Gene Tectonics and TGD

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Abstract

"Gene tectonics" represents a remarkable step of progress in genetics. The study of the evolution of chromosomes involving few basic mechanisms such as mixing of genes within chromosome, fusion of chromosomes along their ends, the insertion of chromosome inside chromosome, and fusion followed by permutations of genes within the composite chromosome allows to study the evolution at the level of entire genome and to understand what the differentiation of lineages and species could correspond at the level of genome. It has been found that the mixing of genes occurs often and does not have drastic effects and one can speak of chromosome conservation whereas the mutations involving several chromosomes are rare.

These findings represent a challenge for the TGD point of view of genetics and together with the recent progress in the number theoretical vision about physics, inspire fresh questions and ideas about genes and chromosomes. In particular, the question of how genes could code for biological functions reduces to the level of space-time dynamics at the number-theoretical level.

In the number-theoretical vision about TGD, biological functions would correspond to polynomials and genes would correspond to composition of polynomials assignable to genes. In zero energy ontology (ZEO), a given polynomial would define a space-time region as an analog of deterministic classical computation and quantum computation would involve their superposition.

1 Introduction

Quantamaganize articles are often highly inspiring. At this time the article "Secrets of Early Animal Evolution Revealed by Chromosome 'Tectonics'" (`https://cutt.ly/OOJbxUz`) provide food for TGD inspired thoughts about genetics.

This led to a little intellectual adventure leading to a proposal for a general answer to two questions. What is the physical counterpart of biological function at fundamental level? How do genes code for biological functions?

1.1 Gene tectonics

Due to the technical restrictions, the research of evolutionary history is strongly concentrated on point mutations so that one has not learned much about the evolution in the scale of the entire genome. This kind of research tries to understand what differentiation to new species and lineages involves at the. level of genes.

In a paper appearing in Science Advances [**?**] (`https://cutt.ly/LOJbaH0`), an international team of researchers led by Daniel Rokhsar has tracked changes in chromosomes that occurred as 800 million years ago. They identified 29 big blocks of genes that remained recognizable as they passed into three of the earliest subdivisions of multicellular animal life. Using those blocks as markers, the scientists deduced how the chromosomes fused and recombined as those early groups of animals became distinct.

The researchers call this approach "genome tectonics". What Rokhsar intuited was that blocks of genes in a given lineage were in good approximation conserved apart from the reshuffling of the genes inside the blocks. One can speak of conservation of chromosomes. This intuition could be tested recently, when enough chromosome-scale genomic information about diverse animal groups became available.

What causes the blocks of genes to stay together? One explanation for the conservation of the blocks is that physical nearness facilitates co-operation in the basic genetic processes such as transcription. This functional explanation applies to Hox genes, which is however a small part of the genome.

An alternative explanation is in terms of genomic inertia. There are only very few mechanisms of genetic reorganization.

1. Remixing occurs within chromosomes so that genes remain linked over the time.

2. In the terminal fusion chromosomes A and B are fused along their ends but genes remain linked with their original fragment.

3. Chromosome A is inserted inside chromosome B.

4. Fusion with mixing involves blending of genomes of the chromosomes A and B. The simultaneous fusion and mixing does not sound plausible whereas fusion followed by mixing is natural and this is what is meant as one learns from the original article [I1]. One speaks about mixing as inversion mutations in this case. If so, only the first three mechanisms serve as basic mechanisms.

Interestingly, the second and third mechanism correspond to basic topological reactions for strings involving reconnection. The mixing within a chromosome corresponds to a permutation of genes within the genome, and the question is whether it could have some natural mathematical description.

Genomic rearrangements are not easy to spread in the population. During meiosis and the formation of gametes all chromosomes must pair with a matching partner. In absence of a partner, odd-sized chromosomes cannot pass to the next generation. Hence broken and fused chromosomes tend to be dead ends. The reshuffling of genes within chromosomes is however possible. There is also a competition with the existing genomes so that the rearrangements have small changes except in small populations.

This picture allows us to make conclusions about genetic evolution. If two species share a similar mixture of two gene blocks, the mixing very probably occurred in the common ancestor. It is also possible to make testable predictions.

Simakov, Rokhsar and their colleagues [**?**] (`https://cutt.ly/7OJbE8U`) used genetic tectonics to learn more about the emergence of some of the earliest animal groups about 800 million years ago. Chromosome fusions in early evolution were studied. How conserved genes passed into early animal lineages during the animals evolution from a common ancestor. Three early lineages represented by demosponges (21 chromosomes), cnidarians (23 chromosomes) cnidarians, bilaterians (24 chromosomes). The researchers found 29 blocks of genes that were highly conserved among their chromosomes.

Using the rules of chromosome fusing and gene mixing that they had identified, the researchers reconstructed the chromosome-level events that accompanied the evolution of these three lineages from a common ancestor. They showed that the chromosomes of sponges, cnidarians and bilaterians all represent distinctive ways of combining elements from the ancestral genome.

1.2 How does gene tectonics relate to the TGD view about genome and its evolution?

1.2.1 Key notions of TGD inspired quantum biology

For several reasons, the proposed mechanisms of evolution at the level of chromosomes are highly interesting from the point of view of TGD.

TGD inspired quantum biology relies on the following key ideas.

1. The view about space-time as 4-surface in $H = M^4 \times CP_2$ leading to the notion of magnetic cody (MB).

2. Number theoretical (adelic) physics predicting the hierarchy of phases of ordinary labelled by the effective Planck constant h_{eff} and behaving like dark matter, p-adic physics as correlates for cognition, and $M^8 - H$ duality predicting that space-time regions are coded by polynomials.

   Number theoretic vision associates evolutionary hierarchies to the inclusion hierarchies of extensions of rationals associated with polynomials P, which at the fundamental level determine space-time via holography. The degree of the polynomial defines effective Planck constant $h_{eff} = nh_0$ serving as a kind of universal IQ characterizing the system.

   MB has large value of h_{eff} serving as a universal IQ, and serves the master and controls the biological body in the role of slave. This leads to the proposal that genetic code has fundamental realization at the level of dark matter in terms of dark proton and dark photon triplets and biochemical realization is a secondary realization.

3. Quite generally, biochemistry emerges as a kind of shadow dynamics. The controlling dynamics of MB is much simpler and control and communications is based on dark photon signalling. Biophotons can be identified as ordinary photons produced from dark photons.

   Resonance is the general communication mechanism. The frequencies associated with the signal select the receiver via resonance condition and the signal itself represented as a frequency modulation is transformed to a sequence of resonance peaks.

   Genetic codons are realized as dark proton and dark photon triplets, which correspond to Galois singlets in a number theoretic picture. Quite generally, bound states correspond to Galois singlets and codons could combine to form genes and larger quantum coherent structures by Galois confinement somewhat analogous to Bose-Einstein condensates.

4. Zero energy ontology (ZEO) in which the quantum state is identified as a superposition of deterministic time evolutions analogous to biological functions or computer programs.

   Polynomials determine space-time surfaces, which in turn are correlates for biological functions so that the notion of biological function reduces to a function as a polynomial with rational coefficients. Functional composition is analogous to a composition of a computer program from modules or of a biological function from simpler ones. The natural proposal is that genes correspond to compositions of polynomials with codons and letters perhaps identifiable as generating functions.

   ZEO provides a new view about quantum measurement theory and predicts that the arrow of time changes in ordinary, "big", state function reductions (BSFRs) and predicts also the occurrence of "small" SFRs (SSFRs) as counterparts of "weak" measurements. This leads to a generalization of thermodynamics and time reversal provides a general mechanism of self-organization and of homeostasis.

1.2.2 Questions

This picture allows us to consider answers to several questions inspired by the article.

What could be the mathematical description for the mixing of genes inside the chromosomes? Why does it have no dramatic effects unlike the recombinations of chromosomes? What does the mixing mean for the biological functions associated with the genes?

What is the fundamental mathematical counterpart for the biological function of a gene? What does construction of chromosomes from genes and various recombinations of chromosomes correspond to in terms of biological functions?

In meiosis chromosomes re-arrange in a new manner. What does this mean at the level of the biological functions?

2 Key ideas of TGD and TGD inspired quantum biology

To consider the questions posed above, one must first introduce some key ideas and notions of TGD.

2.1 Duality between geometric and number theoretic physics

The TGD based view of fundamental physics and also of quantum biology involves in an essential manner the duality of the two visions about physics behind TGD. The geometrization of physics involves generalization of Einstein's program from the geometrization of classical physics to that for the entire quantum physics. Number theoretical vision about physics, which I call adelic physics, brings in number theoretical notions [L3, L4, L8, L9, L13].

1. In the physics as geometry vision [L13], space-time at the fundamental level is identified as a 4-surface in $H = M^4 \times CP_2$, in a loose sense an orbit of 3-surface.

   General Coordinate Invariance (GCI) requires that the dynamics associates to a given 3-surface a highly unique 4-surface at which the 4-D general coordinate transformations act.

This 4-surface is a preferred extremal of the action principle determing space-time surfaces in H and analogous to Bohr orbit. GCI gives Bohr orbitology as an exact part of quantum theory and also holography. The space-time surfaces turn out to be minimal surfaces with singularities analogous to the frames spanning the soap film [L15].

2. In the physics as number theory vision, one considers 4-surfaces in complexified octonionic M^8 determined by octonionic continuations of real polynomials P with rational coefficients. The dynamics reduces to the condition that the normal space of 4-surface is associative (quaternionic). M^8 is analogous to momentum space so that a generalization of momentum-position duality of wave mechanics is in question.

2.2 Space-time surfaces are coded by roots of polynomials

The roots of an irreducible polynomial P continued to a complexified octonionic polynomial, code for a 4-surface in M^8 in turn mapped by $M^8 - H$ by duality to a space-time surface in H [L16, L17, L8, L9].

1. The algebraic roots of P (having rational coefficients) define mass shells $H^3 \subset M^4 \subset M^8$ and these mass shells serve as holographic data defining $M^8 - H$ duality. The duality is defined in terms of a deformation of the real projection M^4_c defining 4-D surface connecting the real projections of the mass shells.

2. The deformation is local $SU(3)$ element g for the subgroup $SU(3) \subset G_2$ of octonionic automorphisms satisfying the condition that the image points $g(m)$ are invariant under $U(2)$. This deformation maps M^4 to CP_2 and defines $M^8 - H$ duality explicitly. An alternative, purely geometric manner to define the duality is by assigning to the normal space of X^4 containing a preferred plane E^2 a point of CP_2 characterizing it.

3. The construction of scattering amplitudes [L16, L17] based on this picture leads to the proposal that by the conservation property the interaction many-particle systems with external particles characterized by polynomials P_i corresponds to a functional decomposition of P_i. The permutations of P_i give rise to different compositions but conserve the roots. There are good reasons to assume that only cyclic permutations can appear in the quantum superposition to which cognitive measurements [**?**] producing as a final state a collection of disjoint surfaces as external particles of the reaction and described by the product of polynomials can be applied.

   Scattering amplitudes are assumed to be dictated by a number theoretic dynamics defined by re-combinations of Galois singlets of many quark states consisting of free quarks with total momenta, which are ordinary integers (quarks have momenta which are algebraic integers) in a unit defined by p-adic length scale associated with the largests ramified prime of P.

2.3 Space-time surfaces and quantum computer programs

The interaction by the formulation of the functional composite has also cognitive interpretation [**?**]: Nature would be doing quantum computations by performing functional compositions.

1. In zero energy ontology (ZEO) [L7] [K3, K4], quantum states are quantum superpositions of deterministic time evolutions analogous to computer programs, biological functions or behaviors.

2. The functional composite would correspond to a decomposition of a computer program to sub-modules, and for rational or even integer coefficients one has a quantum analog of the Turing machine.

   The hierarchy of algebraic extensions of rationals however extends the Turing paradigm. Physical states are however Galois singlets with momentum components, which are integers in suitable scale.

3. The state function reduction (SFR) cascade process reducing the entanglement between different relative Galois groups in the hierarchy of Galois groups defined by the polynomials can be identified as a physical correlate of cognitive analysis [L11]. SFR cascade would be analogous to a halting of a quantum computer program.

4. Biological functions are analogous to (quantum) computer programs. They could be realized as topological quantum computations [K1, K2]. The braids connecting DNA and nuclear membrane or microtubules could code for these programs.

3 The new findings about genes and TGD

In this section the findings of [I1] and their possible implications are considered in the conceptual framework discussed above.

3.1 Dark realizations of the genetic code

The realization of the genetic codons in terms of dark proton - and dark photon triplets [L1, L6] leads to a profound generalization of the notion of the genetic code suggesting a new realization as which could be 2- and even 3-D (the MB of the cell membrane could realize genetic code). Dark DNA codons coding for the same amino-acids differ and the proposal is that dark photons realizations are responsible for what could be called emotional intelligence realized as bioharmony [L1, L6, L12]. The realization in terms of codons and frequencies would be behind the reductionistic "bit" intelligence and holistic and intuitive, emotional intelligence [L2].

The vision about biological control and communications using genetic code realized as 3-chords brings to mind computer language LISP [L12]. Dark codons represented as 3-chords serve as addresses and the message would be coded as frequency and amplitude modulations. The cyclotron resonance sequence at the receiving end transforms the message to a sequence of pulses and also nerve pulse patterns could be produced in this manner.

Codons would correspond to either dark 3-protons or 3-photons identifiable as Galois singlets. Also genes, gene pairs in double DNA strand, and even to chromosomes could be Galois singlets behaving like a single quantum unit having dark proton and perhaps even dark photons counterparts.

Quite generally, these realizations of the genetic code would be induced from the so-called icosa-tetrahedral tessellation of the hyperbolic space H^3 (mass shell) [L12]. The chemical realization of the genetic code would be only a secondary realization. The dynamics of the MB would induce biochemistry as a shadow dynamics of the MB serving as the "boss".

3.2 Genes as composite functions?

There is an intriguing analogy with genetics inspired by the idea that functional compositions define analogs of quantum computer programs.

1. One might say that the roots of P determine the genome of the 4-surface since they fix the boundary data as 3-D mass shells specifying the holographic data fixing $X^4 \subset M^8$ and its image as a minimal surface in H.

2. If the polynomials P of a real variable with rational coefficients (possibly monic polynomials with integer coefficients) satisfy the condition $P(0) = 0$, the compositions of polynomials inherit the roots of the factors in the composition. One can speak of analogs of conserved genes.

3. These analogies inspire the question whether genes or their MBs could indeed correspond to functional composites of polynomials characterizing the 4-surfaces determining the space-time surfaces assignable to genes or their magnetic bodies carrying dark genes as dark matter in TGD sense and controlling the genes. A stronger condition would be that the genes correspond to polynomials and the linear sequence of n genes to the composition $P = P_n \circ ... \circ P_n$. In principle, this would provide a solution to the fundamental question of how genes code for biological functions.

4. The remixings of genes within chromosomes would correspond to permutations of the polynomials P_i in their functional composite. In this picture the mixtures of genes inside the chromosome would correspond to the permutations of polynomials P_i representing genes in the functional composite: $P = P_n \circ ... \circ P_n$ representing chromosomes. The fusion of two chromosomes would in term correspond to the functional composite of $P \circ Q$ of composites of this kind. The simplest genes would correspond to a functional composites of polynomials representing codons, which in turn would correspond to functional composites of 4 polynomials.

5. Suppose that the 64 codons correspond to functional composites of 4 polynomials P_i allowing all permutations. One cannot however assume that the functional composites differing by a cyclic symmetry are equivalent so that the Z^3 equivalence class for the functional composites corresponds to the same amino-acid. One would have $N = 24$ non-equivalent composites corresponding to 24 codons of 3 different polynomials coding for 8 amino-acids, 36 codons with 2 different polynomials coding for 12 amino-acids, and 4 codons containing only a single polynomial coding for 4 amino-acids. The prediction would be unrealistic.

   The letters of codon could however correspond to 4 basic functions and their functional decomposition having codon as its counterpart indeed implies that their order in the composition matters. It is interesting to interpret the symmetries of the genome in terms of functional compositions. The most notable symmetry is almost perfect doublet symmetry with respect to the last letter.

   This symmetry suggests that the basic functions correspond to 2 doublets $D_1 = (f_1, f_2) and D_2 = (f_3, f_4)$ and that the members of the doublet $D_1 \circ f \circ g$ are almost equivalent as also the members of the doublet $D_2 \circ f \circ g$ at the biochemical level (protein transcription).

3.3 Why the reshuffling of genes need not have dramatic effects?

What is the effect of a permitatopm on a general composite polynomial $P_n \circ ... P_1$ at the fundamental level? The functional composite changes in the permutation of the composing functions. In particular, the root spectra of two composites with different order differ. They correspond to inverses of the roots of composites P^k under $(P_k \circ ... P_1)^{-1}$, $k = 1, ..., n$ so that the spectra are not identical although they can be mapped to each other in 1-1 manner. The permutation of genes in chromosomes or codons in genes would correspond to this kind of change for the root spectrum.

At the fundamental quark level this kind of permutation would affect the discrete virtual quark spectrum given by the roots of P appearing as virtual masses in the scattering amplitudes defining zero energy states, and also in the spectrum of Galois singlets [L16, L17] since the sum of quark momenta would be ordinary integer by Galois confinement.

Also the reshuffling of genes could corresponds to permutation of polynomials. Unless the 4 polynomials are commutative, this need not cause too dramatic effects.

This could have an interesting interpretation inspired by the TGD based view of the brain. The sensory data, in very general sense, from the biological body, in particular the brain, are communicated to MB. There is evidence that the brain obeys effective hyperbolic geometry in statistical sense [J1]. Neurons close to each other functionally, but not necessarily physically, are near to each other in this effective geometry.

The TGD inspired explanation [L10] is that these neurons correspond to nearby points at the magnetic body (MB) assignable to mass shell H^3 in H, which indeed obeys hyperbolic geometry. H^3 plays a fundamental role in the number theoretical physics at the level of M^8. This would explain the mysterious looking fact that salamander survives in reshuffling of its neutrons [J2] since this reshuffling does nothing for the image points at MB.

Could the situation be almost similar at the level of genes? Could the reshuffling of genes alter the situation at the level of chemical realization of chromosomes but not at the level of MB. Could this be tested?

3.4 How do the findings relate to Cambrian Explosion

The evolution of chromosomes was studied in a time scale of 500 million years. Interestingly, Cambrian Explosion (CE) took place roughly 500 million years ago and plays a key role in the

TGD based view about biological evolution [L5, L14] . The TGD based view about pre-Cambrian evolution proposes that multicellular life evolved in underground oceans and bursted on the surface of Earth in CE about 500 million years ago.

Amusingly, the plate tectonics would have emerged at that time if TGD is right. Before that the surface of Earth would have been like the surface of Mars now.

The finding that multicellulars have started to evolve already 800 million years ago does not conflict with the TGD picture. The evolution would have occurred underground and its outcome would have bursted to the surface of Earth 500 million years ago.

Monocellulars could have drifted to the surface of Earth much before CE, say 800 million years ago, and managed to survive. For the multi-cellulars, the Earth's surface was however too harsh a place. Their sudden appearance in the CE would have brought to surface genomes, which had experienced fusions followed by mixing. Unless one is ready to believe that the fossils of the intermediaries have disappeared, the interpretation would be that fusion and almost simultaneous mixing must have occurred.

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