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

February 24, 2026

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Abstract

Could TGD provide a concrete view of evolution at the level of genes? How could new genes appear? Genetic engineering (CRISPR) 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.

1 Introduction

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.

1.1 Dark variants of the information molecules

Consider first the key notions and ideas.

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.

1.2 Zero energy ontology and biology

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

1. Zero energy ontology (ZEO) [K1] 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.

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 [L2, L4, L3] space-time surfaces are defined as roots for analytic maps $f = (f_1, f_2) : H = M^4 \times CP_2 \to C^2$. They allow dynamical symmetries $f \to g \circ f$: $g \to C^2 \to C^2$. 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 [L2, L4, L3] allows symmetries realized as maps $g : C^2 \to C^2$. 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 [L1] 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 [L1], 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.

   The polynomials having A_4 as Galois group do not allow a decomposition to a functional composite of polynomials of degree 2. In this sense they are prime polynomials.

   Large enough deformations however change the Galois group and spoil the prime property. If the gene is near the criticality for this deformation, deformation can act as a control operation. This implies that the prime 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.

2 A possible TGD view of DNA transcription and splicing

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.

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 [L1] 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 [L5, L6] 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 [L2, L4]. 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.

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 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 $\to$ RNA $\to$ 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.

3.1 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.

3.2 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 → 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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