How the genetic code is realized at the level of the magnetic body of DNA double strand?

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Abstract

The TGD based model for the genetic code relies on icosa tetrahedral hyperbolic tessellation (ITT) realized in the hyperbolic 3-space H^3 representable as a light-cone proper time constant hyperboloid of light-cone of M^4 or as a mass shell in momentum space. There has been a dramatic evolution in the basic understanding of TGD during 2024-2025 and it is time to

update the views of ITT and also to summarize the recent overall TGD based view about quantum biology. In the sequel we shall discuss a more detailed view of icosahedral tessellation and its concrete realization in biology trying to build a connection with biochemistry and also consider the various hen-egg questions of biology from the TGD point of view.

Also the question whether TGD could provide a concrete view of evolution at the level of genes is considered. Does Nature perform genetic engineering? Can one relate the view about the evolution of cognition at DNA level as emergence of introns to the view of cognition based on hierarchies of maps generating increasingly complex space-time surfaces? One can try to answer these questions using the basic ideas of TGD inspired view of information molecules.

1 Introduction

The TGD based model for the genetic code [L11] relies on icosa tetrahedral hyperbolic tessellation (ITT) realized in the hyperbolic 3-space H^3 representable as a light-cone proper time constant hyperboloid of light-cone of M^4 or as a mass shell in momentum space.

1. The general idea that genetic codons as 6-bit units of ordinary "bitty" intelligence are accompanied by emotional intelligence represented in terms bio-harmonies serving as correlates for emotions. Music indeed expresses and creates emotions [K1] [L3, L6, L7, L11]. This view has far reaching implications. In particular, it means that emotions are present already at the biomolecular level. In the TGD Universe, life is universal and can appear in very many scales. This would be true also for the genetic code realized in terms of the icosa tetrahedral tessellation of H^3 which can appear in arbitrary scales.

2. This interpretation of the genetic code belongs to the category of the intuitive "must-be-true" hypothesis of TGD, whose status has remained unclear. One reason for this is that I am not a specialist in the field of hyperbolic tessellations. Once again I realized that my understanding is far from perfect and decided to clarify my thoughts once again.

3. ITT involves tetrahedra (T), octahedra (O) and icosahedra (I). Genetic code would correspond to a fusion of 3 properly chosen icosahedral Hamiltonian cycles representing 12-note scale (there are many options) and one tetrahedral Hamilton cycle, which is unique. I have an intuitive geometric interpretation for this 3-1 structure: 3 I:s share 3 faces of T. This leaves one free face of T serving as an additional codon. This gives 20+20+20+1=64-3 codons and the missing 3 codons could correspond to stop codons. Also O:s are involved and the intuitive idea is that O is passive in the sense that it represents a void in the sense that the vertices, edges and faces of the octahedron can be regarded as those of octahedron or I. How to make this idea more concrete?

There has been a dramatic evolution in the basic understanding of TGD during 2024-2025.

1. The holography = holomorphy vision reduces the extremely nonlinear classical field equations for space-time surfaces to algebraic equations and the solution is universal and action independent as long as the action is general coordinate invariance and constructible in terms of the induced geometry. Space-time surfaces are analogs of Bohr orbits and this means that no path integral is needed. Quantum TGD reduces to wave mechanics in the "world of classical worlds" (WCW) consisting of Bohr orbits of particles identified as 3-surfaces. The slight non-determinism of these Bohr orbits forces zero energy ontology having dramatic implications in quantum theory and solvings the basic paradox of quantum measurement theory.

2. The understanding of number theoretical aspects of TGD has developed dramatically and the p-adic length scale hypothesis and the hierarchy of dark phases of ordinary matter are now relatively well-understood mathematically. In particular, the p-adic number fields generalize to function fields and this allows us to understand how the p-adic length scales hypothesis emerges.

3. The $M^8 - H$ duality as a generalization of momentum position duality to a 4-D analog of Langlands duality is also understood and the associativity conditions for the 4-surfaces at the level of M^8 can be also solved exactly.

4. The Dirac equation for the spinor fields in H and in causal diamond CD and the induced Dirac equation can be also solved exactly. Color confinement emerges directly from the Dirac equation at the level of H. The basic picture of QCD involves generation of quark gluon phases in the interaction region and hadronization to final states generalized to all interactions. One can say that the Feynman diagrammatics of TGD is understood at the general lefel.

   The dramatic prediction is that there is an entire hierarchy of standard model physics and that the next hadronic physics is already making itself visible at LHC. This suggests a dramatic modification of the existing view about the mechanism producing solar wind and radiation in the Sun.

5. $M^8 - H$ duality leads to an extremely simple view about scattering amplitudes in which free fermions are the only fundamental particles and fermion pair creation corresponds to a V-turn of a fermion line in space-time assignable to 3-D edge of the space-time surface. This would correspond to a defect of the standard smooth structure and give rise to an exotic smooth structure. It turns out that even DNA replication could be understood in terms of the V-turn mechanism applying also to 3-surfaces.

   The view about interactions based on the notion of monopole magnetic flux tubes appearing in all scales led already earlier to a radical reinterpretation of even atomic and molecular physics and it is clear that TGD means a revolution in the entire world view.

6. Most conjectures related to TGD are now on a rather firm ground. Even the Expanding Earth hypothesis, which follows from the TGD based quantum cosmology and is crucial for the TGD view of biology and evolution but certainly raises the eyebrows of most colleagues, has found a lot of new support from various anomalies.

This progress means that it is time to update the mathematical understanding of ITT and related to molecular biology also to summarize the recent overall TGD based view about quantum biology.

In the sequel we develop a more detailed view of icosahedral tessellation and its realization at the level of DNA and other biomolecules and also consider various hen-egg questions of biology from the TGD point of view. One can even ask whether TGD could provide a concrete view of evolution at the level of genes? How could new genes appear? Genetic engineering produces them artificially. Does Nature also perform genetic engineering? Can one relate the view about the evolution of cognition at DNA level as emergence of introns to the view of cognition based on hierarchies of maps generating increasingly complex space-time surfaces? One can try to answer these questions using the basic ideas of TGD inspired view of information molecules.

2 About the genetic code and icosa tetrahedral tessellation of hyperbolic 3-space

2.1 A more precise view of ITT

The ITT in the hyperbolic 3-space H^3 (honeycomb) is completely unique because it includes as cells all Platonic solids, tetrahedron (T), octahedron (O) and icosahedron (I) for which the faces are equilateral triangles. One can characterize the tessellation by giving the numbers of 3-cells meeting at vertices, edges and faces.

Consider first the vertices.

1. The vertex figure of the ITT (see this) represents what an observed at a given vertex sees as intersection of a vertex-centered ball with the ITT. For instane, for cube, vertex figure is square for C(ube) and O, pentangon for I and triangle for T and D(odecahedron).

   For ITT vertex figure corresponds to an Archimedean solid known as icosadodecahedron (ID), which can be regarded as a hybrid of I and D. The 12 pentagons at the vertices of I as vertex figures of 12 I:s and the 20 triangles as vertex figures of 20 T:s correspond to vertices of D. ID has 20 triangular faces and 12 pentagonal faces, totaling 32 faces, with 30 identical vertices, at which two triangles and two pentagons touch, and 60 edges separating a triangle from a pentagon.

2. O is passive in the sense that only 20 I and 12 T but not O meet at the given vertex, hence the attribute "icosatetrahedral". One can say that O represents a void. Octahedron is a lower-dimensional example of this phenomenon: the square defining the vertex figure of O does not define a face appearing at the vertex. Only 4 triangles meet at a given vertex. This brings in mind giant voids of cosmology having galaxies at their boundaries. I have proposed that the tessellations of H^3 realized as cosmological time $a = constant$ hyperboloids in the light-cone of M^4 could explain the observed quantization phenomena for the redshifts [L14]. Could these large voids have something to do with the O:s of ITT?

3. How could one understand the 3-1 correspondence for I:s and T:s? A given T of the vertex figure is surrounded by 3 I:s. This suggests the T+3I defines a unit giving a realization of the genetic code, 4 units of this kind would meet at a given vertex.

   The proposed interpretation of T+ 3I as a unit conformas with the proposed view of the genetic code. I:s have 20 triangular faces and since the I:s have no common faces, this motivates the proposal that the 3I give rise to 20+20+20 icosahedral codons. The I:s would realize a Hamiltonian cycle with a symmetry group which is Z_6, Z_4 or Z_2. Z_2 would act as reflections or rotations. Z_6 cycle is unique, there are 2 Z_2 cycles and a large number of Z_2 cycles.

   The orbits of the symmetry group would correspond to amino-acids. Z_6 would give rise to 3 6-element orbits and 1 2-element orbit. Z_4 would give rise to 5 4-element orbits and Z_2 to 10 2-element orbits. This explains almost exactly the numbers of DNA codons coding for a given amino-acid. The 3 I:s share 3 common faces with T, which leaves one free face for T to which one can assign a tetrahedral genetic codon. The 3 missing tetrahedral faces would correspond to stop codons.

4. Interesting questions concern the interpretation of the cycles. The Hamilton cycle connects the nearest neighbor vertices of the Platonic solid. Does the cycle correspond to a closed monopole flux tube? What does it mean that one face (at least) for a given 3I+T unit is active and represents a codon: does it have protons at its vertices as the alternative realization of the genetic code in terms of the states of 3-proton triplets suggests [L3]? Can the 3I+T units of ITT contain different Hamiltonian cycles so that emotions could be local. Does DNA strand correspond to a linear structure as a substructure of ITT. Is the induction of ITT to 1-D, 2-D and even 3-D structures representing genetic code possible? Could for instance, cell membrane and microtubules represent 2-D realization of the genetic code. Could the brain and even the biological body represent a 4-D realization. Could these realizations be time dependent as the failure of strict non-determinism of the classical dynamics dictated by holography = holomorphy vision suggests: if so, even 4-D realization would be possible.

Also the numbers of cells meeting edges and faces characterize ITT.

1. Edge transitivity means that all edges are symmetry related just as the vertices are. At a given edge I, I, O, and T meet in a cyclic order IIOT.

2. 2 3-cells cells meet at a given face. Only I and T can share faces. and the shared faces correspond to O faces. O does not appear at the vertices, being realized as a "ghost" cell being analogous to the square appearing in O and having no physical realization as a face.

   If one assumes that all I-T interfaces also involve an O interface then the number of 20 O:s surrounded by 3 I:s implies that presence of $4 \times 20 = 80$ O:s assignable to a single vertex. Since each O has 8 faces, there would be 10 O:s per vertex. The numbers of (T,I,O) per vertex would be (20,12,10).

To sum up, the conjecture that the genetic code is realized in terms of ITT is now at a rather firm basis. During the last few years several ideas of TGD have reached a rather strong status as the understanding of the basic mathematical ideas of TGD has increased and TGD is now a mature mathematical theory and can be applied in all scales.

2.2 How the genetic code is realized at the level of the magnetic body of DNA double strand?

Suppose that the proposed view of the ITT realized at the level of the magnetic body (MB) of DNA is correct that dark genetic codons as induction of ITT from the MB of DNA have as a chemical counterpart of DNA or RNA double strand. How the more precise view of ITT affects the earlier model discussed in [L11].

First a couple of facts.

1. The numbers of (T,I,O) per vertex should be (20,12,10) if the T-I interface always involves O. Therefore also DNA codons correspond to faces of O:s and DNA sequences can be identified as a sequence of faces of O:s.

2. 10 DNA codons define the shortests DNA sequence for which the twist is a full multiple of 2π. One should have a sequence of triangles representing genetic codons and each codon should correspond to a face of I and to a 3-chord of a fixed Hamiltonian cycle defining a bioharmony.

This raises the following questions.

1. Does the sequence of 10 O:s correspond to a single ITT vertex and does DNA correspond to a sequence of ITT vertices such that each vertex corresponds to an O and associated 20 T:s and 12 I:s?

2. Do the two DNA strands correspond to separate dark strands or does a single dark strand correspond to both of them as the fact that the DNA strands are conjugates of each other as the latest proposal assumes. Assume this. Single O has 3+3 faces and has two disjoint triangular faces. Could these two faces correspond to DNA codon and its conjugate?

3. This sequence of 10 O:s corresponds to a sequence of 12 I:s. 2 I:s would be "empty" and would not correspond to dark proton triplet: what does this mean? Does this mean that all vertices of the I and T carry ordinary protons and the activation of the codon transforms the ordinary protons of the face to dark proton triplet. I have considered a possible interpretation of this. In the state in which DNA is opened (transcription) the 2 codons would become active and correspond to dark proton triplets.

4. What distinguishes between I and T type active codons? When the dark proton triplet is of T type and when it is of I type? Could the presence of the Hamilton cycle, the assignment of 3-chords to the faces, and resonance interaction allow us to understand this? Does the 3-chord assigned to the face determine whether the dark proton triplet belongs to the T or I type Hamiltonian cycle? Is there some symmetry breaking mechanism selecting from the T type conds the one while the remaining ones act as stop codons. Could the presence of I or T type Hamiltonian cycle in given I or T determine whether it can define an active codon and whether an associated ordinary proton triplet can be transformed to a dark one?

   The cyclotron frequencies assignable to T type codons are different from those assignable to I type codons if the frequency ratio for two subsequent vertices of the cycle is 3/2 for the Hamilton cycle at I in the Pythagorean model.

   Note that the basic problem of the Pythagorean model of harmony (known already by Pythagoras) is that the full Hamiltonian cycle, involving 12 frequency scalings by factor 3/2, does not give quite precisely a full multiple of octaves. One must allow irrational frequency scaling of $2^{1/12}$ on a well-tempered 12-note scale to get rid of the problem. This might relate to the symmetry breaking.

   For a tetrahedron with 4 vertices the frequency ratio should be also such that the cycle spans a multiple of octaves. This is not possible for rational scalings. In any case, I and T options are not consistent and this suggests that the 3-chords select between I and O options. The chords dictated by the character of the Hamilton's cycle select whether the face is of type I or O. The presence of the Hamiltonian cycle would be necessary for the

transformation of the ordinary proton triplets to dark proton triplets and only the I or T type cycle can be realized.

In the standard realization of the code there are 3 stop codons, which are transcribed to mRNA but are not translated to amino-acids. There are 4 codons of type T. There should be a symmetry breaking in the sense that 3 of them are not translated. This could be due to the failure of 3-chord resonance conditions so that there would be no tRNAs with the required resonance frequency triplest. Only a single tetrahedral codon would be translated for the standard realization of the code. This model also allows deviations from the standard realization of the code.

2.3 Pollack effect and ATP→ ADP+P_i transformation

The molecules XP, where X ∈ {A,T,C,G} denote DNA nucleotides, are basic building blocks of DNA. The molecules XP are stable unlike the more complex molecules. The molecules ATP, ADP and GTP, GDP involve 2 or 3 phosphate ions. The latter molecules are essential for the metabolism and appear as carriers of metabolic energy assigned in the TGD view to the dark protons at the magnetic body associated with the molecule. What distinguishes them from the mononucleotides appearing in DNA and RNA?

We talked with Ville-Einari Saari (a member of our Zoom group) about whether it might be possible to build stable negentropic systems with a large Planck constant h_{eff}. Without any stabilizing mechanism, large h_{eff} systems are unstable against the decrease in h_{eff} because their energies increase with h_{eff}, so as free systems they require a continuous energy input and only flow equilibrium is possible. This is the case in the case of XDP and XTP and this makes for ADP and GTP to transfer metabolic energy.

In water, the Pollack effect is a fundamental process and produces dark protons that transform into ordinary ones in an attosecond time scale. This expectation comes from the observation of exotic phases of water with effective stoichiometry $H_{1.5}O$ having attosecond life time. The explanation is that a phase transition in which every fourth proton becomes a dark proton at monopole flux tubes takes place under external energy feed. The negatively charged exclusion zone (EZ) created in the Pollack effect by radiation is an example of this effect. The essential prerequisite for the Pollack effect is external energy feed and TGD has led to various generalizations of the Pollack effect. In particular formation of biomolecules generates binding energy and this could stabilize dark phase [L8, L12, L17] and cold plasmas are excellent candidates for the carriers of stable dark phases.

An illustrative example is provided by transformation of chemical energy to a usable energy as a transition ATP→ ADP +P_i, where P_i is inorganic phosphorus. This process occurs spontaneously. The reverse process requires metabolic energy input and mitochondria are specialized to produce ATP from ADP. The process ADP→ ATP→ ... can be seen as a kind of a karmic cycle.

1. The phosphorus P appearing in ATP and ADP ions is organic. It is not clear what this really means and biologists argue about a mysterious high energy phosphate bond which would carry the metabolic energy to the final uses as ATP transforms back to ADP +P_i. In the TGD framework, the interpretation is that ATP and also ADP involves a dark proton at the MB that neutralizes the negatively charged system and is generated by the generalization of the Pollack effect in the formation of ATP or ADP.

2. The conversion of the chemical energy into a usable form occurs in the mitochondria in a biochemical machine that resembles a rotating turbine of a power plant. 3 ATP are produced in one revolution of the turbine from three ADP. This would strongly suggest that a precursor of dark genetic codon as dark proton triplet is involved.

   Google informs that the lifespan of the ATP varies enormously: when the environment needs energy, its lifespan is shortened. In vivo it varies from a few seconds to about 100 seconds whereas in vitro ATP can be almost stable.

What about DNA and RNA?

1. DNA and RNA have a stable negative charge (as Google informs): there is a negative charge of 3 units per codon. A natural guess is that it corresponds to the exclusion zone (EZ) of

the Pollack effect. This suggests that there must be a stable positive charge in the form of dark proton triplets at the magnetic body associated with the DNA and the proposal is that these triplets define dark codons. What stabilizes the negative charge of DNA and therefore also the dark protons and makes the negentropic state stable.

2. Bound states are formed between phosphates and DNA nucleotides. If their chemical binding energy is so high that the total binding energy, which is reduced by the energy of the dark proton, remains positive, the state is stable. I have suggested earlier [L12] that the formation of biomolecules as bound states can stabilize the dark protons, so the creation of biomolecules would also produce negentropy at the magnetic body. In fact, the formation of biomolecules as bound states during the biological evolution would have generated the dark protons at the monopole flux tubes of their magnetic bodies.

   To sum up, negentropic states can be stabilized in this way and do not require a constant input of metabolic energy to maintain dark h_{eff} in the sense of flow equilibrium. DNA and RNA would be completely exceptional bio-molecules in this respect and would fully deserve the name information molecule.

2.4 How large h_{eff} states are stabilized?

The quantum critical state is unstable by definition because the $h_{eff} \geq h$ states are more energetic than the $h_{eff} = h$ states and spontaneously decay into these.

One way to avoid this would be for the $h_{eff} \geq h$ molecule to form a bound state, for example with a molecule or a larger structure. The electric field of the larger charged structure and that in turn a state where h_{eff} would be stabilized. However, I do not understand the details of the mechanism. How to build a state in which $h_{eff} \geq h$ dark protons are possible in the minimum energy state. Is this possible if only the electromagnetic interaction is involved?

This is a fundamental question. So let's start from a clean table.

1. In the case of DNA and cell membranes, h_{eff} stabilization is related to the presence of electric fields, but do they produce the stabilization or are they a consequence of it?

   A $h_{eff} \geq h$ state and a state bound with another state are created so that the $h_{eff} \geq h$ state stabilizes because the dissociation is no longer energetically favorable. It should be noted that due to their large negative charge DNA and the cell membrane are biologically completely unique. Charge separation does also occur at the level of the brain and the whole body and its sign correlates with the level of consciousness: the sign of the voltage changes during sleep. The Earth itself also has an electric field, which suggests that the biosphere is conscious.

2. In the case of DNA, the bound state would be between phosphate and deoxyribose. Would the large $h_{eff} = h_{em}$ somehow be made possible by the longitudinal and radial electric fields of DNA or is it a consequence of a stabilization mechanism? Maintaining the electric field requires energy, so metabolic energy input is still necessary but at the level of classical fields. But do electric fields maintain dark protons at the monopole flux tubes or vice versa?

   The problem: In the case of DNA, the repulsive energy of the negative charges of the phosphates destabilizes the state. In addition, there is repulsion between the dark protons in the flux tubes. Charge separation, where the dark protons and the phosphate ions are far apart, requires energy because the neutral ground state is of minimum energy.

   The solution of the problem: Some interaction energy must compensate for the increase of the interaction energy. Could strong interactions of the dark protons in the flux tubes, proposed to form dark nuclei with a scale down nuclear binding energy, be involved? The strong interaction would stabilize the repulsive energy of the negative charge of the phosphates, the same would happen for the dark protons. Long range electric field would be a consequence, not the cause.

   (a) The TGD-based model of cold fusion [L1, L2, L5, L20] indeed assumes that the dark protons in the magnetic flux tubes form an analogy of the atomic nucleus and the scaled binding energy of the nucleus would produce the binding energy. Strong interactions in

the TGD sense would play a key role in biology and also in electrolysis. This would be new and revolutionary.

(b) Of course, one could try to cope with just electromagnetic interactions.

i) The negative electrostatic energy would be between the dark protons and the negative charge of the phosphates. One would expect this energy to be small, but is it for flux tubes?

ii) What about the role of water? It can become positively charged (and for example Mg^{2+} ions do), which can produce a Coulomb bound state. Mg^{2+} ions are naturally present in monopole flux tubes, but is the contribution large enough?

iii) The binding energy is related to the bound state between negatively charged phosphates and riboses. The problem is that ribose molecules are not permanently positively charged. This doesn't seem promising.

(c) In the case of the cell membrane, the electric field associated with the membrane potential should accompany large values of h_{eff}. A decrease in the field strength below a critical value would lead to a decrease in the value of h_{em}, perhaps down to $h_{eff} = h$ because h_{em} is proportional to the field value and quantized as an integer. The scale of quantum coherence would be reduced and a nerve impulse would be generated.

The naive Maxwellian assumption would be that a nerve impulse is generated when the voltage is too high: there would be a di-electric breakdown, just as is supposed to happen in a Tesla coil. The fact that exactly the opposite happens is a central mystery of biology. A decrease in h_{em} would explain the mystery. One can pose an interesting and somewhat nosy question: has it really been tested that breakdown is the correct mechanism in Tesla coils?

Also now the strong interactions with monopole flux tubes would stabilize the state.

(d) The negative charge on the surface of the Earth's electric field and the protons and ions in the gravitational flux tubes and electric flux tubes and their strong interaction would stabilize the biosphere as a conscious system.

2.5 Does the presence of ITT at the MB reveal itself in the structure of DNA the surrounding water

Does the presence of ITT at the MB of DNA reveal itself in the structure of DNA and the surrounding water. How does the presence of O:s, T:s and I:s at the MB reflect itself in the properties of chemical DNA and possibly of water? Could the structure of water around DNa reflect the projection of hyperbolic tessellation at 3-D Euclidean space E^3.

Do the octahedrons of the field body have any counterpart in the nearby environment of DNA.

1. Here Google tells that the water around DNA indeed involves octahedral structures besides tetrahedral structures which generally present (see this). They occur in the form of hexahydrated metal cations (see this), such as $[Mg(H_2O)_6]^{2+}$ with positive charge of 2 units. Mg^{+2} ions are bosons and could form Bose-Einstein condensate-like states. The 6 water molecules reside at the 6 vertices of O and its two opposite disjoint faces could correspond to two dark codons generated by Pollack effect from water molecules.

2. These octahedral complexes are commonly found in the major groove or the phosphate backbone region of the DNA, where they are thought to shield the negative charges and stabilize the overall structure. This assumption is natural also in the TGD based view. Only 15 percent of Mg^{+2} ions is estimated to touch phosphate oxygens directly. They would form a kind of cloud, which conforms with the idea that they serve as stabilizers. That they accompany the vertices of the octahedron conforms with the idea that the vertices involve negative charges created as protons are transformed to dark protons.

3. Mg^{+2} ions screen 88-89 percent of the negative DNA charge. If one can assign this kind of octahedron with a net charge of +2 units with each genetic codon, one unit of negative charge remains unscreened for both strands. Fraction 2/3 of total charge would be screened. This is considerably less than 88-89 percent so that not all Mg^{+2} ions would be associated with the vertices of the octahedra.

Could one understand the correspondence between ITT and DNA double strand more concretely? The natural guess is that the vertex figure of ITT relates to the structure of DNA double strand.

1. Could the pentagon associated with the deoxyribose (or ribose in the case of RNA) serve as a counterpart for the pentagon appearing in the vertex figure of ITT? The vertex figure has 12 pentagons, which could correspond to 12 DNA codons defining a cycle in the sense that the total twist angle of the double helix is $3 \times 2\pi$ in the open configuration of the DNA double strand.

   For a non-open double strand 10 DNA codons define a full cycle. One could say that there are 2 missing DNA codons and 2 empty IIT pentagons without dark protons triplets defining a gap separating the dark codons. If the corresponding $[Mg(H_2O)_6]^{2+}$:s, whose opposite triangles would represent DNA codon and its conjugate, are present at all, they should not give rise to dark protons. Mg^{+2} ions giving rise to Bose-Einstein condensate could give rise to quantum coherence at the level of ordinary DNA and make possible the simultaneous generation of 2 dark proton triplets by Pollack effect.

2. Could also Mg^{+2} ions be dark? The findings of Blackman [J1] can be explained in terms of bosonic Ca^{++} ions which have cyclotron frequency 15 Hz in the endogenous magnetic field $B_{end} \simeq .2$ Gauss consisting of gravitational monopole flux tubes. They are dark in the sense that they have a very large gravitational Planck constant $\hbar_{eff} = \hbar_{gr} \sim 10^{15}$ [E1] implying that the cyclotron photons can have energies in the range of visible photons. Mg^{+2} has cyclotron frequency 12.5 Hz for $B_{end} \simeq .2$ Gauss. The crucial assumption is that besides protons, also other metallic ions can be dark in the sense of having large h_{eff}. This suggests that also Mg^{+2} associated with a single codon as a face of ITT is dark in the sense it resides at the MB. The interpretation could be that its wave function is delocalized at the gravitational flux tube of the Earth's surface. When Mg^{+2} is observed its wave function would localize to the surface of Earth, meaning "dropping" from the gravitational flux tube. The effects of electromagnetic radiation with this frequency on DNA could be tested.

   In fact, all metal ions M form $[[M(H_2O)_6]^{2+}]^n$:s complexes (see this). The number of water molecules involved is known as the solvation number and is 6 for the third and fourth period of the periodic table containing Mg and Ca. The bosonic Mg and Ca ions are also involved with microtubules and cell membrane (see this). This gives support for the proposed 2-D realization of the genetic code in terms of dark proton triplets.

3. The ordinary codon should correspond to the dark codon as a triangle at the MB with dark protons at its vertices. At the level of DNA there is no triangle. Could the 1-D quasiperiodic lattice formed by the DNA codons correspond to periodic boundary conditions at the MB so that the linear codon as a unit cell of the lattice has a triangle as a counterpart at the level of ITT? 3 chemically identical pentagons associated with the codon should correspond to a single pentagon at ITT. A single $[Mg(H_2O)_6]^{2+}$ octahedron associated with the major groove should correspond to a single O of ITT? Whether there is indeed only a single O per pair of codon and its conjugate could be perhaps tested. One could argue that symmetry requires that both strands involve $[Mg(H_2O)_6]^{2+}$ octahedron. However, only the other strand is active. This could mean that only its codons contain the $[Mg(H_2O)_6]^{2+}$ octahedron.

4. What about the tetrahedral structures, which also characterize water, around DNA? Here Google informs that in the hydration shell of DNA tetrahedral ordering is present and is essential for the stability of DNA. The presence of tetrahedral ordering could reflect the presence of ITT at the magnetic body associated with DNA and also a region of water environment. There is an enhanced tetrahedral ordering in the DNA minor grooves (see https://pubs.acs.org/doi/10.1021/jp907513wthis). The DNA molecule imprints its helical structure to the tetrahedral structure of water. The TGD interpretation is that the faces of tetrahedra also correspond to the faces of the $[Mg(H_2O)_6]^{2+}$ octahedron. This could be the analog for the I-T faces of ITT identifiable also as octahedral faces? An interesting question is whether the ribose pentagon could somehow correspond to a vertex figure of icosahedron also at the level of DNA.

2.6 Hen-egg questions related to the genetic code

Biology involves a long list of hen-egg questions [L9, L4]. What came first: metabolism, basic information molecules, bio-catalysis, or genetic code? Which biomolecules emerged first: RNA, DNA, or amino acids? TGD provides tentative general answers to these questions in terms of the dark genetic code, whose realization in terms of ITT was present from the beginning. It is instructive to consider these questions in the framework provided by the recent views about the realization of the genetic code in terms of ITT about the emergence of dark matter via the generalization of the Pollack effect. One can also try to develop an overall view.

Consider first the emregence of the basic structures.

1. The dark variants of DNA, RNA, tRNA, amino acids were present from the beginning and realized in terms of dark proton triplets assigned with ITTs at MBs. Stable dark realizations of the DNA, RNA and dark protons at MB were stabilized by the formation of corresponding biomolecules as bound states with the binding energy of the state compensating for the larger energy of the dark proton [L12]. Hence one cannot say which came first.

2. The lifetimes of the basic biomolecules serve as guidelines in the attempts to build an overall view about whether the dark protons at the magnetic body of a biomolecule are relevant for its functioning.

   (a) DNA is extremely long-lived: 521 years in bone. Also the negative charge associated with its phosphates is stable. The TGD based conclusion is that the dark protons at the magnetic body of DNA are stable. There is however a metabolic cost also in this case. The classical long range electric along DNA are a crucial aspect of DNA and make possible large values of h_{em} assignable to the DNA. Also the nuclear membrane potentials are crucial for the survival of the DNA nucleotide. Metabolic energy feed is needed to preserve the charge separations generating the classical electric fields.

   (b) Also the negative charge of RNA is stable but the lifetimes of RNA molecules vary in a wide range. mRNA has a lifetime from minutes to ours and the average lifetime of 2-20 mins. The lifetime can however be much longer, even days and can persist an organism's lifetime. Special RNAs such as tRNA, rRNA, circular RNAs and nuclear RNAs are very stable and long-lived.

   The finite life-time of RNA could be due to the instability of the -OH bond associated with the ribose making possible the transition to the -OH $\rightarrow O^-$ + dark proton at its magnetic body. This would be essential for the ability of RNA to act as a catalyst and could explain the varying lifetime. The stable negative charge of RNA serves as a signature for the presence of dark protons. The dark protons triplets would make possible the communications of RNA with dark DNA and dark tRNA by 3N-resonance.

   (c) Amino acids (see this) do not possess a stable negative charge, which suggests that they do not have dark protons at their magnetic body stably. However, Google AI tells that, a C=O bond in a protein can be temporarily converted into a gem-diol structure ($C(OH)_2$) intermediate in an enzyme's active site during catalytic action. This process is a form of nucleophilic addition of water across the carbonyl double bond, which is often a key step in reactions such as the hydrolysis of peptide bonds (catalyzed by peptidases/proteases) or other reactions involving carbonyl-containing substrates. In the TGD framework this could mean that during the enzyme catalysis a proton from C-OH is transferred to the magnetic body of the protein and drops back later. ATP could quite generally provide the needed metabolic energy to achieve this.

The emergence of communications and control was a crucial step in evolution.

1. Cyclotron frequency triplets as chords assignable to the ITT made possible resonant communications between field bodies by 3N-resonance involving both frequency and energy

resonance. The communications between levels involving different values of h_{eff} (and different length scales) involved only energy resonance and very probably 3N-resonance was replaced by the ordinary resonance. This led to an automatic generation of communication and control networks between field bodies characterized by varying values of h_{eff} and biological bodies. Dark cyclotron radiation and frequency modulated dark Josephson radiation inducing a sequence of pulses at the receiver's end are basic mechanisms suggested by TGD [L13].

2. Large h_{eff} stability possible for DNA and RNA led to a generation of intelligence based on algebraic complexity and to a control by MB. This led to an evolutionary explosion. The electric and gravitational field bodies assignable to the Earth and the Sun were in essential roles [L12].

The emergence of replication was a crucial step. At the chemical level replication reduces to the replication of DNA. A doubling of the DNA strand must occur. In the bio-chemistry approach replication is something which is just accepted.

1. In the TGD framework, the analog of the replication problem is encountered already at the level of particle physics. Fermion fields are free fields in $H = M^4 \times CP_2$ as also the induced spinor fields at the space-time surfaces defined by them: how is fermion pair creation possible at all? The solution is simple and possible only in 4-D space-time: fermion makes a V-turn in time direction generalized [L22]. The vertex of V corresponds to a 3-D edge of the space-time surface [L18, L10, L23] at which the standard smooth structure has a defect [A2, A3, A1]. The magnetic body assignable to the dark DNA as a 3-surface would make a V-turn and induce DNA replication by transcription of the dark DNA to ordinary DNA.

2. What was the first replicator and when did it emerge? This classical question becomes obsolete in the proposed framework. The replication could be a general property of space-time surfaces and therefore of the 3-surfaces associated with the dark DNA molecules realizing ITT at the magnetic body of DNA. There are many interesting questions to be pondered. For instance, how to relate the usual view about the role of various catalysts involved with the replication and what is the role of "big" state function reductions (BSFRs) changing the arrow of time in the process. Could the BSFR have a V-turn as a classical counterpart?

What bio-catalysis is and how did it emerge?

1. In biocatalysis the reactants must find each other in a dense molecular crowd. How can they recognize each other's presence? In the simplest picture the U-shaped monopole flux tubes emerging from the reactants reconnect to form flux tube pairs connecting them. The shortening of the flux tube pair would force the reactants together and could be induced by a reduction of h_{eff} shortening the flux tube lengths.

2. The potential wall preventing the bio-chemical reaction must be overcome. The shortening of the monopole flux tubes could liberate metabolic energy while the reduction of h_{eff} could help to overcome the potential wall. The attachment of a biocatalyst carrying large h_{eff} protons to the reacting system could also provide energy allowing it to overcome the potential wall.

3. How are biocatalysts generated? In general, biocatalysts are unstable. The instability can be inherent or their degradation can be programmed for metabolic reasons since they are needed only when used. If bio-catalysts provide energy to overcome potential walls, they must carry dark protons and their generation requires metabolic energy feed, which also raises the algebraic complexity, "IQ" of the catalysts so that it can take the role of a midwife. ATP is a universal way to provide metabolic energy and dark protons in a standardized way. An alternative option is creation of chemical binding energy making it possible to generate dark protons with large h_{eff}.

4. The dark proton of the catalyst should transform to an ordinary one in the reaction and liberate the energy needed to overcome the potential wall. Catalysts could be either inherently h_{eff} unstable or the instability could be induced in the reaction and induce the decay of the catalyst. Often the catalyst indeed decays after the reaction. Catalysts often have ATPs attached to them and ATP–¿ADP is a basic aspect of catalysis.

   Note that in the translation of mRNA to proteins mRNA serves as a template and degrades after the translation. This could be due to the catalysis of the translation requiring the reduction of h_{eff} inducing a chemical instability. The instability could relate to the -OH sidegroup of the ribose.

3 Could TGD provide a vision about evolution at the gene level?

Could TGD provide a concrete view of evolution at the level of genes? How could new genes appear? Genetic engineering (CRISPR, see this) modifies genes artificially and is realized also in Nature at the level of both DNA and RNA. Also the reverse transcription is realized in Nature. Could Nature realize a kind of R&D and perform genetic engineering. Can one relate the view about the evolution of cognition at DNA level as emergence of introns to the TGD view of cognition based on hierarchies of maps generating increasingly complex space-time surfaces? One can try to answer these questions using the basic ideas of TGD inspired view of information molecules.

3.1 Basic ideas and notions

It is good to start with a discussion of the key notions and ideas.

3.1.1 Dark variants of the information molecules

Dark variants of the basic information molecules residing at the field/magnetic body represent a key element of the TGD inspired quantum biology.

1. The predicts the presence of dark variants of DNA, mRNA, and tRNA associated with flux tubes with codons realized as dark proton triplets. Amino-acids do not carry constant negative charges so that dark proton triplets might not be present at the corresponding monopole flux tubes permanently.

   The hypothesis is that the DNA, mRNA, and tRNA and possibly also AA sequences pair with their dark variants. Resonance coupling by dark 3N-photons would make this possible: N corresponds to the number of codons or AAs). DNA replication, transcription, translation occur at the level of dark DNA and the counterparts of these processes at the level of chemistry correspond to an induced shadow dynamics, a kind of mimicry.

2. There are good reasons to expect that the dark variants of basic information molecules, such as DNA and RNA, consisting of dark proton triplets, are dynamical. This would make possible a kind of R&D lab. How could this be realized? The DNA double strand is not dynamical but RNA is. If the dynamics of RNA is induced from that of dark RNA, dark RNA could make possible experimentation producing new kinds of genes. The living system would evolve actively rather than by random mutations. Of course, also dark DNA could be dynamical and communicate with ordinary DNA resonantly only when in corresponding quantum states.

3.1.2 Zero energy ontology and biology

Zero energy ontology (ZEO) is a basic element of quantum TGD.

1. Zero energy ontology (ZEO) [K2] predicts a fundamental error correction mechanism based on a pair of "big" state function reductions (BSFRs) changing the arrow of time temporarily. When the system finds that something goes wrong, it can make a BSFR and return back in geometric time and restart. After the second BSFR the situation might be better. This

would be a fundamental mechanism of learning and problem solving. And perhaps also a fundamental mechanism of evolution.

2. ZEO inspires the question challenging the Central Dogma of molecular biology: could the time reversals of transcription, of the splicing process of RNA after transcription, and even translation be possible? Are they needed?

   If these processes have space-time counterparts with a slight failure of classical non-determinism, one can expect that these processes are realized in both directions of geometric time. Is there a good reason for their occurrence with a reversed arrow of time? Could the reason be that these processes must correspond to a pair of BSFRs.

This raises several questions.

1. Are the reversals or time reversals for transcription, splicing and even translation possible/needed? This could give rise to non-deterministic reverse engineering of DNA making possible a generation of modified more complex genes at DNA level? Random mutations would be replaced by genetic engineering modifying the existing genome by starting from the protein level would be possible.

2. The strongest form of the proposal is that also the reversal of translation mRNA+tRNA$\rightarrow$ amino acids is possible DNA. There are several strong objections against this proposal. A weaker form of the proposal is that only the reversals of splicing and transcription are possible. Already this could make possible an active evolution at the gene level.

   There is indeed empirical evidence for the occurrence of genetic engineering in Nature: CRISPR occurs in Nature at both DNA and RNA level. Also reverse transcription occurs in Nature. Therefore the question is whether CRISPR in Nature corresponds to addition of introns as reversal of splicing and how it could be realized in the TGD framework.

3.1.3 Holography = holomorphy hypothesis and genes

A naive guess is that the reverse transcription and splicing require the change of the arrow of time. The inverse operation can be realized also without the change of the arrow of time.

1. In holography = holomorphy vision [L15, L19, L16] space-time surfaces are defined as roots for analytic maps $f = (f_1, f_2) : H = M^4 \times CP_2 \rightarrow C^2$. They allow dynamical symmetries $f \rightarrow g \circ f$: $g \rightarrow C^2 \rightarrow C^2$. Functional composition of functions g, in particular iteration, is possible and generates exponentially increasing complexity. Polynomials define one important class of functions g and f.

   Also the inverses of the maps g realized in terms of algebraic functions are possible and the functional composition with them reduces complexity.

2. Holography = holomorphy vision [L15, L19, L16] allows symmetries realized as maps $g : C^2 \rightarrow C^2$. In the simplest situation the maps g are realized in terms of polynomials. The letters of the genetic code could correspond to the roots of degree 4 polynomials g_4 and codons correspond to the functional composites $g_4^{\circ 3}$ defined polynomials of degree 64 representing the 64 genetic codons as its roots. Genes could be constructed as functional powers $g_{64}^{\circ N}$. These functional powers increase the complexity of the space-time surface. The inverses of these maps correspond to algebraic functions and reduce the complexity. Introns would correspond to the functional composites g_4^k and need not correspond to full codons. They would begin with GU and and with AG.

3. Suppose that the composites of maps g making possible cognition realized in terms of the geometric counterparts of dark nucleotides, codons and genes realized at the field body. The inverses of the maps I composed with I allow to eliminate intronic portion I and the operation replacing $g = g_1 \circ I \circ g_2$ with $g_1 \circ g_2 \times I$ would allow to eliminate the intronic portion I so that one would two disjoint space-time surface. Is this operation and its inverse of this operation possible? If so, removal and addition of introns would have a direct description at the level of dark information molecules.

4. Suppose $g = g_1 \circ g_2$ represents a portion of a gene. The Galois group of G of g has the Galois group G_2 of g_2 as normal subgroups so that $G_1 = G/G_2$ is a group. This allows the decomposition of representations of G to a direct sum of tensor products of representations of G_1 and G_2. This makes possible Galois measurements reducing G effectively to $G_1 \times G_2$. An interesting question is whether this could at the space-time level correspond to the reduction $g = g_1 \circ g_2 \to g_1 \times g_2$ so that the space-time surface decomposes to disjoint union of two space-time surfaces. Could the splicing of introns involve the operation $\circ \to \times$ and could the inverse of the splicing involve the operation $\times \to \circ$?

5. The icosa tetrahedral realization of the genetic code [L11] at the level of the field body involves Hamilton cycles for 3 icosahedra and 1 tetrahedron (3I+T). An attractive conjecture is that the 64 triangles of this structure correspond to the 64 roots of the polynomial g_{64}. The highly non-trivial consequence is that the functional composite g_{64}^N defines dark genes. For the simplest option, this would correspond to a monopole flux tube parallel to the ordinary gene but this assumption is not necessary. It is enough that dark genes at the field body are paired with ordinary genes. Dark $3N$-photons make possible communication between them. The scales of gene and dark gene could be widely different.

6. Also dark proton realization of genetic codons is central. They select a triangular face of the icosa tetrahedral tessellation. Codon as a dark proton triplet is associated with the vertices of the triangles of the icosa tetrahedron or tetrahedron such that the 3-chords defined by the cyclotron frequencies for these states for the protons characterize the codon. The transitions between the states of codons induce 3N-chords of light induce opposite transitions in the receiver gene.

7. The letters, codons and genes of the DNA sequence should be in some sense indivisible units, primes one might say. What could this mean mathematically. The functional composites $g_{64} = g_4^{\circ 3}$ representing codon as 3-letters, and g_{64}^N representing gene are not such since Galois group decomposes to a hierarchy of factor groups and normal subgroup at the bottom.

   (a) Polynomials with prime degree have a simple Galois group without normal subgroups and do not have functional decomposition. Could one divide away some root monomials from the polynomial to get prime polynomials. This idea does not conform with the idea that the 3I+T structure corresponds to the union of the roots of g_{64}. It also leads to a problem with met codon *resp.* stop codons: in these cases the polynomials should be of degree 1 *resp.* 3 and degree 1 means a mere comple coordinate change. Dark proton representation of codons allows the selection of one particle face as a geometric representation of codon.

   (b) The observation that polynomials of degree 4 (not prime) allow the alternating group A_4 having 12 elements as a Galois group. A_4 is a subgroup of an icosahedral group with 60 elements obtained by dividing with subgroup Z_5. The Hamilton cycles at icosahedron [L11], representing 12-note scale and defining harmonies with 20 3-chords identifiable as triangular faces of the icosahedron, have subgroup of A_4 as symmetry group.

   A_4 is effectively simple in the sense that the polynomial in question does not allow functional decomposition to polynomials of degree 2. This suggests a solution to the problem. The codons and genes must be such that they can be deformed to in such a way that the Galois group becomes effectively simple.

   This deformation however spoils the composite property. If the gene is near the criticality for thi deformation, deformation can act as a control operation. This implies that the primeness property of the basic unit is dynamical. For instance, genes containing also introns could be effectively prime but small deformation induced by the catalyst could produce a functional composite of the dark gene to $g_1 \circ g_2$: g_1 would contain the intron. The $\circ \to \times$ mechanism could lead to the separation of the portions of the gene corresponding to g_1 and g_2.

In the following various options are studied in the TGD framework. The cautious conclusion is that time reversals of splicing as attachment of introns and transcription are not absolutely

necessary but are favoured by ZEO as a means to induce active evolution. Also a rather detailed view about the connection of genetic code and the cognitive hierarchies predicted by the holography = holomorphy hypothesis emerges.

3.2 A possible TGD view of DNA transcription and splicing

3.2.1 Basic facts about transcription and splicing

If is good to being with some basic facts about transcription and splicing.

1. Consider first the situation at the DNA level before transcription and splicing. The promoter and terminator regions associated with the gene could also be included in the gene because they form a natural unit that is potentially quantum coherent. The codon coding for protein met serves as the start codon for genes at both DNA and RNA level.

   Terminator region is needed since the stop codon does serve as a signal for the end of transcription. Terminator region deforms to a loop which makes it impossible to continue the transcription.

2. In the splicing operation, introns are cut out of the pre-RNA. GU is used to mark the start of an intron and AG is used to mark the end (conjugation symmetry). In splicing, the enzyme spliceosome checks at each step whether it contains GU or AG. GU indicates that the intron part begins and marks the break in the DNA chain. AG indicates that it ends and marks the cutting out of the intron part. Then the part of the gene that precedes and follows the intron that codes for the protein is glued together. Cutting and gluing are the basic operations of DNA surgery, genetic engineering.

3. Note that preventing the transcription of the entire gene is a different epigenetic operation. DNA methylation at CpG (p refers to phosphate bond between C and G) as a chemical barrier prevents the transcription of the entire gene. Is this barrier also realized at the level of dark DNA or is it needed at all? Could it be that the dark photon signal from the field body that initiates the transcription is not received because the methylation has changed the receiving frequency triplet oof the CpG codon so that it is no longer the resonant frequency.

3.2.2 Connection of the genetic code with the hierarchy of functional compositions as representation of cognition

An attractive starting hypothesis is that the genes correspond to 4-surfaces as roots of polynomials $g : C^2 \to C^2$ acting as dynamical symmetries on function pairs $f = (f_1, f_2)$ defining analytic maps $f : H = M^4 \times CP_2 \to C^2$ defining corresponding space-time surfaces as roots $(f_1 = f_2) = (0, 0)$. A second natural assumption it that the polynomials g are obtained from functional compositions of very simple polynomials which are in some sense irreducible or prime.

A natural identification of the letters of A, T, C, G of the genetic code would be as roots of a polynomial of degree $d = 4$, which also allows analytic solutions for the roots. For the sake of simplicity, one can restrict $g = (g_1, g_2)$ to $g = (g_1, Id)$ in the sequel.

1. Why polynomials of degree 4 rather than prime degree 2 or 3 would appear as fundamental polynomials? Could the polynomials of degree 4 have simple Galois group in the sense that functional decomposition $g^{4)} = h_2 \circ i_2$ is not possible?

   The Galois group is a subgroup of S^4 and the isomorphism classes for the Galois group of a quartic are S_4, A_4, D_4 (dihedral), V_4 (Klein four-group), and C_4 (cyclic). A_4 is non-Abelian and has V_4 as a normal subgroup and is not simple. However if A_4 acts as Galois group of a fourth order polynomials, the polynomial does not allow a decomposition $g^{4)} = g^{2)} \to g^{2)}$ so that in this sense it is simple and also the only subgroup with this property. Hence A_4 is unique.

2. Remarkably, the order of A_4 is 12, which is the number of vertices of icosahedron appearing in the icosa tetrahedral model of the genetic code [L11] in which Hamilton cycles through the 12 vertices of icosahedron defines a representation of 12-note scale and the triangular faces define bioharmony consisting 3-chords defined by the cycle.

3. This suggests that a similar phenomenon is possible for the deformations of the composites $g_4^{\circ n}$. In particular $g_4^{\circ 3}$ giving rise to a polynomial g_{64} of degree 64 could be deformed to a polynomial, which does not allow a functional decomposition without changing the Galois group and in this sense defines a basic genetic unit. Also a suitable deformation of $g_{64}^{\circ N}$ could define a gene as an irreducible unit. However, the irreducibility would be a relative notion. For suitable deformations changing the Galois group and functional decomposition becomes possible.

4. What if one modifies $g^{64)}$ so that it becomes a polynomial with prime degree, which does not allow any functional decomposition? Prime degree $d = 61$ is the maximal degree allowing this and corresponds to the number of codons coding for proteins. 3 codons would correspond to stop codons. Could $g^{61)}$ obtained from $g^{64)}$ by dropping 3 monomial factors be associated with protein coding codons? One of the problems is that this proposal is not consistent with the identification of the 64 roots as the triangular faces of the the 3I+T unit of icosa tetrahedral tessellation.

This raises obvious questions.

1. Could DNA codon sequences correspond to an abstraction hierarchy defined by functional composites of polynomials $g^{4)}$? Codons would correspond to the 64 roots as regions of the field body for the deformations of polynomials obtained as functional composites $g^{64)} = g_4^{1)} \circ g_4^{2)} \circ g_4^{3)}$. As a special case, one has $g_4^{1)} = g_4^{12)} = g_4^{3)}$. Holography = holomorphy vision does not however require this. The roots can be solved for the iterates in the general case.

   The degree associated with $g^{64)}$ is $4^3 = 64$. $g^{64)}$ defines a 3-fold extension of the extension E of rationals appearing as coefficients of $g_4^{i)}$ and f so that the Galois group is not simple and allows a decomposition to normal subgroups defining a cognitive hierarchy.

2. What about genes? Gene cannot contain stop codons except at its end. Could genes with N codons correspond to functional compositions of N polynomials $\circ_{i=1^N} g_{64,i}$, having degree 64^N and defining a space-time representative of the gene. Note that the roots of $g_i^{64)}$ are known if they are constructed in the proposed way so that also the genetic polynomials are cognitively very special!

   The irreducibility condition for genes could be realized just as in the case of g_4 by a deformation making the polynomial functionally indecomposable. Criticality would require only a small deformations and this would make the dynamics controllable.

3. In this framework, the addition of introns in the reverse transcription would correspond to the addition of functional composites of $g_{64)}^{\circ K}$ to the functional composite of $g_{64)}^N$ defining the gene. GU is used to mark the start of an intron and AG is used to mark its end. These letter pairs might be special in the sense that cutting and gluing are possible. One possibility is that for these letter pairs it is possible to achieve quantum criticality for the transition to a functional composition of form $g = g_1 \circ g_2$ such that g_2 begins with GU or g_1 ends with AG.

4. The addition/removal of functional composites of $g_{64)}^{\circ K}$ increases/reduces the degree of the polynomial associated with the gene. The processes should involve a deformation making impossible the functional decomposition without changing the Galois group.

What is remarkable is that this picture relates directly to the p-adic length scale hypothesis [L21, L24] stating that primes p near to but smaller than powers of 2 or 3 are in central role physically. TGD leads to a generalization of p-adic number fields to their functional counterparts for which expansion in powers of prime is replaced by expansion in functional powers of polynomials with prime degrees p [L15, L19]. By dividing out k monomial factor one can reduce the degree $d = p^n$ to the prime degree $d = p^n - k$. For $p = 2$ or 3 the roots of the polynomials in the hierarchy can be solved analytically and these hierarchies are expected to be cognitively very special. Genetic code would provide a realization with $d = 4$: if Galois group is alternating group A_4, no functional decompositions to lower degree polynomials are possible. The same could happen also for codons and genes. The discovery of Galois would reflect itself in physics, biology and cognition.

3.2.3 A TGD based model for the transcription and splicing

The basic assumption is that the transcription and also other basic operations at the chemical level are induced by a corresponding process at the level of dark DNA/RNA. The dynamics at the level of dynamics would be induced dynamics, a kind of mimicry.

1. Assume holography = holomorphy vision. Suppose that the coefficient field of the Taylor coefficients of the generalized analytic functions $(f_1, f_2) : H \to C^2$ and functions $(g_1, g_2) : C^2 \to C^2$ are is the extension E of rationals. For simplicity, assume that (f_1, f_2) is ground state in the sense that it does not allow a composition $f = g \circ h$. Assume for the simplicity that the maps g are of the form $g = (g_1, Id)$ affecting only f_1: $f_1 \to g_1 \circ f_1$.

2. The concept of a p-adic function field is essential. p-Adic function field generalizes the notion of p-adic number field and allows category morphism to the ordinary p-adic numbers. p corresponds to the degree of the iterate polynomial. Generalized iteration is possible in the sense that the coefficients of the g polynomial can change step by step in the iteration, but the degree and Galois group are preserved.

3. Suppose that the nucleotides at the space-time surface correspond to the roots of a 4^{th} degree polynomial P_4 and the codons correspond in the case of introns to a 3-fold iteration of P_4 giving P_{64}: this is so because the intronic part can contain stop codons. Gene with N codons would correspond to an N-fold iteration of g_{64} or its generalization allowind deformations of individual polynomials. This assumption is possible and suggested by the connection with icosa tetrahedral realization of the code.

4. The roots for the generalized iterates of g can be solved analytically if they can be solved for the initial polynomial and the roots correspond to 64 different codons. These again are obtained as roots for 3-fold iteration of a 4th degree polynomial and the latter can be solved analytically.

The number theoretical description of the slicing could look like as follows.

1. Intron begins with GU and ends with AG (note the conjugation symmetry). Introns can correspond to all 64 codons apart from the first and last codon. Dark proton triplet selects these special codons. The cutting of intron from the preceding part of pre-RNA corresponds to the $\circ \to x$ operation so that two disjoint space-time sheets are obtained

2. GU resonance for dark codon degrees of freedom in the communication between spliceosome and pre-RNA tells that an intron and splicing are involved. AG resonance indicates that the intron has ended and splicing is taking place. Note that the resonance could induce deformation of the gene transforming its Galois group so that the functional decomposition becomes possible.

   The sequences preceding and following the intron are glued together and now stabilization must take place by a deformation making the polynomial non-decomposable.

3. What would splicing mean at the level of generalized iteration of a function? Pre-RNA would correspond to its own space-time surface. The product $(g_1 \times g_2, Id)$ corresponds to two disjoint space-time surfaces. In the cutting off of an intron, the function $g_1 \circ I \circ g_2$ would be replaced by the function $g_1 \circ g_2 \times I$. The cut operation $\circ \to x$ for the polynomials $I \circ g_2$ and $g_1 \circ I$ would be followed by the gluing operation as the inverse operation $\times \to \circ$ for the polynomial $g_1 \times g_2$. The overall degree of the polynomial would decrease because for a product, the degree is the sum of degrees and for a functional composite, the product of degrees.

3.3 Could the reversals of transcription, slicing and translation allow realization in the TGD inspired quantum biology?

Could the (time) reversals of translation, splicing and transcription make possible active evolution by experimenting with various choices of introns? Consider now what the reverse of the process

leading from DNA to proteins would look like. In the initial state amino acid (AA) sequence and RNA codons are present.

The central dogma of biology states that information is transferred in the direction of DNA → RNA → proteins so that the first guess for the answer is "No". Could ZEO help? The reverse transcription is realized in nature and might be enough.

3.3.1 Reverse splicing and reverse transcription

Introns are believed to control transcription but could also have other functions. In the TGD framework they could also serve as correlates for cognition and emotions realized at the molecular level. Therefore the addition of introns in the (time) reversal of the splicing would be highly desirable. CRISPR, making possible genetic engineering at DNA level, is known to occur in Nature and also at the level of RNA. In the case of RNA it could correspond to a reversal of the splicing. Whether this is the case, is not clear to me.

The reverse splicing would add new introns which give rise to higher control levels in transcription. Could the emergence of the control levels in this way correspond to the compositions $f \to g \to f$ for $f : C^2 \to C^2$ and $f = (f_1, f_2) : H \to C^2$ defining a space-time surface decomposing to a union of regions given by the roots roots $(f_1, f_2) = (0, 0)$.

Reverse transcription (see this) is known to occur in Nature as a basic process. After the reverse transcription, the DNA sequence would replicate to double strand. If the last step would lead to dark DNA strand, which would pair with ordinary DNA. Dark DNA would replicate and this would induce the replication of ordinary DNA strands leading to double DNA strands.

3.3.2 The reversal for the process mRNA → amino-acids is not plausible

Consider first the the reversal of the process: mRNA → amino-acids. mRNA and tRNA would be generated from AA sequence by reverse translation. This step seems to be the most vulnerable part of the process.

1. AA sequence and RNA codons would transform to mRNA and tRNA codons in a process occurring in reversed time time direction. After the first BSFR mRNA and tRNA would appear at the "past" end of increasing causal diamond (CD). After the second BSFR they would appear at the "future" end of the CD. They would apparently pop out of vacuum. One could say that mRNA is reversed engineered from AA. This process is non-deterministic and 1-to-many since many mRNA codons code for a given amino acid.

2. The process would generate tRNA. Usually tRNA is generated by transcribing an appropriate gene to pre-tRNA. After splicing and other kinds of processing the tRNA\ AA is transferred to cytoplasm and AA is added to give the tRNA.

   Suppose that the AA sequence can be feeded to the ribosome machinery (somewhat like AA to tRNA\ AA) operating in the reverse time direction. If so, AA sequence is transformed to mRNA sequence parallel to it by adding mRNA codons from cytoplasm to the increasing mRNA sequence and fusing the counterparts of RNA codons to AAs to give tRNA.

There are several objections against the reverse translation.

1. There exists no "reverse ribosome enzyme" for the reverse translation from protein to DNA. Could the time reversal occurring in BSFR be involved? Could the ribosome machinery operate in the opposite time direction and in this way make possible reverse translation?

   After the first BSFR, the time reversed process would generate mRNA and tRNA from AA sequence and RNA codons and their counterparts in the cytosome and this looks like a decay of mRNA in standard time direction.

2. The tRNA counterpart of RNA could be called tRNA\ A. Is a gene activating its generation needed or does the cytosome contain enough tRNA\ A generated in the translation. If not, information transfer to DNA to activate it is needed.

   It deserves to be noticed that for years ago I considered the possibility that originally AA sequences catalyzed the formation of RNA sequences and decayed in the process. Then the

roles were changed: RNA sequence started to be generated by AA sequence. This process would have been analogous to the reverse translation.

3. The map RNA $\rightarrow$ proteins is not invertible: this is however not a problem from R&D point of view since it would make possible generation of new DNAs. Furthermore, ZEO is motivated by the small failure of classical determinism for the dynamics of the space-time surfaces. Non-determinism is necessary if one wants to realize R&D lab.

4. Protein folding could be seen as the problem. The protein should be unfolded first but this process occurs routinely under metabolic energy feed. Proteins also suffer modifications after translations but even this is not a problem if one wants to make living organism R&D lab.

5. Is it really possible that reverse translation would not have been observed? Could a more prosaic and realistic option be the decay of AA sequence to AAs and the fusion of AAs and tRNA-AA codons to tRNA occurring in the standard view about generation of tRNA. Indeed, since AA sequence does not carry a negative constant charge density, h_{eff} hypothesis suggests that it is not accompanied by a dark variant consisting of dark proton triplets (as I have suggested earlier).

   One might hope that quantum coherence allows the reverse translation to occur for the entire AA or sequence or part of it, at least with some probability. If so, the RNAs combine in the process to RNA sequence accompanied by dark RNA.

6. One can also consider the possibility that the reverse translation is dropped away so that one would have only the reverse transcription. This would be enough to produce the introns.

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