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

February 11, 2026

Matti Pitkänen

orcid:0000-0002-8051-4364.
email: matpitka6@gmail.com,
url: http://tgdtheory.com/public_html/,
address: Valtatie 8, as. 2, 03600, Karkkila, Finland.

Contents

Abstract

Could TGD 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.

1 Introduction

Could TGD 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.

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, could be dynamical. This makes 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. Zero energy ontology (ZEO) 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.

4. 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.

   Could the time reversal of the entire sequence decomposing to transcription of DNA to RNA followed by the splicing of RNA to mRNA followed by the transformation of tRNA and mRNA to AA sequence and mRNA codons produced from tRNA and from the decay of mRNA look like if possible at all? This would give rise to non-deterministic reverse engineering of DNA making possible a generation of modified more complex genes? What would be nice is that random mutations would be replaced by genetic engineering modifying the existing genome by starting from the protein level would be possible.

5. 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.

In the following these alternative hypotheses are studied in the TGD framework. The cautious conclusion is that time reversals of splicing as attachment of introns and transcription are enough 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 Could the time reversals of the basic genetic processes allow to understand genetic evolution?

Introns are believed to control transcription but could also have other functions. In the TGD framework they could also serve as correlates for cognition emotions realized at the molecular level. The key question is whether the time reversals of translation, splicing and transcription could make possible active evolution by experimenting with various choices of introns.

2.1 Could one consider the reversal of the translation of DNA to proteins?

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 $\rightarrow$RNA $\rightarrow$ proteins so

that the first guess for the answer is "No". Could ZEO help? There is evidence for the reverse transcription and it might be enough to consider a weaker option involving reverse transcription.

1. At the first step mRNA and tRNA would be generated from AA sequence by reverse translation. This step seems to be the most vulnerable part of the process.

   (a) 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.

   (b) 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.

   The basic objections against reverse translation will be considered later.

2. The second step would be time reversal of splicing. I would add to the mRNA obtained in this way pieces of RNA. Non-determinism could be involved and only in special cases the outcome would be the RNA produced in the transcription of the original DNA. This is also so because a given AA corresponds to several RNA codons. Also this step would involve the R&D aspect process giving rise to active evolution.

3. This would generate 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 $f \to g < sub > ordm; < /sub > f$ 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 $(f_1, f_2) = (0, 0)$. For $g = (g_1, Id)$ with degree $d = n$ the number of roots increases by factor n. The prime degrees $d = 2$ and $d = 3$ are favoured since in these cases the roots of the iterates can be solved analytically.

   $d = 4$ is the maximal degree allowing analytic expressions for the roots and a good guess is that it corresponds to the letters A,T,C,G of the code assignable to the roots of $g^{4)}$.

4. The third step would be time reversal of transcription. In general it would not produce DNA equivalent with the DNA coding for AA sequence. Time reversed splicing would increase the complexity of the DNA. After this the DNA sequence would replicate to double strand.

5. If the dark variant of the reverse process leading from dark AA sequence to dark DNA can occur, 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.

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 come to the rescue? 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.

To sum up, the first step of the reverse process is clearly the vulnerable part of the proposal but it is not necessary.

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

An attractive idea is that the genes correspond to 4-surfaces as roots of polynomials $g < sub > ordm; < /sub > f$ defining corresponding space-time surfaces and that the polynomials g are obtained as or from functional compositions of very simple polynomials. 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 following.

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 so that functional decomposition $g^{4)} = h^{2)} < sub > ordm; < /sub > i^{2)}$ 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 $g^{4)} = g^{2)} < sub > ordm; < /sub > g^{2)}$ 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. Could DNA codon sequences correspond to an abstraction hierarchy defined by functional composites of polynomials $g^{4)}$? Codons would correspond to polynomials obtained as functional composites $g^{64)} = g_1^{4)} < sub > ordm; < /sub > g_2^{4)} < sub > ordm; < /sub > g_3^{4)}$ and codons would correspond to the 64 roots of g. As a special case, one has $g_1^{4)} = g_2^{4)} = g_2^{4)}$ but holography = holomorphy vision does not require this also the roots can be solves for the iterates in general case.

   The polynomial degree associated with $g^{64)}$ is $4^2 = 64$. $g^{64)} = g_1^{4)} < sub > ordm; < /sub > g_2^{4)} < sub > ordm; < /sub > g_3^{4)}$ defines a 3-fold extension of the extension E of rationals appearing as coefficients of $g^{64)}$ and f so that the Galois group is not simple and allows a decomposition to normal subgroups defining a cognitive hierarchy.

4. One should understand why codons special units of DNA. What if one modifies $g^{64)}$ so that it becomes a simple polynomial with prime degree allowing no functional decomposition so that codon would represent irreducible cognition? 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 associated with the stop codons?

5. What about genes? Gene cannot contain stop codons except at its end. Could genes with N codons correspond to functional compositions of N polynomials $g_i^{61)}$, $i = 1, ..., N$ having degree 61^N and defining a space-time representative of the gene. Note that the roots of $g_i^{61)}$ are known if they are constructed in the proposed way so that also the genetic polynomials are cognitively very special!

   The simplicity condition for the genetic polymials could be realized by dropping out k monomial factors associated with the roots so that the the degree $d = 61^N - k$ is prime. Genes correspond to irreducible cognitions obtained from composite cognitions by dropping k genes. Could these non-allowed genes be analogous to stop codons? What could this mean?

6. In this framework, the addition of introns in the reverse transcription would correspond to the addition of functional composites of $g_k^{61)}$ to the functional composite of $g_i^{61)}$ defining the gene. The added composites should be somehow distinguishable from the codons coding for proteins. Note that it is not quite clear whether the order for functional compositions is the same as the linear order along the gene.

   The addition functional composites of $g_k^{61)}$ increases the degree of the polynomial associated with the gene. This could imply that it is not anymore a prime polynomial. The dropping of the introns in splicing could mean a reduction to the original prime polynomial with a simple Galois group.

2.3 Connection with p-adic length scale hypothesis

What is remarkable is that this picture relates directly to the p-adic length scale hypothesis [L4, L5] 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, L3]. 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 $d = 4$ and for codons and genes one would have prime degree. The discovery of Galois would reflect itself in physics, biology and cognition.

REFERENCES

Books related to TGD

Articles about TGD

[L1] Pitkänen M. About tessellations in hyperbolic 3-space and their relation to the genetic code . https://tgdtheory.fi/public_html/articles/tessellationH3.pdf., 2023.

[L2] Pitkänen M. About Langlands correspondence in the TGD framework. https://tgdtheory.fi/public_html/articles/Frenkel.pdf., 2024.

[L3] Pitkänen M. A more detailed view about the TGD counterpart of Langlands correspondence. https://tgdtheory.fi/public_html/articles/Langlands2025.pdf., 2025.

[L4] Pitkänen M. A refined view of the phenomenology of hadron physics and p-adic mass calculations. https://tgdtheory.fi/public_html/articles/padmass2025.pdf., 2025.

[L5] Pitkänen M. Does the notion of Teichmüller element cure the problem of p-adic mass calculations due to the slight failure of Lorentz invariance? https://tgdtheory.fi/public_html/articles/padmass2026.pdf., 2026.