcription, and translation would be induced by their dark variants. One can even extend this vision: perhaps also ordinary nuclear physics and its scaled up counterpart explaining "cold fusion" are parts of evolutionary hierarchy of nuclear physics in various scales.

3. Nature could have a kind of R&D lab allowing to test various new candidates for genes by using transcription and translation at the level of dark counterparts of the ordinary basic biomolecules.

1.2 Conditions on the model

The model must satisfy stringent conditions.

1. Both the basis A, T, C, G and A, U, C, G as basic chemical building bricks of RNA and DNA must have emerged without the help of enzymes and ribozymes. It is known that the biochemical pathway known as pentose-phosphate pathway (see `http://tinyurl.com/y9akkwok`) generates both ribose and ribose-5-phosphate defining the basic building brick of RNA. In DNA ribose is replaced with de-oxiribose obtained by removing one oxygen.

   Pyrimidines U, T, and C with single aromatic ring are are reported by NASA to be generated under outer space conditions (see `http://tinyurl.com/y7sh9zk4`). Carell *et al* [I4] (see `http://tinyurl.com/z65kpyo`) have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons. TGD inspired model for the mechanism involves dark protons [L7] [**?**].

   Basic amino-acids are generated in the Miller-Urey type experiments (see `http://tinyurl.com/4q2arv`). Also nucleobases have been genererated in Miller-Urey type experiments [I6].

   Therefore the basic building bricks can emerge without help of enzymes and ribozymes so that the presence of dark nuclei could lead to the emergence of the basic biopolymers and tRNA.

2. Genetic code as a correspondence between RNA and corresponding dark proton sequences must emerge. Same true for DNA and also amino-acids and their dark counterparts. The basic idea is that metabolic energy transfer between biomolecules and their dark variants must be possible. This requires transitions with same transition energies so that resonance becomes possible. This is also essential for the pairing of DNA and dark DNA and also for the pairing of say dark DNA and dark RNA. The resonance condition could explain why just the known basic biomolecules are selected from a huge variety of candidates possible in ordinary biochemistry and there would be no need to assume that life as we know it emerges as a random accident.

3. Metabolic energy transfer between molecules and their dark variants must be possible by resonance condition. The dark nuclear energy scale associated with biomolecule could correspond to the metabolic energy scale of .5 eV. This condition fixes the model to a high extent but also other dark nuclear scales with their own metabolic energy quanta are possible. In fact, the dark nuclear binding energy for $k = 151$ scaled up from the typical value of the ordinary nuclear binding energy about 1 MeV is .5 eV.

1.3 Vision

The basic problem in the understanding of the prebiotic evolution is how DNA, RNA, amino-acids and tRNA and perhaps even cell membrane and microtubules . The individual nucleotides and amino-acids emerge without the help of enzymes or ribozymes but the mystery is how their polymers emerged. If the dark variants of these molecules served as templates for their generation one avoids this hen-and-egg problem. The problem how just the biomolecules were picked up from a huge variety of candidates allowed by chemistry could be solved by the resonance condition making possible metabolic energy transfer between biomolecules and dark nuclei.

The basic question is to what p-adic length scales $L(k)$ DNA, RNA and amino-acids correspond. The original hypothesis was that the p-adic length scale assignable to dark DNA is consistent with the radius of ordinary DNA. It however turned out that this implies that the binding energy scale of corresponding dark nuclear physics is too high for the recent biology. Also the assumption that the dark variant of DNA double strand is horizontally scaled up variant of ordinary DNA strand excludes this identification since it requires that the horizontal size scale of dark DNA strand is larger than that of ordinary DNA strand.

DNA coil has radius $L(151) = 10$ nm and this suggests that dark DNA radius does not correspond to the radius of ordinary DNA (as assumed in the original version of this text) but to the p-adic length scale $L(151)$, where $k = 151$ corresponds to first Gaussian Mersenne prime belonging to the group $k = 151, 157, 163, 167$. The primes $k > 151$ would correspond to higher level coilings of DNA. From this hypothesis one ends up to the proposal that RNA, tRNA, and amino-acids correspond to $k = 149$. This picture follows essentially from the contraints posed by various biological anomalies.

Also the smaller primes $k = 127, 131, 137, 139$ can be present in pre-biotic evolutions. This hierarchy of dark nuclear physics leads to a vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compare it to PAH world hypothesis.

The vision about dark matter as a controller of biomatter leads to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures related to by radial scaling to their counterparts at the level of ordinary biomatter. This is supported by p-adic length scale hypothesis and thermodynamical considerations. These 2-D structures could represent 2-D variants of 1-D structures represented by DNA, RNA, and amino-acids with each node of lattice representing code letter.

Thermal constraints allow cell membrane of thickness about 5 nm as am additional realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. For $k = 149$ metabolic energy quantum is predicted to be .5 eV. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is just at the verge of thermal threshold. This could be understood in terms of minimization of metabolic resources. For bosonic singly charged ions the Josephson energy would be below the thermal threshold. The notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum.

Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is $E_{ex}(151) = .25eV$. Of course, the replacement of $E_{ex} = 1$ MeV for ordinary nuclei with $E_{ex} = 2$ MeV would give $E_{ex}(151) = .5$ eV so that one must take these estimates as order of magnitude estimates only. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

The great vision would be that hierarchy of dark variants of DNA, RNA, amino-acids and their replication, transcription, and translation would be behind biological replication in various scales. Ordinary bio-chemistry would be shadow dynamics doing its best to mimic what happens at the level of dark matter. The reduction of bio-physics to that of dark matter level would mean a huge simplification of the vision about living matter.

The picture that I discussed in the original version of this chapter involved several uncertainties and open questions. During the years, TGD itself has developed and I decided to add to end of the

chapter the recent view about the genetic code as a section title "Genetic code in terms of dark nucleon triplets". This is the year 2022 view about dark nucleon realization of the genetic code.

2 About dark variants of DNA, RNA, and amino-acids

To make progress one must construct a concrete model for the dark nuclei. The recent picture relies strongly on various anomalies to which TGD provides a solution. The TGD inspired model for "cold fusion" leads to the notion of dark nuclear physics - actually hierarchy of them labelle by the values of $h_{eff}/h = n$ and corresponding p-adic length scales. Second basic idea [L2] is that cylindrical variants of EZs discovered by Pollack [L2] give rise to the dark counterparts of DNA, RNA, and amino-acids as dark proton sequences. tRNAs would be analogs of tritium and ^{3}He. Pollack effect serves as a strong constraint for the model. Also the effects of ELF em fields on vertebrate brain [**?**] combined with the rather recent finding about clustering of RNA II polymerase molecules [I5] exhibiting Comorosan effect [I9] provide valuable constraints on the model [L16]. The outcome of the arguments is that single strand of DNA, mRNA, tRNA and amino-acids most naturally correspond to $k = 149$ and double stranded DNA to $k = 151$.

Remark: The following argumentation is kind of Sherlock-Holmes-ing using all possible hints as constraints to select between imagined options rather than glorious march from axioms to theorems and thus not science in the usual sense.

2.1 Dark variant of DNA

Concerning the identification of the size scale of dark DNA one can consider several options. The first guess was that the scale is same as for ordinary DNA: L(141)=.34 nm obtained by scaling from the distance of protons in the $k = 127$ dark nucleus implicated by the findings of Holmlid *et al* [**?**, **?**] [L3]. It however turns out that the p-adic length scale assignable to dark DNA is most naturally $k = 151$ corresponding to the thickness 10 nm of DNA coil. The hypothesis that the integer k labelling p-adic length scale is prime is attractive working hypothesis leaving very few options under consideration. The options $k = 137$ and $k = 149$ are excluded since the pairing of dark DNA and ordinary DNA would not be possible without the coiling of ordinary RNA around dark DNA. This leaves only options for which $k \geq 149$ for prime values of k.

Remark: The p-adic length scale associated with a system is defined to be $L(k)$ if the size of the system is in the half open interval $[L(k), L(k+1))$. One can also consider the possibility that p-adic length scale corresponds to the upper end of $[L(k-1), L(k))$.

2.1.1 General considerations

Consider first some background.

1. The TGD based model leads to the proposal for a formation of this kind of dark nuclear strings such that the distance between protons is rather precisely electron Compton length $L_e \simeq .4 \times 10^{-12}$ meters explains "cold fusion" in terms of dark nucleosynthesis which should have preceded ordinary nucleosynthesis by heating the material to the temperature required by it [L9] [K5].

   Dark nucleosynthesis would have produced part of heavier nuclei outside stars. The binding energy scale for dark nuclear physics would be scaled down like 1/length and 2.6 MeV binding energy per nucleon for ^{3}He of the ordinary nuclei would be scaled down by a factor 2^{-11} to 1.3 keV. Note however that it is excitation energies of order 1 MeV what matters and would scale down to .5 keV. This level does not yet correspond to biology as we know it but could be one step in the evolutionary hierarchy leading from nuclear physics also based on nuclear strings to biology involving increase of Planck constant $h_{eff}/h = n$ identifiably as the dimension of algebraic extension of rationals characterizing the complexity of the dynamics.

2. These dark nuclei have $h_{eff}/h = n = 2^{11}$ (or near to it) and cannot be those responsible for the dark variants of biomolecules since the distances of dark protons given by electron Compton length are much shorter than the distance between DNA nucleotides about .34 nm, which is roughly 142 times the electron Compton length 2.4×10^{-3} nm.

3. The distance between the dark protons appearing as counterparts of DNA nucleotides should be larger than that between ordinary DNA nucleotides. The simplest assumption that dark DNA coil is a horizontally scaled variant of DNA coil with same twisting angle so that DNA nucleotides are projected horizontally to their dark counterparts at the surface of a cylinder. Once the p-adic length scale of this cylinder is given, the distance between dark protons is fixed by p-adic scaling from the distance between dark protons for $k = 127$ case - that is electron Compton length. In the case of uncoiled RNA/AA one could have also a coil rotating around the ordinary RNA/AA.

   The distance between dark nucleotides must be longer than the distance $3 \times .34 \sim 1$ nm taken by single ordinary DNA codon. If k is prime this leaves only $k = 149$ or $k = 151$ into consideration.

4. The negative charge of DNA and RNA assignable to one oxygen of phosphate combining with ribose and DNA/RNA base could come from the tubular EZ formed in the formation of DNA. The negative charge of phosphates and the positive charge of dark protons could guarantee the stability of pairs of dark proton sequences and ordinary RNA and DNA.

   DNA strand has radius of $R = 1$ nm. The Debye length R_D of DNA gives rough idea about the scale above which the negative charge of DNA nucleotides associated with the phosphates screened. R_D should be longer than R: otherwise it is not possible to speak about charge of DNA only atomic length scales. One should have $R_D > R$: otherwise it does not make sense to assign negative DNA charge except in atomic length scales. The simplest option is that dark DNA has size scale $L(151)$.

   Remark: The rough estimates depend on how one identifies p-adic length scale. For the identification as $L(k) = \sqrt{5}L_e(k)$ motivated by the mass formula for electron, one would have $L(k) = \sqrt{5}L_e(k)$ giving $L(141) = 0.67$ nm. With this interpretation the estimate for the screening radius would be still shorter than R.

   Remark: Scaled up hadron physics would be associated with flux tubes of the magnetic body of the codon at which one would have nucleons as 3-quark color singlets. I have already earlier proposed that scaled variants of hadron physics [K8] appear in TGD inspired biology. One motivation comes from honeybee dance [A1]!

The pairing dark AAs with positive charge with ordinary AAs might lead to problems since 16 AAs are neutral. The only charged AA residues are Lys (+), Arg (+), Asp (-) and Glu (-).

1. The formation mechanism for dark proton sequences gives for dark AAs a large positive charge. AAs are however not accompanied by negatively charged phosphate ions. Does charge neutrality require that the dark bonds between dark proton has negative charge so that one has effectively neutron?

   Dark weak interactions correspond to large value of n [L9] so that in DNA length scale their proceed as fast as electromagnetic interactions (weak bosons would behave like massless particles below scaled up weak scale). This could make possible β decays changing the charges of the bonds between dark protons or dark neutrons [L9] and lead to a stability by β emission.

2. Proteins in water environment have a charge due to protons or electrons attaching to them. This charge depends on pH and becomes negative above certain critical pH. One might think that the limit of very large pH (no protons) corresponds to the situation in which the electrons of EZ attach to AAs.

Dark codons do not have decomposition to letters whereas ordinary codons have. In a well-defined sense one could say that dark code is "holistic" whereas the ordinary code is "reductionistic".

1. This brings in mind western written language in which words decompose to letters. In some eastern languages the symbols of written language correspond to entire words. Do these differences correspond at deeper level to ordinary and dark genes. Could the analytic and holistic aspects of cognition relate to the differences between ordinary and dark code.

2. One cannot exclude the entanglement between codons and evolution as emergence of entanglement even suggests this. Could this kind of entanglement give rise to basic units of DNA, in particular genes and introns. Could the decomposition of gene into coding regions and introns correspond to a decomposition to unentangled products of internally entangled pieces. This would increase exponentially the degrees of freedom involved and explain why organisms with practically the same code can be at so different evolutionary levels. In the splicing process when intronic portions are cut out from DNA sequence. Do the remaining pieces of RNA get entangled or does the decomposition of dark RNA to unentangled pieces have some meaning? Note that also ordinary RNA would be entangled or entangled. Could introns provide the means for decomposing the coding RNA to unentangled pieces.

3. The most natural possibility is that entanglement contains superposition of codon sequences in which each sequence codes for the same AA. The chemical codons appearing in the superposition have different masses and chemical properties but in zero energy ontology (ZEO) this is possible. Situation would be like for a superconductor in which coherent state means superposition of states with different numbers of Cooper pairs and thus different fermion number in standard ontology but in ZEO this problem disappears.

2.1.2 Why one must have $k = 151$ for dark DNA

It was already found that for prime values of k the options $k < 149$ are not possible for dark DNA since ordinary DNA should coil around dark DNA. There is also second objection against prime $k < 149$ from energetics inspiring the hypothesis DNA corresponds to $k = 151$.

1. The scaling of the dark nuclear binding energy $E_b \sim 7$ MeV per nucleon as $L(107)/L(k)$ predicts very high binding energies for primes $k < 149$. For instance, $k = 139$ would correspond to the scaled binding energy $E_b(139) = E_b L(107)/L(139)$, $E_b \sim 7$ MeV, which is typical nuclear binding energy. This gives $E_b(139) = E_b/2^{(139-107)/2} = .14$ keV. For $k = 139$ the typical nuclear excitation energy $E_{ex} = 1$ MeV scales dow to 20 eV, which is still very high but could correspond to energies of atomic transitions. For $k = 151$ it E_b scales down to 3.5 eV. The typical dark excitation energy for $k = 151$ is $E_{ex}(151) = .5$ eV and the identification as a nominal value of metabolic energy quantum is attractive. Dark nuclear physics might therefore control biochemistry using dark nuclear transitions as a tool to provide desire energy currency.

2. The TGD based explanation of Pollack effect provides a consistency test for the idea [L2] [L2]. In Pollack effect IR light (besides either kinds of energy feeds) induces the formation of negative charged exclusion zones (EZs) in water bounded by gel phase. In TGD based model this would correspond to the formation of dark proton sequences at magnetic flux tubes. The scale of dark nuclear binding energy would be most naturally in eV scale. The binding energy scale of hydrogen atoms in water molecules is about 5 eV which suggests that the binding energy scale for dark protons sequences is smaller since otherwise energy would be liberated. This would suggest $k = 149$ as will be found.

3. One can imagine that an external perturbation induces

   (a) a transition in which the proton bound to water molecule transforms to its dark variant in higher energy state or

   (b) that the proton goes over a potential wall, whose height is measured in eV:s.

   If the dark nuclear binding energy is higher than the binding energy of proton in water molecule, the process should liberate energy and could occur spontaneously unless high potential wall prevents it. Hence the first option seems the only realistic one. Note that one could consider the cancellation of dark nuclear binding energy and repulsive Coulomb energy which scale in the same manner as function of p-adic length scale so that still the net energy would scale increase in shorter p-adic length scales.

Pollack effect suggests that if k is prime, one must have $k = 149$ for dark proton sequences formed in Pollack effect.

1. For $k = 149$ one has $E_b(151) \sim E_b/2^{(149-107)/2} = 3.5$ eV for $E_b = 7$ MeV, which is in UV range slightly above the visible range. The binding energy of hydrogen atom in water is about 5 eV which would require the incoming radiation to have energy 1.5 eV which is indeed in IR range. This option looks therefore realistic.

2. For $k = 151$ one would have $E_b(151) \sim 7MeV/2^{(151-107)/2} = 1.75$ eV, which just above the IR energy range. Now the energy needed to transform ordinary protons to dark protons in Pollack effect would be in UV range so that this options seems to be excluded.

This argument suggests that dark proton sequences generated in Pollack effect are analogs of single DNA strand, which would naturally correspond to $L(149) = L(151)/2$. Also RNA would naturally correspond to this scale.

1. $L(151) \simeq 10$ nm is the thickness of coiled DNA double strand. The size scale of dark nucleons would be $L(151)$ and the dark DNA strand should be horizontally scaled variant of ordinary DNA strand by a scaling factor $\lambda \sim L(151)/.33$ nm $= 30$. DNA double strand would be obtained by a transversal scaling from the ordinary DNA double strand.

2. The higher coilings of DNA could correspond to higher horizontally scaled variants of DNA corresponding to $k = 157, 163, 167$. $k = 167$ would correspond to nuclear membrane length scale of 2.5 μm. The emergence of nuclear membrane in $k = 151$ length scale would have been accompanied by the emergence of dark DNA in this scale. Cell membrane could correspond to $k = 173$ and p-adic length scale 17.6 μm. Neurons have size varying from 4-100 micrometers (the definition of size depends on whether one includes axons) and might correspond to $k = 179, 181$ and length scales of .16 mm and perhaps even .32 mm.

The only justification for this speculative picture is that it is consistent with the other basic ideas about TGD inspired quantum biology.

1. Cisse *et al* [I5] found that RNA II polymerase molecules cluster during transcription and their dynamics involves multiples of the time scale $\tau = 5$ seconds. Comorosan reported long time ago that just these time scales are universal bio-catalysis [I9]. The TGD inspired model [L16] for the findings of Cisse *et al* allows to sharpen the TGD based view about quantum biology considerably.

2. The basic parameter of the model is the value of gravitational Planck constant $\hbar_{gr} = GM_Dm/v_0$ assigned to magnetic flux tubes mediating gravitational interactions. Already earlier work gives estimates for the value M_D of dark mass and velocity parameter v_0 and the model leads to the same estimates. The identification of the values of τ as Josephson periods assuming the potential difference V along flux tubes connecting reacting molecules is universal and same as over neuronal membrane fixed the value of h_{gr}. The value of V along flux tube serving as Josephson junction would be universal and equal to membrane potential. Josephson radiation would have energies coming as multiples ot ZeV just above the thermal energy at physiological temperatures fixed by the membrane potential.

3. The model forces the conclusion that the endogenous magnetic field B_{end} has at its upper bound $B_{end} = .2$ Gauss deduced from the findings of Blackman about effects of ELF em fields on vertebrate brain [**?**]. The earlier ad hoc hypothesis was that $B_{end} = .2$ Gauss is minimum value of B_{end}. Furthermore, for the required value of h_{gr} $B_{end} = .2$ Gauss corresponds to dark cyclotron energy of .12 keV, which is surprisingly large energy at the upper end of UV band: the earlier intuitive guess was that energy scale is in visible range.

   Also harmonics of cyclotron frequencies were found to have effects so that really large energy scales are involved with the interaction of ELF radiation and one can ask whether this picture really makes sense. This raises a question about the mechanism of the interaction of ELF em radiation with living matter. One also wonder why the ELF radiation has effects on both behavior and physiology.

   Assume

   (a) that dark photons with energies coming as multiples of .12 keV are in question,

(b) that these dark photons excite dark cyclotron states in the cellular length scale deduced from flux quantization and

(c) that the dark cyclotron photons radiated as the excited cyclotron states return to the ground states perform some control action on ordinary DNA coil - this is in accordance with the basic vision about the role of magnetic body.

X rays have energy range varying from 100 eV to 100 keV and wavelengths varying from 10 nm to .01 nm. The wavelength of an ordinary photon resulting from dark photon with energy of .12 keV would be of order 10 nm, the radius of DNA coil for $k = 151$!

Could this energy induce an analog of standing em wave in transversal degrees of freedom of DNA perhaps transformable to many phonon state with very large number of photos and thus classical acoustic wave? This would allow to understand how cyclotron harmonics can have non-trivial effects. The effects of ELF radiation on behavior and physiology could be understood as gene expression induced by the irradiation.

Both dark cyclotron radiation and radiation generated in dark nuclear transitions could have biological effects

1. Can one relate energy scale of .12 keV associated with dark cyclotron radiation to atomic physics? The ionization energies behave as Z_{eff}^2/n^2, where Z_{eff} is nuclear charge minus the charge of the closed shells. Z_{eff} is also reduced by electronic screening by other valence electrons. The binding energies of valence electrons decrease with the principal quantum number n so that only $n = 2$ row of the periodic table might allow so high ionization energies for valence electrons.

   Oxygen is certainly the first candidate to consider. The ionization energy for oxygen is .12 eV from an estimate assuming that the effective nuclear charge is 6 (with the contribution of 2 valence electrons subtracted). The actual value is 68.9 eV: the reduction is due to electron screening. This value is smaller than the estimate estimate for $E_b = .12$ keV and since harmonics of this energy are involved, the interpretation in terms of ionization does not make sense.

2. Not only oxygen but also heavier elements are ionized in living matter and at least to me this has remained more or less a mystery. Could dark photons emitted by dark nuclei of MB perform control by inducing the transitions and even ionization of oxygen and other biologically important atoms. The process could proceed also in opposite direction. The energy scale would correspond to that of nuclear excitations scaled down by the above ratio of p-adic length scales. If the energy scale of ordinary nuclear excitations is taken to be about 1 MeV, the dark energy scale for $k = 127$ assignable to the dark nuclei created in "cold fusion" is keV. For $k = 131$ the scale would be 250 eV and above the ionization energy scales for valence electrons. For $k = 137$ the scale would be 17 keV. These dark nuclear transitions could generate dark photons inducing transitions of atoms and even ionizations.

2.2 What about dark variants of RNA, tRNA, and AAs?

Also RNA and AAs should have dark variants and one should understand their role. Suppose that the integer k characterizing the p-adic length scale is prime. The vision about RNA era preceding DNA era suggests that RNA accompanying dark RNA is at lower level in the evolution, and hence the value of h_{eff} is smaller for dark RNA than for dark DNA. Also the p-adic length scale for RNA would be shorter.

1. The most natural option is that RNA corresponds to $k = 149$ as also single DNA strand. This would conform with the above suggestion that the Pollack effect generates $k = 149$ dark proton sequence (dark RNA?). DNA double strand would correspond to $k = 151$.

   The emergence of $k = 151$ level would mean the emergence of structures with scale characterized by $L(151)$. This includes DNA double strand forming a coil with thickness $L(151)$ and nuclear and cell membranes. During RNA era these structures would have been absent.Both DNA double strand and cell membrane have binary structures. Therefore single

DNA strand and lipid layer could correspond to $k = 149$. In transcription DNA opens and double strand becomes pair of strands having naturally $k = 149$. Therefore mRNA should have also $k = 149$.

2. If AAs correspond to $k = 149$ then also tRNA should correspond to $k = 149$. On the other hand, tRNA does not form strands and should be more elementary structure than RNA. Could tRNA corresponds to $k = 139$ or $k = 137$? This would require that also the attached AA would correspond to $k = 139$ or $k = 137$, which does not look plausible.

   Remark: TGD vision assumes tRNA was present already at RNA era and the role of AA in tRNA was to catalyze RNA replication. In fact, RNA could have been just tRNA at very early stages.

What about AAs? The following arguments suggest that one has $k = 149$ for both AAs and RNA.

1. For dark AAs one can imagine p-adic evolutionary hierarchy analogous to that for DNA. In TGD inspired vision AA sequences emerged together with DNA. Proteins can appear also as coils. Since mRNA pairs with single DNA strand and AAs with mRNA, it seems that AAs should correspond to $k \geq 149$?

2. One could however argue that AAs are building bricks rather than information molecules and k could be rather small for dark AAs. Dark AAs should pair with proteins. Pairing without coiling is possible only if the length per letter is same as the length per AA and thus same as for DNA letter, which is longer than the length taken by $k = 139$ dark proton. Also this suggests $k = 149$ for dark AAs and their coiling around the ordinary AAs.

2.3 Clustering of RNA polymerase molecules and Comorosan effect

Once again I had good luck: I received a link (see `http://tinyurl.com/y7bego83`) to a highly interesting popular article telling about the work by Ibrahim Cisse at MIT and his colleagues [I5] (see `http://tinyurl.com/y9wzt5yl`) about the clustering of RNA polymerase proteins in the transcription of RNA. Similar clustering has been observed already earlier and interpreted as a phase separation giving rise to protein droplets [L20]. Now this interpretation is not proposed by experiments but they say that it is quite possible but they cannot prove it.

I have already earlier discussed the coalescence of proteins into droplets as this kind of process in TGD framework [**?**] [L20]. The basic TGD based ideas is that proteins - and biomolecules in general - are connected by flux tubes characterized by the value of Planck constant $h_{eff} = n \times h_0$ for the dark particles at the flux tube. The higher the value of n is the larger the energy of given state. For instance, the binding energies of atoms decrease like $1/n^2$. Therefore the formation of the molecular cluster liberates energy usable as metabolic energy.

Remark: h_0 is the minimal value of h_{eff}. The best guess is that ordinary Planck constant equals to $h = 6h_0$ [L6, L17] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`.

2.3.1 TGD view about the findings

Gene control switches - such as RNA II polymerases in DNA transcription to RNA - are found to form clusters called super-enhancers. Also so called Mediator proteins form clusters. In both cases the number of members is in the range 200-400. The clusters are stable but individual molecules spend very brief time in them. Clusters have average lifetime of $5.1 \pm .4$ seconds.

Why the clustering should take place? Why large number of these proteins are present although single one would be enough in the standard picture. In TGD framework one can imagine several explanations. One can imagine at least following reasons.

1. If the initiation of transcription is quantum process involving state function reduction, clustering could allow to make this process process deterministic at the level of single gene in spite of the non-determinism of state function reduction. Suppose that the initiation of transcription is one particular outcome of state function reduction. If there is only single RNA II

polymerase able to make only single trial, the changes to initiate the transcription are low. This could be the case if the protein provides metabolic energy to initiate the process and becomes too "tired" to try again immediately. In nerve pulse transmission there is analogous situation: after the passing of the nerve pulse generation the neuron has dead time period. As a matter of fact, it turns out that the analogy could be much deeper.

How to achieve the initiation with certainty in this kind of situation? Suppose that the other outcomes do not affect the situation appreciably. If one particular RNA polymerase fails to initiate it, the others can try. If the number of RNA transcriptase molecule is large enough, the transcription is bound to begin eventually! This is much like in fairy tales about princess and suitors trying to kill the dragon to get the hand of princess. Eventually comes the penniless swineherd.

2. If the initiation of transcription requires large amount of metabolic energy then only some minimal number of N of RNA II polymerase molecules might be able to provide it collectively. The collective formed by N molecules could correspond to a formation of magnetic body (MB) with a large value of $h_{eff} = n \times h_0$ and controlling the molecules and inducing its coherent behavior. The molecules would be connected by magnetic flux tubes.

3. If the rate for occurrence is determined by an amplitude which is superposition of amplitudes assignable to individual proteins the rate is proportional to N^2, N the number of RNA II polymerase molecules. The process for the cluster is reported to be surprisingly fast as compared to the expectations - something like 20 seconds. The earlier studies have suggests that single RNA polymerase stays at the DNA for minutes to hours.

   Clustering could allow to speed up bio-catalysis besides the mechanism allowing to find molecules to find by a reduction of $h_{eff}/h = n$ for the bonds connecting the reactants and the associated liberation of metabolic energy allowing to kick the reactants over the potential wall hindering the reaction.

Concerning the process of clustering there are two alternative options both relying on the model of liquid phase explaining Maxwell's rule assuming the presence of flux tube bonds in liquid and of water explaining its numerous anomalies in terms of flux tubes which can be also dark (see `http://tinyurl.com/ydhknc2c`).

1. **Option I**: Molecules could form in the initial situation a phase analogous to vapour phase and there would be very few flux tube bonds between them. The phase transition would create liquid phase as flux tube loops assignable to molecules would reconnect form flux tube pairs connecting the molecules to a tensor network giving rise to quantum liquid phase. The larger then value of n, the longer the bonds between molecules would be. This kind of model [**?**] (see `http://tinyurl.com/yassnhzb`) is used to explain the strange findings that a system consisting of plastic balls seems to show primitive features of life such as metabolism.

2. **Option II**: The molecules are in the initial state connected by flux tubes and form a kind of liquid phase and the clustering reduces the value of $h_{eff}/h = n$ and therefore the lengths of flux tubes. This would liberate dark energy as metabolic energy going to the initiation of the transcription. One could indeed argue that connectedness in the initial state with large enough value of n is necessary since the protein cluster must have high enough "IQ" to perform intelligent intentional actions.

Protein blobs are said to be drawn together by the "floppy" bits (pieces) of intrinsically disordered proteins. What could this mean in the proposed picture? Disorder would mean absence of correlations between building bricks of floppy parts of the proteins in translational degrees of freedom.

1. Could floppiness correspond to low string tension assignable to long flux loops with large n assignable to the building bricks of "floppy" pieces of protein? Could reconnection for these loops give rise to pairs of flux tubes connecting the proteins in the transition to liquid phase (Option I)? Floppiness would also make possible to scan the environment by flux loops to get in touch with the flux loops of other molecules and in the case of hit (cyclotron resonance) induce reconnection.

2. In spite of floppiness in this sense, one could have quantum correlations between the internal quantum numbers of the building bricks of the floppy pieces. This would also increase the value of n serving as molecular IQ and provide molecule with higher metabolic energy liberated in the catalysis.

2.3.2 About Comorosan effect and clustering of RNA II polymerase proteins

What about the interpretation of the time scales τ equal 5, 10, and 20 seconds appearing in the clustering of RNA II polymerase proteins and Mediator proteins? What is intriguing that so called Comorosan effect [I9, I3] involves time scale of 5 seconds and its multiples claimed by Comorosan long time ago to be universal time scales in biology. The origin of these time scales has remained more or less a mystery although I have considered several TGD inspired explanations for this time scale is based on the notion of gravitational Planck constant [K20] (see `http://tinyurl.com/yb8fw3kq`).

One can consider several starting point ideas, which need not be mutually exclusive.

1. The time scales τ associated with RNA II polymerase and perhaps more general bio-catalytic systems as Comorosan's claims suggest could correspond to the durations of processes ending with "big" state function reduction. In zero energy ontology (ZEO) there are two kinds of state function reductions [L12]. "Small" state function reductions - analogs of weak measurements - leave the passive boundary of causal diamond (CD) unaffected and thus give rise to self as generalized Zeno effect. The states at the active boundary change by a sequence of unitary time evolutions followed by measurements inducing also time localization of the active boundary of CD but not affecting passive boundary. The size of CD increases and gives rise to flow of time defined as the temporal distance between the tips of CD. Large reductions change the roles of the passive and active boundaries and mean death of self. The process with duration of τ could correspond to a life-time of self assignable to CD.

   Remark: It is not quite clear whether CD can disappear and generated from vacuum. In principle this is possible and the generation of mental images as sub-selves and sub-CDs could correspond to this kind of process.

2. In [K20] I proposed that Josephson junctions are formed between reacting molecules in bio-catalysis. These could correspond to the shortened flux tubes. The difference $E_J = ZeV$ of Coulomb energy of Cooper pair over flux tube defining Josephson junction between molecules would correspond to Josephson frequency $f_J = 2eV/h_{eff}$. If this frequency corresponds to $\tau_J = 5$ seconds, h_{eff} should be rather large since E_J is expected to be above thermal energy at physiological temperature.

   Could Josephson radiation serve as a kind of of synchronizing clock for the state function reductions so that its role would be analogous to that of EEG in case of brain? A more plausible option is that Josephson radiation is a reaction to the presence of cyclotron radiation generated at MB and performing control actions at the biological body (BB) defined in very general sense. In the case of brain dark cyclotron radiation would generate EEG rhythms responsible for control via genome and dark generalized Josephson radiation modulated by nerve pulse patterns would mediate sensory input to the MB at EEG frequencies.

   A good guess motivated by the proposed universality of the Comorosan periods is that the energy in question does not depend on the catalytic system and corresponds to Josephson energy for protein through cell membrane acting as Josephson junction and giving to ionic channel or pump. The flux tubes themselves have universal properties.

3. The hypothesis $\hbar_{eff} = \hbar_{gr} = GMm/\beta_0 c$ of Nottale [**?**] for the value of gravitational Planck constant [K18, K12, K13, **?**] gives large $\hbar$. Here $v_0 = \beta_0 c$ has dimensions of velocity. For dark cyclotron photons this gives large energy $E_c \propto \hbar_{gr}$ and for dark Josephson photons small frequency $f_J \propto 1/h_{gr}$. Josephson time scale τ_f would be proportional to the mass m of the charged particle and therefore to mass number A of ion involved: $f_J \propto A$ possibly explaining the appearance of multiples of 5 second time scale. Cyclotron time scale does not depend on the mass of the charged particle at all and now sub-harmonics of τ_c are natural.

The time scales assignable to CD or the lifetime-time of self in question could correspond to either cyclotron of Josephson time scale τ.

1. If one requires that the multiplies of the time scale 5 seconds are possible, Josephson radiation is favoured since the Josephson time scale proportional to $h_{gr} \propto m \propto A$, A mass number of ion.

   The problem is that the values $A = 2, 3, 4, 5$ are not plausible for ordinary nuclei in living matter. Dark nuclei at magnetic flux tubes consisting of dark proton sequences could however have arbitrary number of dark protons and if dark nuclei appear at flux tubes defining Josephson junctions, one would have the desired hierarchy.

2. Although cyclotron frequencies do not have sub-harmonics naturally, MB could adapt to the situation by changing the thickness of its flux tubes and by flux conservation the magnetic field strength to which f_c is proportional to. This would allow MB to produce cyclotron radiation with the same frequency as Josephson radiation and MB and BB would be in resonant coupling.

Consider now the model quantitatively.

1. For $\hbar_{eff} = \hbar_{gr}$ one has

$$r = \frac{\hbar_{gr}}{\hbar} = \frac{GM_D m}{c\beta_0} = 4.5 \times 10^{14} \times \frac{m}{m_p}\frac{y}{\beta_0} \quad .$$

   Here $y = M_D/M_E$ gives the ratio of dark mass M_D to the Earth mass M_E. One can consider 2 favoured values for m corresponding to proton mass m_p and electron mass m_e.

2. $E = h_{eff} f$ gives the concrete relationship $f = (E/eV) \times 2.4 \times 10^{14} \times (h/h_{eff})$ Hz between frequencies and energies. This gives

$$x = \frac{E}{eV} = 0.4 \times r \times \frac{f}{10^{14} Hz} \quad .$$

3. If the cyclotron frequency $f_c = 300$ Hz of proton for $B_{end} = .2$ Gauss corresponds to bio-photon energy of x eV, one obtains the condition

$$r = \frac{GM_D m_p}{\hbar\beta_0} \simeq .83 \times 10^{12} x \quad .$$

   Note that the cyclotron energy does not depend on the mass of the charged particle. One obtains for the relation between Josephson energy and Josephson frequency the condition

$$x = \frac{E_J}{eV} = 0.4 \times .83 \times 10^{-2} \times \frac{m}{m_p} \times x\frac{f_J}{Hz} \quad , \quad E_J = ZeV \quad .$$

   One should not confuse eV in ZeV with unit of energy. Note also that the value of Josephson energy does not depend on h_{eff} so that there is no actual mass dependence involved.

For proton one would give a hierarchy of time scales as A-multiples of $\tau(p)$ and is therefore more natural so that it is natural to consider this case first.

1. For $f_J = .2$ Hz corresponding to the Comorosan time scale of $\tau = 5$ seconds this would give $ZeV = .66x$ meV. This is above thermal energy $E_{th} = T = 27.5$ meV at $T = 25$ Celsius for $x > 42$. For *ordinary* photon ($h_{eff} = h$) proton cyclotron frequency $f_c(p)$ would correspond for $x > 42$ to EUV energy $E > 42$ eV and to wavelength of $\lambda < 31$ nm.

   The energy scale of Josephson junctions formed by proteins through cell membrane of thickness $L(151) = 10$ nm is slightly above thermal energy, which suggests $x \simeq 120$ allowing to identify $L(151) = 10$ nm as the length scale of the flux tube portion connecting the reactants. This would give $E \simeq 120$ eV - the upper bound of EUV range. For $x = 120$ one would have

$GM_E m_p y/v_0 \simeq 10^{14}$ requiring $\beta_0/y \simeq 2.2$. The earlier estimates [**?**] for the mass M_D give $y \sim 2 \times 10^{-4}$ giving $\beta_0 \sim 4.4 \times 10^{-4}$. This is rather near to $\beta_0 = 2^{-11} \sim m_e/m_p$ obtained also in the model for the orbits of the 4 inner planets as Bohr orbits.

For ion with mass number A this would predict $\tau_A = A \times \tau_p = A \times 5$ seconds so that also multiples of the 5 second time scale would appear. These multiples were indeed found by Comoran and appear also in the case of RNA II polymerase.

2. For proton one would thus have 2 biological extremes - EUV energy scale associated with cyclotron radiation and thermal energy scale assignable to Josephson radiation. Both would be assignable to dark photons with $h_{eff} = h_{gr}$ with very long wavelength. Dark and ordinary photons of both kind would be able to transform to each other meaning a coupling between very long lengths scales assignable to MB and short wavelengths/time scales assignable to BB.

   The energy scale of dark Josephson photons would be that assignable with Josephson junctions of length 10 nm with long wavelengths and energies slightly above E_{th} at physiological temperature. The EUV energy scale would be 120 eV for dark cyclotron photons of highest energy would be fixed by flux tube length of 10 nm.

   For lower cyclotron energies forced by the presence of bio-photons in the range containing visible [K4, K6] and UV and obtained for B_{end} below .2 Gauss, the Josephson photons would have energies below E_{th}. That the possible values of B_{end} are below the nominal value $B_{end} = .2$ Gauss deduced from the experiments of Blackman [**?**] does not conform with the earlier ad hoc assumption that B_{end} represents lower bound. This does not change the earlier conclusions.

   Could the 120 eV energy scale have some physical meaning in TGD framework? The corresponding wavelength for ordinary photons corresponds to the scale $L(151) = 10$ nm which correspond to the thickness of DNA double strand. Dark DNA having dark proton triplets as codons could correspond to either $k = 149$ or $k = 151$. The energetics of Pollack effect suggests that $k = 149$ is realized in water even during prebiotic period [L14] (see `http://tinyurl.com/yalny39x`). In the effect discovered by Blackman the ELF photons would transform dark cyclotron photons having $h_{eff} = h_{gr}$ and energy about .12 keV. They would induce cyclotron transitions at flux tubes of B_{end} with thickness of order cell size scale. These states would decay back to previous states and the dark photons transformed to ordinary photons absorbed by ordinary DNA with coil structure with thickness of 10 nm. Kind of standing waves would be formed. These waves could transform to acoustic waves and induce the observed effects. Quite generally, dark cyclotron photons would control the dynamics of ordinary DNA by this mechanism.

   It is natural to assume that $B_{end} = .2$ Gauss corresponds to the upper bound for B_{end} since magnetic fields are expected to weaken farther from the Earth's surface: weakening could correspond to thickening of flux tubes reducing the field intensity by flux conservation. The model for hearing [K16] requires cyclotron frequencies considerably above proton's cyclotron frequency in $B_{end} = .2$ Gauss. This requires that audible frequencies are mapped to electron's cyclotron frequency having upper bound $f_c(e) = (m_p/m_e) f_c(p) \simeq 6 \times 10^5$ Hz. This frequency is indeed above the range of audible frequencies even for bats.

For electron one has $h_{gr}(e) = (m_e/mp) \times h_{gr}(p) \simeq 5.3 \times 10^{-4} h_{gr}(p)$, $\hbar_{gr}(p)/\hbar = 4.5 \times 10^{14}/\beta_0$. Since Josephson energy remains invariant, the Josephson time scales up from $\tau(p) = 5$ seconds to $\tau(e) = (m_e/m_p)\tau(p) \simeq 2.5$ milliseconds, which is the time scale assignable to nerve pulses [K17, K7].

To sum up, the model suggests that the idealization of flux tubes as kind of universal Josephson junctions. The model is consistent with bio-photon hypothesis. The constraints on $h_{gr} = GM_D m/v_0$ are consistent with the earlier views and allows to assign Comorosan time scale 5 seconds to proton and nerve pulse time scale to electron as Josephson time scales. This inspires the question whether the dynamics of bio-catalysis and nerve pulse generation be seen as scaled variants of each other at quantum level? This would not be surprising if MB controls the dynamics. The earlier assumption that $B_{end} = 0.2$ Gauss is minimal value for B_{end} must be replaced with the assumption that it is maximal value of B_{end}.

3 TGD view about the emergence of chemical life

Consider first the basic assumptions.

1. Dark DNA, RNA,... emerged before chemistry and serve as templates for ordinary DNA, RNA,... The replication, transcription, and translation for ordinary DNA, RNA,... are induced by the corresponding processes for their dark counterparts.

2. Dark proton sequences are associated with tubular EZs in water generated by Pollack effect.

3. The amount of entanglement measured by entanglement negentropy (having a well-defined meaning in adelic physics [L11]) is expected to increase gradually during evolution. Hence one expects generation of more and more entangled sequences of dark nucleons. At the bottom - perhaps ordinary nuclear physics - one would have the product states of dark nucleons. Perhaps dark nuclear physics with $n = 2^{11}$ came next. After that came $n = 2^{18}$ dark nuclear physics. But which came first: dark variants amino-acids, tRNA, RNA, or DNA and their chemical counterparts? And could one see even genes as entangled codon sequences coding for the same protein?

3.1 The quantum vision about the prebiotic evolution

The following vision about quantal prebiotic evolution beginning from amino-acids suggests itself. The basic idea is that all processes took place at dark level and induced the processes for ordinary biomolecules in water environment. Even the enzyme and ribozyme actions essential in recent biology would be replaced with corresponding actions at dark level and biochemistry would reduce to shadow dynamics.

1. Amino-acids are easiest to produce (as Miller-Urey experiment demonstrated (see `http://tinyurl.com/4q2arv`)) requiring no enzymatic action and there is just single chemical amino-acid per dark RNAs coding for it. Therefore the pairs of amino-acids and their dark variants could have emerged first. Note that proteins were not yet present.

   Remark: Vivo-vitro difference could mean that dark partner of biomolecule is present in vivo and missing in vitro.

2. DNA requires cell membrane. This requires RNA emerged after amino-acids. This implies that dark variants of dark tRNA, their pairing with tRNA and the pairing of dark RNA with RNA emerged next?

   This picture supports that the old TGD inspired idea about the role of tRNA during RNA era. Dark tRNA would have made possible the replication of dark RNA sequences (rather than the translation of RNA to amino-acid sequence) during this era. The dark amino-acid of dark tRNA would have served as a catalyst inducing the addition of dark RNA codon to the growing RNA sequence. No chemical transcription machinery nor DNA was needed at this stage. This would solve one hen-or-egg problem.

3. After that a revolution would have occurred. For some reason dark amino-acids began to attach to the growing sequence of amino-acids and dark RNA codon was left alone. What prevented dark RNA codon to attach to the growing dark RNA sequence? Was it the emerging entanglement between dark codons giving rise to genes as entangled pieces of DNA that made this impossible.

   This means entanglement also between the ordinary codons, which makes sense only in ZEO. If possible at all this entanglement should respect genetic code so that entangled superposition would involve only codons coding for the same amino-acid so that the translation to a single amino-acid sequence rather than their quantum superposition is possible. If more general superpositions are allowed the translation process would be like state function reduction to amino-acid sequence.

4. At this step the replication of both dark and ordinary RNA was lost and it seems that dark DNA-DNA pairs replicating dark DNA and transcribing it to dark RNA and inducing corresponding process at the level of chemistry must have emerged at the same time.

The emergence of DNA requires also the emergence of cell membrane. Could the emergence of cell membrane relate to the emergence of dark nuclei in the p-adic length scale $L(k)$, $k = 149$ and could the double layered structure of cell membrane serve as an analog for that of DNA double strand? Could lipid layers correspond to 2-D analogs of DNA strand with lipids taking the role of codons?

5. Could the full genetic code emerged in step-wise manner as proposed earlier [K1, K19]? Genetic code can be seen in a good approximation as a fusion of 16-letter code and 4-letter code. This might be understood if the entanglement of dark codons emerges first as entanglement of only two first letters.

What gave rise to the correspondences between dark DNA, RNA, tRNA, amino-acids and their dark variants? How the amino-acids and nucleotide bases were selected?

1. The basic principle would be the condition that metabolic energy can be transferred between chemical and dark levels. This is possible if there identical transition energies in the spectra of biomolecules and their dark variants making possible resonance.

2. Metabolic energy quantum in the range .4-.5 eV should correspond to the excitation energy scale of dark dark nuclear physics if $E_{ex} = 1$ MeV is taken as the estimate for a typical nuclear excitation energy. Hydrogen bonds also correspond to this energy scale but this might be just what is needed to give rise to coherent metabolic activity.

   The original proposal was that dark DNA associated with ordinary DNA corresponds to $k = 141$ assignable to the ordinary DNA but this proposal predicts $E_{ex}(141) = 16$ eV. This proposal turned out to be unrealistic also in other respects. $k = 149$ assignable to dark RNA predicts $E_{ex}(149) = .5$ eV and is a more plausible option in many other aspects. Also lower values of k than $k = 149, 151$ might be present - at least during the prebiotic stage. Pollack's findings however support the view that the irradiation of water with IR light generates dark proton sequences with $k = 149$. Does this mean that the evolutionary level of water is raised to $k = 151$ in presence of gel phase binding the water sample? Note that "cold fusion" [L3, L9] might be interpreted as creation of $k = 127$ dark proton sequences.

To sum up: for DNA,RNA, and tRNA the emergence of entanglement would have created the chemical counterparts of quantum superpositions: ZEO is necessary since in positive energy ontology superpositions are highly implausible.

There are some questions to ponder.

1. Why the decomposition into triplets? Does resonance condition for the metabolic energy transfer select triplets as basic units and also the RNA-amino-acid correspondence? Do also intronic regions have triplets as basic units?

   One ends up to a prediction of vertebrate genetic code also from a model of music harmony [L1]. In fact, the model explains also its slight variation and the 2 additional amino-acids. Could this help to understand why the triplet code is so unique.

2. Could one imagine that also quarks and antiquarks were involved? Could dark nucleon pair with dark quark with same spin and isospin and color confinement forces dark proton triplets? Dark quarks indeed define a representation for A,T,C, G. In the model of topological computation [K1, K19]. I have actually speculated with the possibility that dark quarks and antiquarks are paired with ordinary DNA codons.

3. Could dark conjugate protons or their triplets of parallel dark DNA strands form Cooper pairs or does pairing of dark protons triplets (their conjugates) with dark quarks (anti-quarks) give rise to bosonic states?

3.2 Unidentified Infrared Bands as a test for the proposal

Unidentified Infrared Bands (UIBs) are an ill-understood phenomenon associated with radiation coming from interstellar space. There are also other analogous phenomena having no explanation in terms of molecular transitions [K3] and one can ask whether they could be seen as signatures of dark nuclear physics.

1. UIBs are observed around bands around IR energies $E \in \{.11, .20, .375\}$ eV.

2. Poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`) are known to generate UIBs [K3]. Therefore the UIBs from interstellar space could originate from PAHs.

3.2.1 TGD based models for UIBs

TGD suggests several explanations for UIBs involving new physics related to the p-adic length scale hypothesis and $h_{eff}/h = n$ hierarchy.

1. For years ago I discussed a model for UIBs based on p-adic length scale hypothesis [K3]. The idea was that protons "drop" from atomic space-time sheet with $k = 137$ to a larger space-time sheet to $k_1 > 137$ space-time sheet and the difference of zero point kinetic energies is liberated as radiation [K3]. The proposal was that the zero point kinetic energies give rise to a hierarchy of metabolic energy quanta.

   Second possibility is phase transition in which the size of the $k = 137$ space-time sheet increases to $k_1 > 137$ and liberates the difference of zero point kinetic energy. For the third option energy preserving phase transition increasing $h_{eff}/h = n$ by a factor $(k_1 - k)/2$ followed by a phase transition reducing the value of h_{eff} back to the initial one but without change of the size of the space-time sheet would liberate the difference of zero point kinetic energies.

2. Could dark nuclear transitions explain UIBs? For $k = 149$ as the p-adic length scale of DNA letters would give nuclear energy scale $E = .5$ eV equal to the metabolic energy quantum by scaling 1 MeV for the ordinary nuclei by factor $2^{149-107}/2 = 2^{21}$ (here the original version of text contained error: this claim was made for $k = 141$). This energy has correct order of magnitude but is too high an energy for UIBs but there are of course also smaller energies possible for the nuclear excitations possibly explaining the UIBs.

3. What about hydrogen bonds? The strength of hydrogen bond - essentially the bond energy - is in the range .4-.5 eV -, which as such does not correspond to the average UIB energy, which come approximately as three lowest powers of two. The range of bond energies is .1 eV is smaller than the smallest UIB energy .11 eV.

   UIBs can be associated with hydrogen bonds if there are states of bond with higher bond energy. They could correspond to higher values of $n = h_{eff}/h$ for the de-localized dark proton associated with the bond (analogous to de-localized valence electron). For instance, if the energy of the bond corresponds to the cyclotron energy of proton in a magnetic field associated with the bond, it is proportional to n.

   The photon energies come approximately as powers of 2. If the favored values of n are in bands around $n = 2^k$ favored by the p-adic length scale hypothesis, one has hopes of understanding the band structure in terms of transitions reducing the value of k.

Membrane potential (see `http://tinyurl.com/chylvs9`) plays a key role in metabolism and one can wonder whether UIBs might relate to the potential energies defining energies $E_J = ZeV$ of Josephson photons associated with membrane if it acts like Josephson junction like structures associated with the prebiotic lifeforms.

1. Membrane potential energy varies in the range (.04, .08) eV (cell interior is negatively charged). Excitable cells (able to generate action potentials) include neurons, muscle cells, endocrine cells, and some plant cells. The average value for them is around .06 eV and further depolarization makes these cell more excitable. This suggests that the instability is caused by thermal radiation with nearly the same energy. The threshold for the generation of the action potential E_{act} is in the range $(.050, .055)$ eV. Interestingly, during ageing neurons become more hyperpolarized and therefore less excitable. In photoreceptors the resting potential energy can be as low as .03 eV making them very sensitive to light.

2. In TGD inspired quantum biology axonal membrane can be seen as a generalized Josephson junction [K14, K15, K17] decomposing nanoscopically to Josephson junctions defined by cell

membrane proteins. The protein as junction would correspond to a magnetic flux tube along which various charged particles with $h_{eff} = n \times h$ flow possibly as supra currents. As a special case cell membrane acts like an ordinary Josephson junction. In this case the increment of the electrostatic energy of the Cooper pair over membrane given by $E_J = 2eV$ defines the energy of the smallest quantum of Josephson radiation.

The intensity of thermal radiation at temperature T as function of photon energy E has a peak at $E \simeq 3T$, which for room temperature about $T = .03$ eV gives $E_{max} = .09$ eV. The energy ZeV of Cooper pair should be larger than E_{max}. For critical action potential one has $E_{act} = 0.1$ eV, which is slightly above $E_{max} = .09$ eV so that the action potential has minimal value and thus minimizes metabolic energy costs and implies quantum criticality with temperature as a critical parameter.

Note however that for energies below E_{max} the intensity of thermal radiation decreases so that also these energies might serve as Josephson energies: this and the fact that incoming photons have intensity higher than termal background at this energy could explain why some photoreceptors can have $eV = .03$ eV.

3. Could also Josephson radiation relate to UIBs? The Josephson energy of Cooper pair for the membrane potential is around $E_J = 0.1$ eV, which corresponds to the lowest UIB band, which could thus correspond to action potential .05 eV of excitable membrane. The higher bands would correspond roughly to two octaves suggesting that the action potentials in these case are roughly .1 eV and .2 eV. Quantum criticality would suggest that temperatures scale like the energies of the bands slightly higher than $E_{max} \simeq 3T$.

Metabolic energy transfer between magnetic body and biological body (defined in very general sense for any system) is possible if the spectra of transition energies share common transition energies. Therefore the spectrum of transition energies assignable to hydrogen bonds could have many transition energies common with that assignable to dark nuclear transitions and second and third explanation could be consistent with each other.

3.2.2 Model for hydrogen bond

The explanations of UIBs in terms of hydrogen bonds encourages to consider a concrete model for the hydrogen bond as flux tube. This suggests a connection with metabolism at cellular level involving transfer of protons through cell membrane against potential gradient assumed to take place as dark protons carrying the metabolic energy and providing it to ADP-ATP process after their return.

1. The simplest model for the proton inside flux tube is as particle in 1-D flux tube with magnetic field. Unless the magnetic field strength and/or n is very large, the kinetic energy in the direction of flux tube dominates and phase transition would change the scale of kinetic energy proportional to n^2 for fixed flux tube length. For $n = 2^k$ this would give too strong dependence of photon energies on k.

2. On the other hand, if the flux tubes are flux loops of the magnetic body of molecule their lengths naturally scale as n and the longitudinal kinetic energy is not affected in the transition. The cyclotron energy proportional to n would change and for $n \sim 2^k$ one obtains qualitatively correct behavior.

   For proton in magnetic field of $B_{end} = .2$ Gauss the cyclotron frequency is 300 Hz and corresponds to $E_c(B_{end}) = 1.2 \times 10^{-12}$ eV. The identification of $E_c(B) = .5$ eVs would give $E_c(B) = n(B/B_{end}) \times E_c(B_{end}) = E_c(B) = .5$ eV. An estimate for B for the flux tube of hydrogen bond comes from flux quantization: $eBS = 1$ holds true for unit quantum of flux and for flux tube radius of one Angstrom this would give $B/B_{end} \sim 5 \times 10^8$. This gives the estimate $n \sim 10^8 \sim 2^{27}$. The rather large value conforms with the general vision for the values of n for dark protons whereas dark electrons of valence bonds would have much smaller values. The emergence of dark protons could be seen as the transition from chemistry already involving n as characterizer of valence bonds [L10] to bio-chemistry.

3. The identification of the metabolic energy quantum in terms of cyclotron energy could apply also in the case of cellular metabolism. The model for the generation of ATP from ADP assumes that protons are pumped by the energy coming from nutrient molecules against the membrane potential.

   The membrane potential correspond to energy of .05 eV but metabolic energy quantum is 10 times larger. This looks like an inconsistency, which in thermodynamical approach is resolved by introducing of chemical potentials. In genuine quantum approach the introduction of thermodynamics quantities is not allowed.

   The general vision about metabolic energy as a tool to increase $h_{eff}/h = n$ defining kind of molecular IQ suggests that the transformation to dark proton at magnetic flux tube along which proton can travel through the membrane is responsible for the most of the energy needed for pumping. After the dark proton has returned through cell membrane it transforms to ordinary proton and liberates the metabolic energy and makes possible ADP-APT transformation.

   The above model assumes that the lengths of hydrogen bonds as flux loops scale like n. This makes possible the reconnection of flux loops coming from opposite sides of the membrane to pair of flux tubes along which dark protons can flow. Similar picture applies also to other biologically important ions.

   The general view about superconductivity in TGD Universe [K14, K15] suggests that reconnection can give rise to a Cooper pairs of protons with members at separate flux tubes. Also Cooper pairs of electrons and biologically important ions could form by the same mechanism.

3.3 PAH world hypothesis from TGD point of view

The so called PAH world hypothesis (see `http://tinyurl.com/ycxm9zes`) has been proposed as a prebiotic era preceding RNA world. As a matter of fact, PAH world hypothesis inspired more a detailed development of TGD based model for dark nuclei.

Let us first list some properties of poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`).

1. PAHS consist of aromatic rings glued together along sides. By definition aromatic rings have delocalized electrons. In benzene, which is the classical and simplest example of PAH, the electronic state is quantum superposition of states in which bonds and double bonds alternate along the ring but are shifted by 60 degrees with respect to each other. Naphtalene has two aromatic rings and anthracene and pnenanthtrene have 3 rings.

2. PAHs are very stable non-charged non-polar molecules and are very common in Earth. They are found in coal and tar deposits and produced in an incomplete combustion of organic matter. PAHs are poisonous. For instance, tobacco smoke contains PAHs with carcinogenic effects. The stability of PAHs motivates the belief that a large fraction of carbon in the interstellar space consists of PAHs.

3. Benzene in difficult to detect in in the interstellar space since the rotational symmetry does not allow to detect rotational transitions. Recently however nitrobenzene was detected so that benzene and more complex PAHs presumably exist in interstellar space (see `http://tinyurl.com/yap9ksrg`).

Benzene and more complex PAHs can give rise to more complex aromatic by hydrogenation, oxidation, carboxylation, and nitrogenation and led also to the basic building bricks of DNA and amino-acids and PAHs are proposed to have played important role in prebiotic life.

1. PAH world hypothesis states that the polymer like sequences of PAHs serve as scaffoldings for the formation of RNA like polymers (see `http://tinyurl.com/ycxm9zes`). The key motivation is that the distances between PAHs are same as between RNA and DNA bases: 3.4 nm. The proposal is that during PAH era RNA nucleosides A, U, C, G were attached to PAHs by hydrogen bonds.

2. Second hypothesis is that formaldehyde molecules [(H_2C)=O] formed valence bonds with RNA bases and with each other giving rise to sequences analogous to the phosphate-ribose backbone of RNA. The sequence of disjoint CO=:s was replaced with the sequence ..(C-R)-O-(C-R)-O-.. with R denoting the RNA nucleoside. After this hydrogen bonds were split and the precedessor of RNA was detached from the PAH scaffolding. Later the pre-RNA strands were folded to form double pre-RNA strands similar to ribozymes. The problem is to understand how the formaldehyde backbone was replaces with more stable phosphate-ribose backbone.

In TGD framework dark nuclei would serve as scaffolding, which however does not detach from the corresponding biomolecules. The distances between dark variants of biomolecules would explain why the two distances are the same. Very many molecules, including PAHs, can attach around dark RNA/DNA and the periodic structure would be reflect the properties of dark nuclei. This could explain UIBs as emission bands of both dark nuclei and hydrogen bonds essential for the pairing and the transfer of metabolic energy between ordinary and dark biomolecules. Also in DNA double strand hydrogen bonds could serve similar function. If thermal radiation excites higher energy states of nuclei, the emission of UIBs depends on temperature. Perhaps this could be tested.

UIBs could therefore serve as a direct signature of dark nuclear physics. If dark nuclei are not associated with PAHs in vitro or in an environment not containing water, UIBs would be absent.

3.4 Did RNA replicate in codon-wise manner during RNA era?

3.5 Did RNA replicate in codon-wise manner during RNA era?

There was an interesting popular article in Spacedaily with title "*Scientists crack how primordial life on Earth might have replicated itself*" (see `http://tinyurl.com/y92ng5vd`). The research paper [I8] is titled "*Ribozyme-catalysed RNA synthesis using triplet building blocks*" and published in eLife (see `http://tinyurl.com/ya5qyjfn`).

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

These findings are highly interesting in TGD framework. In TGD the chemical realization of genetic code is not fundamental. Rather, dark matter level would provide the fundamental realizations of analogs of DNA, RNA, tRNA, and amino-acids as dark proton sequences giving rise to dark nuclei at magnetic flux tubes [L14] (see `http://tinyurl.com/yalny39x`). Also ordinary nuclei correspond in TGD Universe to sequences of protons and neutrons forming string like entities assignable to magnetic flux tubes.

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

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

1. During RNA era amino-acids associated with pre-tRNA molecules would served as catalysts for replication of RNA codons. The linguistic mode would have been "holistic" during RNA era in accordance with the findings of the above experiments. RNA codon would have been the basic unit.

2. This would have led to a smaller number of RNAs since RNA and RNA like molecules in tRNA are not in 1-1 correspondence. A more realistic option could have been replication of subset of RNA molecules appearing in tRNA in this manner.

3. Then a great evolutionary leap leading from RNA era to DNA era would have occurred. AA catalyzed replication of RNA would have transformed to a translation of RNA to proteins and the roles of RNA and AA in tRNA would have changed. [Perhaps the increase of h_{eff} in some relevant structure as quantum criticality was reached led to the revolution]

4. At this step also (subset of) DNA and its transcription to (a subset of) mRNA corresponding to tRNA had to emerge to produce mRNA in transcription. In the recent biology DNA replicates and is transcribed nucleotide by nucleotide rather than using codon as a unit so that helicases and DNA and RNA polymerases catalyzing replication and transcription should have emerged at this step. The ability of DNA to unwind with the help of helicase enzyme helping DNA to unwind is essential for the transcription and translation of DNA. Therefore helicase must have emerged together with the "analytic linguistic mode" as an analog of written language (DNA) decomposing codons to triplets of letters. This would been a crucial step in evolution comparable to the emergence of written language based on letters. Also the counterpart of RNA polymerase and separate RNA nucleotides for transcription should have emerged if not already present.

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

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

5. How DNA could have emerged from RNA? The chemical change would have been essentially the replacement of ribose with de-oxiribose to get DNA from RNA and U$\rightarrow$ 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 [L14] (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 [L6, L17] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`).

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

1. The proposal is that 3-chords assignable to nucleotides as music of light with allowed 64 chords defining what I have called bio-harmony is essential for the resonance [L18, L19, L17](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 [L1, L18] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/ydhxen4g`) based on the fusion of icosahedral (12 vertices and 20 triangular faces) and tetrahedral geometries by gluing icosahedron and tetrahedron along one face, provides a model as Hamiltonian cycle and produces genetic code as a by-product. Different Hamiltonian cycles define different harmonies identified as correlates for molecular moods.

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

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

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

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

   (b) One could have

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

   .

   (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 [L1].

   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.

4 Improved reckless speculation about higher level variants of dark genetic code

In an earlier article I represented what I called reckless speculations about higher level variants of genetic code (see [L14] for the updated version of the original article). The speculations turned out to be not only reckless but to contain besides an unrealistic working hypothesis for p-adic length scale of dark DNA also a numerical error in the estimate of dark nuclear excitation energy scale leading to a wrong track.

The wrong working hypothesis was the assumption that ordinary DNA, RNA, etc correspond to same p-adic length scale as their dark variants. Simple argument shows that the dark scales must result via radial scaling of the typically linear structures such as DNA, RNA, etc and also 2-D structures such as membranes and microtubules giving rise to 2-D lattice like realizations of genetic code generalizing the ordinary 1-D realizations.

Also new improved picture conforms with the vision that dark realizations of genetic code at various p-adic length scales serve as controllers of the ordinary biochemistry, which is kind of shadow dynamics. Replication, certainly one of the most mysterious feats of living matter, would reduce to the replication at the level of dark DNA in various p-adic length scales involved. This would be a huge simplification.

A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h_0 = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier. A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier [K10].

4.1 Ideas

Consider first the general ideas.

1. The assumption of prime values for k in $L(k)$ would pose extremely tight constraints on the allowed p-adic length scales and values of h_{eff}/h_0. One would have $k \in \{127, 131, 137, 139, 149\}$ and $k \in \{151, 157, 163, 167\}$ and $k \in \{173, ..\}$ at least at the level of dark matter. So predictive an idea deserves to be killed, if not anything else.

   A further motivation for these speculations is that the Gaussian Mersenne primes $M_{G,k=}(1+i)^k - 1$ for $k \in \{151, 157, 163, 167\}$ define p-adic length scale $L(k) \propto 2^{k/2}$ between 10 nm assignable to the neuronal membrane and 2.5 μm assignable to cell nucleus: so many Gaussian Mersenne in so short length scale range is a number theoretical miracle.

2. Cell membrane consisting of two lipid layers (see `http://tinyurl.com/h9a2hsq`) is a binary structure as also DNA double strand. DNAs replicate as would do also RNAs during RNA era. Also cells and therefore also cell membranes replicate so that the analogy might make sense. Since processes like translation and transcription do not occur, cell membrane might serve as 2-D as analog of RNA: the counterpart of RNA era might prevail at these levels. Neuronal membrane might correspond to 2-D analog of DNA.

   So: could various 2-D structures such as nuclear membrane, cell membrane, neuronal membrane, and microtubuli correspond to a new level in the hierarchy of dark codes for which genes and their dark variants would be 2-D rather than 1-D structures? One would have 2-D lattices of codons. Could there be entire hierarchy of them assignable to certain p-adic length scales? As 2-D realizations could be paired with their dark variants so that one could speak of dark variants of various membrane like structures. This applies also to microtubuli.

   The idea that dark variants of DNA, RNA, and AAs are their radially scaled up variants generalizes also. The processes like replication of cell could be induced by a much simpler replication of 2-D dark DNA. This kind of pairing hierarchy could be behind miraculous looking replication of entire organisms. p-Adic fractality and hierarchy of dark DNAs could lurk behind the curtains.

3. The structures of ordinary bio-matter and also their dark variants assumed to control them are characterized by p-adic length scales. How these p-adic length scales could relate? The natural idea inspired by scaling invariance is that the dark variants of 1-D linear structure and 2-D structures formed from ordinary bio-matter are obtained by radial scaling consistent with p-adic length scale hypothesis, and guaranteeing that the distances between building bricks are scaled to the size scales of dark variants of DNA and other basic molecules. This rule makes sense also for the 2-D structures. For instance, it would scale up the p-adic length scale $L(143)$ characterizing lipid to $L(149)$ assignable to single dark RNA strand or $L(151)$ assignable to dark double DNA strand.

4. One can argue that cell membrane - in particular neuronal membrane - is highly dynamical unlike RNA. In ZEO however dynamical evolutions of space-time surfaces as preferred extremals - correlates for behaviors - replace 3-D static patterns as basic entities so that the emergence of cell membrane might mean dark genetic code for dynamical patterns analogous to deterministic computer programs defining predetermined dynamical patterns. In central nervous system nerve pulse patterns coded by dark RNA could provide similar coding of behavioral patterns.

5. I have claimed in earlier publications that the lipid double layer defining cell membrane has thickness $L_e(151) = 10$ nm: actually the thickness is $L_e(149) = 5$ nm for ordinary cells and 8-10 nm - roughly $L_e(151)$ - only for neuronal membranes. Therefore the emergence of neuronal membranes could be seen as an evolutionary step in p-adic and thus number theoretic sense. Needless to say, this little difference might be absolutely crucial for undestanding why neurons are at higher evolutionary level than ordinary cells. It would be nice if this difference could correspond to an increase of $h_{eff}/h_0 = n$ and p-adic length scale of ordinary and dark membrane like structure by a factor 2.

   There is double cell membrane associated with mitochondria. The thickness of the two double membranes is about 7 nm so that they might correspond to $k = 149$. The double membrane would have roughly the thickness 22 nm. If this structure is a functionally coherent structure it would corresponds to $L_e(153)$ and could be controlled by its dark counterpart.

6. I have proposed that the flux tubes connecting the dark DNA sequences above lipid layer to those associated with DNA could make possible to realize topological quantum computation [K1, K19] in terms of braiding induced by the 2-D liquid flow induced by nerve pulse patterns at nuclear membrane. Flux tubes might be associated with cytoskeleton and define an analog of central nervous system at the level of cell. A rough estimate for the numbers of codons for human DNA of length about 1 m and the number of codons allowed by the surface of the nuclear membrane are of order 10^9 so that the proposal might make sense.

   This proposal generalizes and has many alternative forms. For instance, microtubules inside axons could be connected by flux tubes to the surface of axons.

   One could also consider braidings between ordinary and dark levels, say braiding of flux tubes connecting lipid layers of neuronal membrane to 2-D analog of dark DNA. This braiding would code quantum computer programs and be part of coding of nerve pulse patterns inducing 2-D flow of lipids to memories represented as braidings. Quite generally, the braidings could be very naturally between ordinary and dark variants of structures considered.

4.2 Could cell membrane and neuronal membrane realize genetic codons as 2-D structures?

In the sequel I discuss in more quantitative level the idea that cell membrane and neuronal membrane realize analogs of genes as 2-D structures.

4.2.1 The p-adic length scales associated with the dark variants of 2-D structures?

Consider next the p-adic length scales associated with the structures considered.

1. The thickness of ordinary cell membrane corresponds roughly to $L_e(149) = 5$ nm whereas the coiling associated with the cell membrane corresponds to $L_e(151)$. Also neurons correspond

to $L_e(151)$. Could $k = 149$ *resp.* $k = 151$ define levels of ordinary cell *resp.* neuron in the hierarchy of dark nuclear physics?

2. Cell membrane consists of lipid bilayer. The lipid layer has three parts (see `http://tinyurl.com/h9a2hsq`).

   - The totally hydrated layer nearest to water is hydrophilic head group, which in the case of phospholipids contains negatively charged phosphate. This phosphate layer has thickness $.7 - 1.0$ nm.
   - Below it is a partially hydrated layer of thickness .3 nm, which corresponds to $L(141)$: this of course puts bells ringing!
   - Hydrophobic lipid tail layer below it is dehydrated. The thickness of single lipid layer is 1.25-1.75 nm and would correspond to the p-adic length scale $L_e(145) = 1.2$ nm. $k = 145$ is not prime.

3. The phosphate layer analogous to phosphate-ribose backbone and the thickness $L(141)$ of partially hydrated layer suggests that it corresponds to EZ created in Pollack effect so that there would be parallel dark RNA sequence along axon (possibly helical as for microtubules). In the case of cell membrane would have lattice like system formed from dark protons, and maybe even dark neutrons (as an analog for the neutron halo in some nuclei).

4. If the recent biology is the analog of RNA era for $k = 149$ codes, their manifestations could be seen as analogs of RNAs and the number of different lipids associated with the cell membrane could give some idea about their number. Cell membrane could perhaps be seen as a 2-D analog of RNA polymer. Cell division implying membrane replication would be induced by dark RNA replication. Even the analogs of tRNA and AAs but not proteins might be present if one takes the analogy very seriously. Could one identify pairs of lipids and some molecules analogous to proteins appearing in cell division?

What kind of general conditions can one pose on the dark variants of DNA, RNA, and AAs?

1. Dark variant of 2-D variants of DNA, RNA, or AAs realizing the hierarchy of dark codes should control their analogues or possibly some other molecules coded by them. The coupling would be by resonance. This suggest the hierarchy of codes uses as building bricks simpler structures by starting from 1-D structures and building from them more complex structures. Hence the natural hypothesis is that the 2-D variants of proteins consisting of a 2-D lattice like structure formed from proteins is in question.

2. The geometric aspect of membrane dynamics would be determined by basic dynamics of TGD determined by action, which is a generalization of charged point-like particle coupling to Maxwell field by replacing the particle orbit with 4-D surfaces. This allows as special case minimal surfaces such as deformations of cosmic strings giving magnetic flux tubes. Cell membranes should correspond to extremals for which coupling to Kähler force is non-trivial as it indeed is by membrane potential. This because static closed surfaces, in particular spherical layers, are not possible as minimal surfaces. Remarkably, these extremals are not analogs of external particles (geodesic lines) but correspond to interaction regions. This conforms with the fact that cell membrane is a self-organization pattern requiring a continual feed of metabolic energy.

   The 2-D dark variants of DNA, RNA, and AAs would be involved mostly with the control the electro-chemistry of membrane like structures. Of course their geometrodynamics would induce also morphogenesis of ordinary bio-matter.

   Also enzymes and ribozymes would have dark variants controlling their behavior. Folded protein represents an interesting example about possibly 3-dimensional graph like structure in which the protein forms an analog of Hamilton's cycle going through all points of the graph defined as a lattice with nearest neighbors connected by edges without self-intersections. This hypothesis is rather powerful since for Hamiltonian cycle do not necessarily exist for an arbitrary graph.

3. In the case of cell membrane membrane proteins are the natural candidate for the building bricks. They indeed have an active role and serve as both channels and pumps and in the case of the neural membrane this role is especially important. Membrane proteins are identified in TGD framework as generalized Josephson junctions. In the case of cell membranes mebrane proteins having length of about 5 nm (5 AAs) or 10 nm (10 AAs) going through the membrane are an excellent candidate for the basic building brick. One could see the basic structure either as 2-D structure built from membrane proteins or 3-D structure build from AAs. Membrane proteins would form kind of generalized protein as a 2-D lattice of proteins and accompanied by their dark variants or of 2-D dark variants of RNA or DNA coding for them and identifiable as radial scalings of these proteins to $k = 149$ or $k = 151$.

   The model for topological quantum computation [K1] suggesting that DNA codons of are connected to lipids of cell membrane could be modified so that dark DNA, RNA, or AAs associated with membrane proteins are connected to them by flux tubes which can get braided. This would allow the quantum control of the 2-D protein like structure and make it effectively single quantum coherent Josephson junction as suggested in the quantum model for nerve pulse [K17].

The original proposal was that there might exist an analog of genetic code for lipids. The number of different lipids is however too high to allow any simple correspondence. Lipids have also rather passive role in the dynamics of the cell membrane: their serve as signal pathways, provide metabolic energy, and serve as signal pathways (see `http://tinyurl.com/z7d7osm`). The proposal however deserves to be explained.

1. Both sides of the lipid bilayer of cell membrane could pair with 2-D lattice of dark RNA whose size scale would be obtained by radial scaling giving rise to what might be called dark cell membrane. In the case of neuronal membrane the dark lattice would consist of pairs of dark DNA codon and its conjugate. In the case of axon one could have the analog of dark DNA strand extended to a cylinder containing bundles of these strands at its surface. Lipid layers would be 2-D analogs of 1-D DNA strands in this case.

2. Lipids would be analogs of ordinary RNA codons and dark RNA codons would code for them: this would predict 64 different lipids in cell membrane. Single dark RNA would correspond to the size scale of single lipid given by $L(143) = 2L(141) = .625$ nm. The dark nuclear physics would correspond to $k = 149$. The number N of parallel dark RNA strands would be roughly the circumference of the axonal lipid layer divided by the size of single lipid about $L(143) = .625$ nm given by $N \sim 2\pi \times L_e(167)/L_e(143) = \pi \times 2^{24} \sim 5 \times 10^6$.

4.2.2 Thermodynamical constraints

Could this totally irresponsible speculation about p-adic hierarchy of dark nuclear physics and genetic codes survive thermodynamical constraints?

1. The condition that metabolic energy quantum is not below thermal energy at physiological temperatures poses constrains on the model. I have considered several identifications of the metabolic energy quantum. These identification need not be mutually exlusive.

   - One interpretation is as 1-D zero point kinetic energy of proton at tubular space-time sheet of atomic size with transversal length scale $L(137)$. This energy is invariant under scalings induce by increase of h_{eff} since h_{eff}^2/L^2 is not changed.
   - Second identification of metabolic quanta would be as energies assignable to hydrogen bond and its dark variants.
   - Third identification of the metabolic energy quantum would be as scaled variant of $E_b(k) = 2^{(k-107)/2}E_b$ of typical dark nuclear binding energy $E_b =\sim 1$ MeV. The value would be about .5 eV for $k = 149$ and .25 eV for $k = 151$.

2. Note that the action potential assignable to $k = 151$ neuronal membrane is around .05 eV (the membrane potential for some photoreceptors is .03 eV). In TGD Universe the cell membrane

can be seen as Josephson junction decomposing in an improved resolution to membrane proteins acting as Josephson junctions [K14, K15]. Josephson energy of Cooper pair is twice this - that is $E_J = 0.1$ eV slightly above the maximum $E_{max} = 3T = .09$ eV of the thermal distribution at physiological temperature.

3. As far Josephson radiation are considered, for $k = 151$ membrane would be a quantum critical system. Quantum criticality could give rise to instability making possible the generation of nerve pulses. During nerve pulse the dark protons at the dark space-time sheet would return to the neuronal membrane and destroy the ionic equilibrium. Also the temperature criticality of consciousness manifesting itself as the generation of hallucinations during fever could be understood. For $k = 151$ the situation would be overcritical and will be discussed separately.

The Josephson energy of Cooper pair is scaled down to $E_J = .1$ eV near to $E_{max} = .09$ eV. This is slightly above the thermal energy but one could still argue that Josephson radiation cannot carry information. Or could Nature have found the means to overcome this potential problem? The notion of generalized Josephson junction central in TGD inspired theory of EEG as communications from brain to MB [K17, K7] could save the situation.

1. For the generalized Josephson junction the energy of quantum of Josephson radiation is $E = E_J + \Delta E_c$, where ΔE_c is the difference of cyclotron energies at the two sides of the membrane. E_c is proportional to $h_{eff} = n \times h$ and large enough value of n guarantees that E_c is above $E_{max} \simeq 3T$ irrespective of the value of the membrane potential. The variations of the membrane potential modulate Josephson frequency, and are proposed to provide a coding of sensory data defined by nerve pulse patterns communicated to MB.

2. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis [K13, **?**] guarantees the spectrum of cyclotron energies is universal and does not depend on the mass m of the charged particle being in the range of visible and UV energies of photons (this allows to deduce information about the values of mass M and velocity parameter $v_0 < c$): bio-photons would be produced in energy conserving phase transitions transforming dark photons to ordinary ones [K4, K6].

3. If MB itself (a structure which has size scale of Earth at EEG frequencies around 10 Hz) has low enough temperature, this would allow to overcome the limitations caused by the thermal masking of the ordinary Josephson radiation so that the frequency modulations by nerve pulse patterns could code for the sensory data. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis indeed allows very large values of h_{eff} for which ordinary cyclotron energies proportional to h_{eff} would be ridiculously small for the ordinary value of h.

What about the situation for massive particles like proton? Now Maxwell-Boltzmann (Gaussian) distribution is a good approximation and for effectively D-dimensional system the value of distribution is reduced by $1/e$ at thermal energy $E_{cr} = DT/2$. One could argue that above this energy thermal masking can be avoided. For $D = 1$ at magnetic flux tubes this would give $E_{cr} = T/2 = E_{max}/6$. At $T_{phys} = .03$ eV one would have $E_{cr} = 0.15$ eV. Metabolic energy quantum would be above E_{cr} for $k = 151$. Even $k = 153$ possibly assignable to mitochondrial double membrane can be considered but represents an upper bound at physiological temperatures.

Remark: In TGD view about information processing in brain [L8] active linear neuron groups relate to verbal cognition and 2-D neuronal groups relate to the geometric cognition associated with the decomposition of perceptive field to objects. At cellular level DNA and cell membrane could perhaps be seen as counterparts for these structures. In TGD framework neuronal membrane is proposed to be a constructor of sensory representations communicated to the magnetic body (MB) using generalized Josephson radiation whereas motor control by MB has been assumed to take place via DNA [K9].

4.3 DNA packing problem and p-adic length scales

DNA manages to pack huge amount of DNA to single cell nucleus. For instance, human DNA as length of about 1 meter. This is achieved by a hierarchical coiling structure involving 3 levels with highest level identifiable as chromatides and the lowest level defined by nucleosomes (see `http://tinyurl.com/yat5cm4y`) wound around histon isomers linked together by straight portions

of DNA. One can find a detailed representation of the 4-levelled packing of DNA (see `http://tinyurl.com/ybxv6w4v`).

There are 4 levels involved. Could they relate to the Gaussian miracle primes $k = 151, 157, 163, 167$? The general proposal is that the products of powers of small primes define the scale hierarchy. There is evidence that at least the powers of 2 and 3 define p-adic length scales, which would correspond also to dark scales. The simple guess is that the dark scales are identical to the ordinary p-adic scales.

- The diameter of the nucleosome is 11 nm $= 1.1L(151)$, which suggests $k = 151$. Chromatosome consists of histone H_1 plus nucleosome.
- Nucleosomes coil to form a fiber of diameter $d = 30$ nm. This scale is $3L(151)$.
- At the next level loops of average length 300 nm $= 30L(151) \sim 32L(151)$. This level is only intermediate level in packing.
- These loops compress and fold to 250 nm $=25L(151) \simeq 3 \times L(157)$, $L(157) = 8L(151)$ wide fiber. Thus third harmonic of also the miracle length scale $L(157)$ would be involved.
- This fiber compresses a tight coil of radius 700 nm $= 70L(151) \simeq 64L(151) = L(163) = 640$ nm giving rise to the chromatid fiber of chromosome. $k = 163$ is the third miracle length scale.
- Chromosomes have width 1400 nm which corresponds to the scale $L(165)$.

The 3 levels $k = 131, 157, 163$ seem to be realized although not in the simplest manner. Nuclear membrane would correspond to $L(k = 167) = 2.5$ μm. For $n = h_{eff}/h_0$ these levels would correspond to the values n of form $n = 2^r 3^s$.

Consider next nucleosome.

1. DNA wraps of around histone octamers forming a cubical structure consisting of 8 smaller cubes (octamers). There are 2×4 histones forming two identical layers. The 4 histones H_{2A}, H_{2B}, H_3, H_4 of given layer are not identical. There is also histone H_1 attached to the entire structure. The incoming DNA double strand enters to the upper end of H_1 and leaves from its lower end. H_1 is related to the secondary coiling. The wrapping gives rise nucleosomes as helices with two turns and containing about 146 base pairs making 48 codons plus 2 base pairs.
2. According to the standard model of nucleosome double DNA strand wraps around the analog of a spool formed from an octamer consisting of two identical units above each other consisting of 4 different histones. The incoming DNA strand enters the upper 4-histone unit and winds once around it and then does the same for the lower unit before leaving the nucleosome.

One can construct a rough TGD inspired model for this structure (not completely realistic) to get a concrete idea about what is involved.

1. The size scale of the cube like structure is $L(151) = 10$ nm so that single histone corresponds to a cube with side roughly about $L(149) = 5$ nm. One can estimate the total length L of the wire from the equation $z = xR\phi/\pi$, $R \sim L(149)$, $\phi \in [0, 4\pi]$, as $L = \sqrt{1 + \pi^{-2}} 4\pi R$. For $R \sim L(149)$ and $h = L(151)$ this gives $L \sim 66$ nm, There are roughly 146 DNA base pairs and 48 whole codons ($144 = 3 \times 48$ base pairs) and each codon has length about 1 nm. This gives total length of 48 nm. The reduction of radius R by factor $r = 48/66 = 3/4$ to $R = 3L(149)/4$ would give a correct value of L

   According to the representation for the hierarchy of packings (see `http://tinyurl.com/ybxv6w4v`), the diameter of the structure is $d = 1.1L(151)$ rather than small and the height of the structure is smaller in the illustration. This width is however not consistent with the helix structure for any value of the height.

2. If the double DNA strand is accompanied by a dark double strand of radius $L(149)$, the situation is like having a band of width $L(151)$ going around the spool. The dark double strand covers an area, which is 4/3 times the spool area. The horizontal thickness of the entire dark structure is about $d_D = (7/4)L(151)$. If the radius of DNA double strand is $r = L(151)$ the area covered by the double strand is roughly twice the area of the spool. This suggests that one should identify the p-adic length scale of DNA double strand as its diameter about $L(151)$ rather than its radius.

Remarks:

1. While trying to understand nucleosomes in TGD framework, I encountered an interesting side result related to Hamiltonian face paths and Hamiltonian cycles on octahedron, which to my best understanding must correspond to Hamiltonian paths and cycles on cube. The octahedral face paths can be identified as closed paths connecting the middle points of the centers of a cube. The 8 histones define a decomposition of the entire cube to 8 sub-cubes. The idea was that Hamiltonian face cycles in these cubes could give up to tight packing of 6 codons. The number of the Hamiltonian paths for cube is 64 (see `http://tinyurl.com/ybqw6zpt`) and the number of cycles is 6! Single genetic codon would dictate the choice of the Hamiltonian path on cue! Although the idea did not work (the length of, it led to ask whether the Hamiltonian cycles on octahedron or their duals at cube might have some biological relevance.

2. A further interesting finding is that the sequence of 8 quints defines a piece of 12-note scale proceeding by quints as steps between nearest neighbor vertices (using octave equivalence) in the icosahedral model of harmony [L1, L21] based on 12-note scale could be interpreted as cubic Hamiltonian cycle giving rise to the notes $F, C, G, D, A, E, H, F\sharp$. This gives the notes of C major scale with 7 notes plus tritonus $F\sharp$ defining half-octave as 8:th note. One could also identify the cycles as consisting of the notes of 8-note scale along cycle in the usual order $C, D, E, F, G, A, H, F\sharp$ based on standard notion of nearness for which neighboring vertices correspond to neighboring notes of the scale. Allowed 3-chords would correspond to triplets containing no neighboring notes. The Hamiltonian cycle for cube is unique apart from isometries as also for tetrahedron and dodecahedron.

4.4 Microtubules as quantum critical systems

Also microtubules (see `http://tinyurl.com/y8km9vve`) are 2-D structures having a strong resemblance with the lipid layers of cell membrane. Could a higher level representation of genetic code similar to the one proposed for cell membranes make sense for them. Also now one can imagine that the microtubular surface is accompanied by its dark variant realizing 2-D dark genes, dark RNA, or dark proteins with scaled up size. The p-adic prime should correspond to $k > 151$ so that higher level realization of genetic code would be in question. In the case of axons a possible identification for the dark scale would be as the radius of the axonal membrane.

1. Microtubules are hollow cylinders with outer *resp.* inner diameter equal to 24 *resp.* 12 nm (the scales differ by factor 2) so that their thickness is 12 nm is same as the inner radius and would correspond to $L(151) = 10$ nm. They decompose to 13 parallel helical filaments consisting of 13 tubulin proteins having size scale of order $L_e(151)$.

2. Tubulins are dimers of α and β tubulin and the pairs are oriented along the helical filament. One can estimate the size of α and β tubulin by diving the circumference of 24 nm of the microtubule with the number of filaments, which is 13. This gives for the size scale of tubulin the estimate $R_{tub} \sim 12$ nm not far from $L(151)$. This supports the view that p-adic length scale $L(151)$.

   The size scale of the transversal volume associated with lipid is roughly .62 nm that is $L(143) = 2L(141)$ so that they could correspond to $k \in \{141, 143\}$, presumably $k = 141$. Therefore one could see microtubules as scaled up variants of cell membrane with scaling factor $2^{(151-141)/2} = 2^5 = 32$. Similar scaling would take place for the value of $n = h_{eff}/h$ giving $n = 2^{23}$ so that microtubules would represent a higher level of evolution identified as increase of n. Microtubules have indeed emerged after cell membrane.

3. It has been proposed that the α and β conformations of tubulin give rise to bit or even qubit. If this were the case, single helical filament rotating one full turn would have 2^{13} states and carry 13 bits of information. 13 independent filaments would have $2^{26} \simeq 64 \times 10^6$ states and carry 26 bits of information. One could also think of codon as sequence of 13 filaments with the states of filaments representing 2^{13} letters of the code.

4. Microtubular surface has rather high charge density and is polarized: the almost stationary end has negative local charge density roughly equal to that of DNA whereas the growing end has lower surface charge density. One manner to control the charge of the tubulin dimer is in terms of the charge states of GDP and GTP by ionization of the phosphates. Maximal negative charge for tubulin dimer would be 5 units.

   Microtubules are highly dynamical objects with inherent instability and have varying length: one might say that microtubules are quantum critical objects. Quantum criticality and thus instability might relate to the fact that the metabolic energy quantum is very near to thermal energy at room temperature.

   The dynamics for the length of microtubule could be induced from the dynamics of EZ involving the flow of protons between microtubule and its magnetic body defined by dark DNA. The gradient in charge density would make possible positive net charge density at the growing end of the microtubule.

   In ZEO it looks reasonable to argue that the dynamical patterns are coded by a generalization of genetic code just as computer programs code for deterministic dynamical patterns.

5. What could the dark code behind the dynamics be? The α- and β tubulins of tubulin dimer involve GTP (see `http://tinyurl.com/ybtjluaf`) *resp.* GDP (see `http://tinyurl.com/y8uok7kq`). In the case of DNA one has XMP, $X = A, T, C, G$. The analogs of dark RNA sequences would contain mere G and the information coded by the tubulin would be determined by the conformation of the tubulin dimer giving 1-bit code. This looks somewhat disappointing.

   If the charge states of the phosphates of GDP and GTP can vary and all charge combinations for phosphates are possible, one has 2^3 charge states for GTP and 2^2 charge states for GDP. Together with the bit associated with the tubulin conformation this would give 2^6 states and realize 6 bits of the ordinary genetic code! One would have 2-D realization of the genetic code analogous to that proposed for the lipid layer with the state of tubulin analogous to RNA codon.

   This coding together with thermal criticality would make microtubule a dynamical object since the deviation of the tubulin charge from -1 units would spoil charge local charge neutrality of tubulin-dark RNA pair.

I have proposed that flux tubes connecting tubulins to the lipids of the axonal lipid layer could give rise to topological quantum computation [K1, K1]. The size scale of lipid is about $L_e(141)$ and that of tubulin about $L_e(151) = 32L_e(141)$, and the radius of axonal membrane is by two orders of magnitude larger than microtubular surface. Hence this proposal does not look realistic unless one assumes that sub-structures of cell membrane with size scale of order $L_e(167)/L_e(151) = 2^8$ larger than tubulin size represented as space-time sheets with cell nucleus size $L(167)$ have flux tube connections to tubulins.

This kind of map would give rise to a kind of abstraction about what happens at the level of axonal membrane integrating out un-necessary details. This abstraction is natural since microtubules would indeed correspond to a higher level of cognitive hierarchy. Roughly $N = 2^{16}$ lipids would contribute to the information received by single tubulin. Could nerve pulse patterns can induce braiding of the flux tubes in this scale?

5 Freaky DNA

The popular article "*Freaky Eight-Letter DNA Could Be the Stuff Aliens Are Made Of*" (see `http://tinyurl.com/y5wb7cm8`) tells about very interesting discovery related to astrobiology, where the possible existence of variants of DNA and other bio-molecules are of considerable interest.

The article "*Hachimojii DNA and RNA: A genetic system with eight building blocks*" (see `http://tinyurl.com/y2mcjb4r`) published in Science tells about a discovery of a variant of DNA with 8 letters instead of 4 made by Hoshika *et al* [I2]. By using an engineered T7 RNA polymerase this expanded DNA alphabet could be transcribed into Hachimoji variant of RNA. The double strand structure of hachimoji DNA is similar to that of ordinary DNA and it is thermodynamically stable.

No amino-acid (AA) counterparts assigned to the hachimoji RNA were engineered: this would require the existence of translation machinery. The possible existence of also additional AAs leads to the speculation is that both alien life forms utilizing this kind of extended code could have evolved. One can also ask whether mere synthetic hachimoji RNA could be enough for synthetic life.

The abstract of the article gives a more technical description about what has been achieved.

> *We report DNA- and RNA-like systems built from eight nucleotide "letters" (hence the name "hachimoji") that form four orthogonal pairs. These synthetic systems meet the structural requirements needed to support Darwinian evolution, including a polyelectrolyte backbone, predictable thermodynamic stability, and stereoregular building blocks that fit a Schrödinger aperiodic crystal. Measured thermodynamic parameters predict the stability of hachimoji duplexes, allowing hachimoji DNA to increase the information density of natural terran DNA. Three crystal structures show that the synthetic building blocks do not perturb the aperiodic crystal seen in the DNA double helix. Hachimoji DNA was then transcribed to give hachimojii RNA in the form of a functioning fluorescent hachimoji aptamer. These results expand the scope of molecular structures that might support life, including life throughout the cosmos.*

If the additional code letters for DNA (8 code letters instead of 4) really carry information, the number of codewords is extended by factor $2^3 = 8$ giving $2^9 = 512$ code words. What the number of AAs would be, can be only guessed: the simplest guess is that also now the number is scaled up by factor 8 but this is only a guess.

In the sequel I consider hachimoji code from TGD perspective. The natural guess is that the hachimoji code corresponds to 8 copies of the ordinary genetic code in some sense. TGD predicts two basic realizations of the genetic code corresponding to dark genetic code and bio-harmony.

1. In the case of the dark code it is possible to imagine an extension of the code based on the notion of dark nucleus and the number codons is multiplied by 8. In the case of bio-harmony fusion of 8 copies of bio-harmony allows to realize hachimoji code.

2. I have considered two basic realizations of bio-harmony [L1, L21] giving also realization of genetic code. The first realization is as a fusion of 3 icosahedral harmonies and tetrahedral harmony. Second realization is as a fusion of 2 icosahedral harmonies and 1 toric harmony. These constructions do not however allow any elegant geometric interpretation since two different geometries are involved in both cases.

   During writing I was forced to reconsider this problem and realized that a fusion of 2 icosahedral harmonies with 20 chords and 2 dodecahedral harmonies with 12 chords produces genetic code with 20+20+12+12=64 codons. Icosahedral and docecadedral harmonies correspond to dual tessellations of sphere so that bio-harmony can be represented as a bundle over sphere with two notes represented as points of the fiber. Hachimoji harmony is obtained by replacing 2-point fiber with 8×2-point fiber. The presence of the dual tessellations conforms with the fact that Eastern music uses micro-intervals, which rather naturally correspond to 20-note dodecahedral scale.

3. The reason why for the hachimoji code could the basic problem of the music scale realized in terms of rational frequency ratios. Already Pythagoras was aware of this problem. The construction of the scale as powers of quint (3/2-fold scalings of the basic frequency) using octave equivalence produces with 12 iterations 7 octaves but only approximately: the 12th iterate does not quite correspond to the basic note in the octave equivalence. Performing the 12-fold iteration 8 times gives therefore a refined scale with each note replaced with 8 almost copies identifiable as hachimoji scale.

4. A further discovery was that the quint scaling appearing in the earlier model can be replaced with a unique scaling, which is same for icosahedral and dodecahedral codes. One must however generalize the notion of Hamiltonian cycle by introducing the analog of gauge symmetry in a discrete bundle over sphere and allowing to generate new Hamiltonian cycles from given cycle by gauge transformations. In this manner one obtains extremely rich harmony from single basic chord transposable to $CEG\sharp$.

5.1 Icosa-tetrahedral and icosa-dodecahedral bioharmonies as candidates for genetic code

Both the icosa-tetrahedral [L1] and icosa-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 [L15]. The basic reason is that the third harmony corresponds to doublets. One cannot exclude the possibility of several equivalent representations of the code.

5.1.1 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, oneas $A_5 \times Z_2$ 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 $Z_2 \times Z2$ 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 on 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 dublets. These 4-plets would correspond to (phe, tyr, his, gln, asn, lys, asp, glu, cys, stop-doublet) This leaves (stop,trp) double 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.

5.1.2 Dodecadedral 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 is 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.

5.1.3 Is icosa-dodecahedral harmony consistent with the genetic code?

One must check whether icosa-dodecahedral 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.

2. 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.

3. 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.

1. 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?

2. 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?

3. 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 [L19]!

   The condition that orbits of different cycles do not interesect 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 icosa-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).

4. 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 $24 \to 22$ 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.

5. 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 [L19]. 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.

5.2 Hachimoji code and realizations of genetic code suggested by TGD inspired quantum biology

The discovery of Hachimoji code relates interestingly to two realizations of the genetic code inspired by TGD based quantum biology.

1. The first realization is dark genetic code with codons realized as 64 3-proton states made of dark protons having non-standard value $h_{eff} = n \times h_0$ of Planck constant [L14]. The hierarchy of Planck constants is predicted by adelic physics providing physical correlates for correlation in terms of p-adic physics [L11]. Dark genetic code would be fundamental in

TGD and bio-chemical realization would be kind of shadow or mimicry of it and not even complete in some cases. One cannot talk about letter decomposition for dark proton triplets since the 3-proton states are entangled.

2. Second realization relies on the notion bio-harmony [L1, L21]: the realization of the genetic in terms of 3-chords of bio-harmony emerged as a by-product from a model of harmony.

5.2.1 Does dark realization of genetic code allow hachimoji code?

Could one realize hachimoji codons as dark codons?

1. If the proposed dark proton triplets [L14, L13] is the only fundamental realization of genetic codons, the real information storage capacity should not increase but the correspondence between dark codons and chemically realized codons would not be 1-to-1 but 1-to-8. Furthermore, the transcription of dark DNA to ordinary one would not be possible in 1-to-1 manner so that hachimoji code could not have evolved.

2. One can however imagine of having also neutrons rather than only protons in the dark nuclear string. If one can have both dark protons and neutrons, one could obtain effectively 8 letters. Also the number of dark RNA codons and perhaps also of ordinary AAs would increase - presumably by factor 8. Since the dark nucleons would be located along magnetic flux tube, Fermi statistics, which does not allow protons to have the same position, would not affect the situation and one would indeed obtain just the factor 8.

   There is however an objection. Dark proton sequences would be generated by the formation of exclusion zones in Pollack effect [L2] [L2], and would be stable against transformation to those containing neutrons since the energy needed to transform proton to neutron is about MeV and huge in the scale of biochemistry.

Is it possible to overcome this objection?

1. TGD inspired nuclear physics relies on nuclear string model [K11] for which unexpected correlations between nucleons (EMC effect) provide support. Nucleons would be connected bo nuclear string by color bonds having quark and antiquark at their ends. Bonds could be color neutral and color confinement would make the bonds stable.

   The bonds connecting nucleons to nuclear string would have u/d type quark and antiquark at their ends and could have total charges +, -1, and 0. This would predict new exotic states of nuclei with binding energy differences of order keV (small scale compared to MeV scale of nuclear binding energies). There is evidence for keV energy scale.

   In fact, several scaled variants of dark nuclear physics are predicted [L14], and the nuclear binding energy scale would behave like $1/L$, where L is the size scale of dark nuclei identifiable as p-adic length scale in TGD framework. Even dark nuclear binding energy scale of order metabolic energy quantum of order .5 eV can be considered.

2. Same would apply to dark nuclei formed from dark protons. The bonds connecting dark protons to nuclear string could also have total charge +1,-1, and there could exist two states with charge 0. Only 3 spin states analogous to those of (neural) ρ_0 meson are accepted in the original model whereas neural pion-like state is not allowed. Now the states analogous to both ρ_0 and ρ_{-1} are accepted. One can denote the bond as $B(q)$, $q = 0, +1, -1$.

   The pair $p + B(-1)$ would behave like neutron effectively. The pair $p + B(1)$ would have charge +2 and could be be unstable due to repulsion whereas neutron like state could be stable by attraction. This could give rise to an effective doubling of letters.

   Remark: A possible objection is that the neutral ρ meson like color bond is expected to have energy higher than neutral pion by spin-spin splitting as in the case of ordinary mesons. A good argument for throwing out the pion-like bond is needed.

5.2.2 Is the realization of hachimoji code in terms of bio-harmony possible?

What about the realization of hachimoji code as a bio-harmony [L1, L21]? Bio-harmony makes it possible to transfer the genetic information at the level of dark variants of basic bio-molecules (also RNA, AAs, and tRNA) in terms of 3-chords of dark photons coupling via frequency resonance. The coupling to ordinary variants of DNA would take place via energy resonance and involve the transformation of dark photon to ordinary photon or vice versa coupling. Music expresses and induces emotions and the music of dark photons would provide fundamental expression of emotions realized at the bio-molecular level [L18].

5.2.3 Can one scale the number chords of bio-harmony by factor 8 by using icosa-dodecahedral bio-harmony?

The number 64 of 3-chords defining the bio-harmony should be scaled up by 8. As far as chords are considered, each note appearing in the chord should be doubled.

1. There are two variants for bio-harmony. 12-note scale is represented as a Hamiltonian cycle defined as a closed path (by octave equivalence) going through all vertices of as tessellation of sphere or torus and not intersecting itself. Both icosahedron and tetrahedron can be regarded as tessellations of sphere by triangles.

   The first realization [L1, L21] involves fusion of 3 Hamiltonian cycles at icosahedron defining 20 chord harmony H_{20} each and 1 cycle at tetrahedron defining 4-chord harmony H_4. This gives 20+20+20+4=64 3-chords defining the codons.

   Second realization [L15] is a fusion of 2 20-chord harmonies H_{20} defined by Hamiltonian cycles at icosahedron and 24-chord harmony H_{24} by cycle associated with torus tessellation. The fusion of two icosahedral cycles gives 20+20 3-chords and torus cycle gives 24 chords: 64 altogether. There are large number of Hamiltonian cycles and their fusions would correspond to different emotional states.

2. Can one imagine any modification of the model giving rise to 8-fold increase of the basic chords? One can consider doubling of the 4 basic frequencies to 8. For instance, splitting of each frequency could correspond to the doubling of the code letters. One can also imagine that each triplet of dark nucleons (dark neutron would be now dark proton+the bond with varying charge) corresponds to its own cyclotron frequency triplet so that 8-fold increase of 3-chords would become possible.

3. Could one have a geometric interpretation for the 8-fold increase of 3-chords realized as faces of Platonic solid or toric triangular tessellation. Could summand in the sum of 3 icosahedral harmonies and one tetrahedral harmony (of 2 icosahedral and toric harmonies) be replaced with an analog of tessellation having 8-fold number of triangles? The splitting of each triangle to 8 smaller equilateral triangles so that the 12-note scale would have now $8 \times 12 = 96$ notes, is not possible since the side of the smaller triangle should be $2^{-3/2}$ times smaller than that of the original triangle: inverse integer scaling would be required.

4. The simplest manner to get 8-fold scaling for the number of chords is some kind of fusion of 8 octaves of bio-harmony. By octave equivalence the 8-letter code would bring new information at the level of bio-harmony perceived in an improved resolution only. New information would require that the fused scales differ slightly. A natural interpretation for the fusion would be as formation of a discrete bundle structure in which 8-fold increase of notes of the scale corresponds to 8-point fiber.

   The fusion of fundamental harmonies with 20, 4 or 24 3-chords is used in the proposed models of bio-harmonies. The geometric interpretation of the fusion is not quite clear. For a fusion of 3 icosahedral code one could imagine a discrete bundle structure in which 3 copies of note as points of icosahedron form a 3-point fiber. The addition of tetrahedron could be seen as a union of icosahedron and tetrahedron with gluing along common face. This does not however fit with the bundle interpretation.

   Same applies to the union of 2 icosahedral codes with $(V, F) = (12, 20)$ and 1 toric code with $(V, F) = (20, 24)$. One could ask whether the latter option could allow interpretation

as singular bundle structure such that in the fiber space two tori collapse to spheres. This would correspond to a disappearance of 4 faces so that one has 20 faces instead of 24. This does not look like an attractive option.

5. Could one find a realization of the code consistent with the bundle interpretation? Could one have 64 codons by using fusion of 2 icosahedral and 2 dodecahedral codes (forget for a moment that the faces of dodecahedron are pentagons!)? Dodecahedron has 20 vertices (maybe 20-note scale might relate to micro-intervals used in Eastern music) and 12 faces. The fusion would give 20+20+12+12= 64 chords. Dodecahedral harmony is unique since there is only single Hamilton's cycle.

   One would have only single topology and the interpretation as fiber space with 2 points in the fiber would make sense if the dodecahedral tessellation is constructed as a dual of icosahedral one with new vertices as centers of icosahedral triangles. Music, even the music of light realized as triplets of dark photons with frequencies equal to those of the chords of bioharmony, expresses emotions and this leads to the suggestion that emotions are expressed even at the level of bio-molecules [**?**] Therefore I cannot avoid the temptation to ask whether the uniqueness of the dodecahedral harmony could relate to the eastern notion of empty mind empty of any emotions and thoughts.

6. For this realization of bio-harmony the fusion of 8 bio-harmonies could be seen as a transition to a higher hierarchy level considering structures made of structures and would produce the required number 96 of notes. These bio-harmonies would have slightly different 12-note scales. Octave equivalence would suggests that 12-note scale is effectively replaced with $8 \times 12 = 96$ note scale. The interpretation in terms of fiber space structure with 2×8 points in the fiber would make sense.

5.2.4 The problem of Pythagoras a motivation for the fusion 8 copies of bio-harmonies

Could one imagine any justification for the fusion of 8 copies bio-harmonies possibly with slightly differing scales? A problem that teased already Pythagoras suggests this kind of justification!

1. The basic problem of Pythagorean scale based on rational frequencies realized as quints of the basic frequency modulo octave equivalence is that octave equivalence is not quite exact. The octave projections by scaling by a power of 2 of the scale in higher octaves to the lowest octave do not quite quite co-incide with the 12-note scale assigned with it: the reason is that no power of $x = 3/2$ can exactly co-incide with power of 2 so that $x^{12} = 2^7$ is true only with 1 per cent accuracy.

   Pythagoras who firmly believed that Nature relies on the arithmetics of rationals was even ready to believe that Nature is imperfect! In TGD framework one could say that only the cognition based on rationals is imperfect (also cognition using algebraic numbers is predicted to be possible and evolution would mean increase of the complexity for the extension of rationals). Tempered scale would require the powers of algebraic number $x = 2^{1/2}$ to belong to the extension.

   The problem is that Pythagorean scale seems however to have a deeper meaning (people with absolute ear love it) [L4]. Could some number of octaves - say 8 - give a more precise mathematical model of music experience in the case of people having absolute ear? Could it be that people with absolute ear have a better pitch resolution and are able to distinguish between notes of 96-note scale?

   Remark : The realization of 12-note scale using irrational frequency ratios coming as $2^{1/12}$-powers of the fundamental frequency does not have problem with octave equivalence.

2. The 8×12-note would be obtained as follows. One performs first 12-fold iteration to get 12-note scale. The 12th iterate is very near to the basic note by octave equivalence. After that one repeats 12-iteration 7 times so that each note in the original 12-note scale is mapped to 8 notes. These notes must be within interval corresponding to half-note (say E-F), which corresponds to the scaling $r = 2^{1/12}$ in good approximation. This gives the condition $(x^{12\times 8}/2^8)^8 < r$ giving the condition $x < 2 \times r^{1/(8\times 12)} = 2 \times 2^{1/96} \simeq 2.0145$ satisfied for $x_8 = 27/17$.

3. The construction of bio-harmony was based on the assumption that the subsequent vertices along Hamiltonian cycle (neighboring points of tessellation) are related by the scaling of frequency by $x_7 = 3/2$ (Hamiltonian cycle would correspond to quint cycle especially familiar for jazz musicians) and projecting to the basic octave. 12 scalings of this kind give slightly more than 7 octaves ($(3/2)^{12} \simeq 129.746..$ rather than $2^7 = 128$): there relative error is about 1 per cent. $x_7 = 3/2$ would suggest 7 rather than 8 copies of the basic bio-harmony.

   Quint rule is consistent with 8-fold repetition of the basic 12-iteration but one can imagine also alternative rules for generating the notes of the scale using powers of some number x reduced to basic octave. Could a simple choice for $x = x_8$ give $x_8^{12} = 2^8$ in a better approximation than $x_7 = 3/2$ gives $x_7^{12} = 2^7$? The replacement $x_7 = 3/2 \to x_8 = (3/2) \times y$, where y is rational approximation for $2^{1/12}$, gives a natural guess for x_8. For $y = 18/17$ giving $x_8 = 27/17$ (to be compared with $x_7 = 27/18$ one obtains $x_8^{12}/2^8 = 1.006...$, so that the error is .6 per cent whereas for $x_7 = 3/2$ the corresponding error is around 1 per cent. Note that $p = 17$ is Fermat prime of form $F_n = 2^{2^n} + 1$ near to power of 2. Primes near power of two are in fundamental role in TGD.

4. It will be found that the recent proposals for bio-harmony have drawbacks, and that a more elegant identification of bio-harmony as a fusion of icosahedral and dodecahedral harmonies leads to a replacement of powers of quints ($C - G$) with powers of slightly larger interval ($C - G\sharp$) and a generalization of Hamiltonian cycle by introducing the analogy of gauge symmetry.

5.2.5 Details of the icosa-dodecahedral harmony

Consider now the details of the icosa-dodecahedral harmony.

1. Dodecahedral harmony involves $n_{20} = 20$ notes. The generalization of the quint cycle means that the frequencies in the basic octave are obtained from the base frequency as scalings by octave equivalence: $f/f_0 = x_{20}^k/2^{r(k)}$, $k = 0, 1, .., 19$ with $r(k)$ fixed by the condition that $1 \leq f/f_0 \leq 2$. x_{20} is a rational number determined by the condition that x_{20}^{20} is as near as possible to power $2^{k_{20}}$, where k_{20} can have several values.

   $k_{20} = 12$ gives $x_{20} = 127/40$ as optimal choice. $x_{20}^{20}/2^{12} = 1.0007$, so that the error is very small. What puts bells ringing that Mersenne prime 127 appears in the numerator of x_{20}: it appears also in the model of genetic code based on Combinatorial Hierarchy [K9].

2. One can argue that the values of x should be such that 20-note scale shares the notes of 12-note scale under octave equivalence. This requires that x_{12} and x_{20} differ by a power of 2. For $n_{12} = 12, k_{12} = 8$ $x_{12} = 127/80 = x_{20}/2$ gives $x_{12}^{12}/2^8 = 1.0007$, which is an excellent accuracy. Note that x_{12} is not very far from quint $x = 3/2$. 20-note scale shares under octave equivalence the notes of 12-note scale in the sense that one has $x_{12}^r 2^{-r} = x_{20}^r$.

   8 icosahedral octaves emerges a as a prediction of icosa-dodecahedral codes and this is the number of octaves required by hachimoji DNA. Presumably there is a connection between these two identical numbers.

3. To get some idea about dodecahedral harmony one can use the fact that $x_{12} = 1.5875..$ is near to $2^{8/12} = 1.5874...$, which corresponds to the interval $C - G\sharp$ rather than quint $C - G$. For case b) the notes of 4 pentagons containing 4-edge would can be transposed to $CG\sharp ECG\sharp$ so that the notes begin to repeat themselves approximately and one would indeed obtain only 3-chords modulo octave equivalence! If the notes of 3-chord correspond to same power of x, all 3-chords would be of the same type: the melancholic 3-chord with which so many finnish tangos end! Since the repetition is not exact the notes of dodecahedral scale cover the entire octave. The basic $CEG\sharp$ chord transponated by the powers of x_{20} covers entire octave.

4. For 8 pentagons of type a) one would obtain 3-chord transposable to $CG\sharp E$ and 2-chord transposable to $CG\sharp$.

5. Should one allow also for the icosahedral harmonies only chords for which the notes belong to the cycle and triangle? This would allow 3-chords for triangles containing two edges of

the cycle: these chords would be of type CGD involving two quints. Triangles containing single edge would correspond to 2-chords with separation by quint. The triangles containing no edges would correspond to notes. The choice of the note would not be unique. The model of icosahedral harmony indeed predicts this kind of 3-chords. For instance, dissonant chords involving 3 subsequent notes are possible [L1] and more natural interpretation would be as possible notes of melody.

5.2.6 Is gauging of sphere needed to make icosa-dodecahedral harmony non-trivial?

There is also a second objection. If the notes of the chord correspond to same power of $x_{20} = 127/40$, only the notes $C, EC, G\sharp$ would appear in the 3-chords the approximation that $x^{20}/2^{12} = 1$ as is obvious from the fact that one $x_{20} \simeq 2^{4/12}$. Both icosahedral and dodecahedral harmonies based on $x_{20} = 127/40$ would be trivial. As noticed, one obtains the 20 transposes of this chord but having only chords with same structure looks still trivial.

1. One could solve the problem by allowing combinations of notes of 3-chord with different values of k in x_{20}^k (or x_{12}^k). The division of octave to 20 (12) notes guarantees that the chords obtained in this manner allow to realize very rich repertoire of harmonies. Essentially $20^3 = 8000$ chords become possible. What looks like a weakness of Pythagorean view about music based on rationals would become a strength.

   The analogy with the non-uniqueness of gauge choice in gauge theories is obvious. Gauge transformations changing the value of k in local manner give new Hamiltonian cycles from given cycle. Mathematically this solution looks elegant since one can also choose $x_{20} = 127/40 = 2x_{12}$. This also gives 8 octaves for icosahedral harmony as hachimoji code requires.

2. Although the proposed solution is mathematically elegant, it is interesting to look also for the case $x_{12} = 3/2$. The first problem is that x_{12}^{20} deviates 20 per cent from base note, and would correspond to $E\flat$ rather than C. What is however nice is that the notes for a pentagon containing 4-edge would correspond to C, G, D, A, E, H. From these one can select major chords CEG, GHD, and minor chords ACE, EGH. One could obtain the basic harmonies from the dodecahedral part by allowing all possible choices.

   Could one assume a slightly modified quint scale and different scales for icosahedron and dodecahedron? Icosahedral and dodecahedral scales are roughly consistent if k_{20} corresponds to an integer multiple of k_{12}. For $k_{12} = 7$ and $k_{20} = 2k_{12} = 14$ one has $x_{12} = 3/2$ and $x_{20} = 13/8$. One has $x_{20}^2 0/2^{14} = 1.006$. One has $x_{20}/x_{12} = 13/12 = 1.08..$ to be compared with $2^{1/12} = 1.059...$ The difference is more than half-note that x_{20} corresponds roughly to $C - G\sharp$ interval as for $x_{20} = 127/40$ as above. Therefore this option does not look attractive.

5.2.7 Summarizing

Some concluding remarks are in order.

1. Hachimoji DNA turned out to be extremely inspiring discovery also from TGD point of view and led to a more refined vision about bio-harmony with elegant mathematical interpretation.

2. If the above arguments make sense, one cannot avoid the question whether the fact that some people have absolute ear mean that genetic code with 8-fold number of codons is realized at the level of dark codons and bio-harmony? Chemical realization would have been probably discovered.

3. 8×12-note scale would allow discretized glissandos and also discretized blue notes appearing in popular music. Purely electronic production of this kind of music using computer programs is possible using Garage Band or some other similar program, and it would be interesting to test how the discretized glissando is heard.

   One can imagine also instruments producing this kind of music. A hybrid of piano and violin comes first in mind. The keys of piano would be replaced by keys sensitive to touch - the technology used in smartphones would allow to realize this. The 8 1/16 notes associated with a given ordinary half-note would correspond in an increasing order to linearly ordered

regions along the key, and one could change the note or chord by shifting the fingers along the key. The strength of touch could code for the volume. The chords of the harmony do not consist of arbitrary notes of the 8×12 note scale but are obtained by transposing the chords of the basic bio-harmony. This would help enormously in playing since one can shift all fingers along the keys defining the chord.

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