**Article**

# Many-sheeted DNA: Basic Ideas

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**Abstract**

The problems of how genes code information about the morphology of organism and how this information is expressed, belong to the great puzzles of the developmental biology. A closely related mystery is the differentiation of cells. The notion of the genetic program is far from precise and it is not clear how close the analogy with a computer program is. There are also several problems which challenge the basic dogmas of genetics.

1. Only 1 per cent of DNA of human genome actually codes polypeptides. Eukaryote genes contain intron sequences which are transcribed into hnRNA but snipped of when hnRNA is transformed mRNA in process called slicing. The higher the evolutionary level of organism, the higher the fraction of introns is. Molecular Darwinists see introns as "junk DNA" but there is evidence that introns are far from junk. For instance, the splicing of intron contribution from hnRNA to give mRNA can give several different outcomes depending on the stage of development of the organism and introns are crucial for the effectiveness of immune system. Hence one can wonder whether intronic mRNA and protein mRNA could both form the real output of gene subprograms serving in some sense as input for other gene subprograms. This interpretation obviously conflicts with "gene-single protein" dogma in its basic form.
2. There are large amounts of highly repetitive DNA which is silent. One can wonder whether there is some fundamental mis-understanding involved. Could it be that this DNA is analogous to control DNA not transcribed to RNA and therefore not all useless. There is also active repetitive DNA.
3. There is large amount of silent DNA in control sections between genes. Could it be that this silent DNA expresses itself in some nonchemical manner? Chemical expression is very slow, translation rate being twenty aminoacids per second, and one can wonder whether life might have invented faster modes of gene expression and control of gene expression.
4. Plant genome is often by a factor of hundred longer than human genome. One could argue that the complexity of organism is measured by the length of the shortest program coding the organism. It is however not at all obvious how the genome of plants could be more redundant than human genome since repetitive sequences common to all animals are present. Introns are in fact more frequent in human genome. This suggests that some new unidentified degrees of freedom giving rise to complexity might be present and that the chemistry of DNA in the sense of standard physics is perhaps not all that is needed to understand genetic program.
5. Various self-organization process such as self-assembly and de-assembly are very frequent in living systems. The problem how genes give rise to morphology of the organism is poorly understood. This forces to challenge the dogma of genetic determinism. One should be able to understand what is determined by genes and what is determined by self-organization and whether the genes of the standard physics are enough.

In the first part of the article basic facts about genetics are introduced and the notion of many-sheeted DNA is introduced as a possible solution of the above discribed problems. In the second part of the article a model of genetic program will be developed and some TGD inspired ideas about regulation of morphogenesis are discussed.

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# 1 Introduction

The problems of how genes code information about the morphology of organism and how this information is expressed, belong to the great puzzles of developmental biology. A closely related mystery is the differentiation of cells. The notion of genetic program is far from precise and it is not clear how close the analogy with a computer program is. There are also several problems which challenge the basic dogmas of genetics.

1. Only 1 per cent of DNA of human genome actually codes polypeptides. Eukaryote genes contain intron sequences which are transcribed into hnRNA but snipped off when hnRNA is transformed mRNA in a process called slicing. The higher the evolutionary level of organism, the higher the fraction of introns is. Molecular Darwinists see introns as "junk DNA" but there is evidence that introns are far from junk. For instance, the splicing of the intron contribution from hnRNA to give mRNA can give several different outcomes depending on the stage of the development of the organism and introns are crucial for the effectiveness of the immune system [4] . Hence one can wonder whether intron mRNA and exon mRNA could both form the real output of gene subprograms serving in some sense as input for other gene subprograms. This interpretation obviously conflicts with "gene-single protein" dogma in its basic form.

2. There are large amounts of highly repetitive DNA which is silent. One can wonder whether there is some fundamental mis-understanding involved. Could it be that this DNA is analogous to control DNA not transcribed to RNA and therefore not at all useless. There is also active repetitive DNA.

3. There is large amount of silent DNA in control sections between genes. Could it be that this silent DNA expresses itself in some nonchemical manner? Chemical expression is very slow, translation rate being twenty aminoacids per second, and one can wonder whether life might have invented faster modes of gene expression and control of gene expression. Also the question whether there is a relation to the typical frequency scales of brain consciousness of order 10 Hz, which can be related to the magnetic transition frequencies, can be raised.

4. Plant genome is often by a factor of hundred longer than human genome. One could argue that the complexity of organism is measured by the length of the shortest program coding the organism. It is however not at all obvious how the genome of plants could be more redundant than human genome since repetitive sequences common to all animals are present. Introns are actually more frequent in human genome. This suggests that some new unidentified degrees of freedom giving rise to complexity might be present and that the chemistry of DNA in the sense of standard physics is perhaps not all that is needed to understand genetic program.

5. Various self-organization process such as self-assembly and de-assembly are very frequent in living systems. The problem how genes give rise to morphology of the organism is poorly understood. This forces to challenge the dogma of genetic determinism. One should be able to understand what is determined by genes what is determined by self-organization and whether the genes of the standard physics are enough.

The reason why the above mentioned problems have turned out to be so untractable might be due to a wrong view about space-time. Many-sheeted space-time concept of TGD might be absolutely crucial for the expression of genetic code. DNA itself might involve many-sheeted space-time structures coding faithfully the topology of the body parts. This many-sheeted structure of DNA could allow to understand the miraculous looking features of DNA replication and differentiation of cells. TGD based view of evolution as p-adic evolution implied by the basic quantum theory, should be a crucial element of the picture. Together with the p-adic length scale hypothesis it leads to precise quantitative predictions and a general model for genetic program based on the many-sheeted space-time concept. The model explains also why introns are present only in eukaryotic genome. Most importantly, it seems that the statements

represented by the dynamical intron-exon decompositions of genes and defining Boolean algebra, could represent our conscious beliefs and thus affect our behavior as conscious beings. Notice the beautiful connection between matter and mindgenes code the information, not only about the material structure of organism, but also about its belief system. Thus without introns, the pariah class in the society of bio-molecules regarded as 'junk DNA' by always-so-imaginative reductionistic materialists, we would have no world views and belief systems! In this article one possible TGD inspired view about genetic code and its realization is discussed in detail.

## 1.1 The notions of magnetic body and dark matter

The notion of magnetic body is central in the TGD inspired theory of living matter. Every system possesses magnetic body and there are strong reasons to believe that the magnetic body associated with human body is of order Earth size and that there could be hierarchy of these bodies with even much larger sizes. Therefore the question arises what distinguishes between the magnetic bodies of Earth and human body.

The vision about dark matter hierarchy labelled partially by a hierarchy of values of Planck constant coming as $\hbar_{eff} = n\hbar$. The original proposal was that the favored values of the integer $n$ are $n = \lambda^k$, $\lambda \simeq 2^{11}$ (near to the ratio of proton and electon masses) but this assumption is un-necessarily restrictive. Even without this assumption one ends up with to a rather concrete view about the hierarchy of magnetic bodies and implies a natural generalization leading to the notion of super- and hyper genes.

TGD inspired biology in its recent form (see the chapters in [17]) involves also other TGD inspired concepts, which are barely mentioned in this two-part article for the simple reason that the articles were written first time for about eighteen years ago and have been gradually updated since then. Mention only the notions of zero energy ontology (ZEO) and negentropic entanglement. The most recent summary about TGD inspired theory of consciousness - highly relevant also to quantum biology in TGD Universe - can be found in [19]. The chapter about dark photons as biophotons [18] should also give a view about the role of electromagnetic fields in TGD based quantum biology. In particular, a rather detailed view about the central role of magnetic body emerges. It would be highly rewarding to process the material of these articles in light of the updated vision about living matter.

## 1.2 Many-sheeted DNA

The replacement of the DNA of standard physics with many-sheeted DNA suggest surprisingly simple model for how organism's morphology is coded and decoded to DNA.

1. How the morphology of body is coded?
   The most striking feature of DNA is its one-dimensionality. According to work of Mae-Wan Ho, living systems are liquid crystals [1] . Liquid crystals are effectively one-dimensional since the layers of the liquid crystal consist of homogenous liquid phase determined by macroscopic characteristics such as pH, temperature, ionic concentrations and electric fields. This suggests that the structural information coded into DNA could be essentially information about the macro- properties of the layers of liquid crystal. This would make 1-dimensional coding of the body plan using DNA sequences very natural. Kind of contraction of the body parts to DNA sequences having many-sheeted structure could be in question! This coding would preserve the topological structure of the many-sheeted space-time surface representing the expression domain of the gene. The structure of the expression domains of maternal genes and Hox genes [8] controlling morphogenesis supports this picture.

2. How DNA is expressed?
   The very naive first guess is that during growth various thin space-time sheets associated with DNA gradually grow and are glued together by the join along boundaries contacts and form the space-time sheets associated with their expression domains. Somewhat exaggerating, many-sheeted DNA would represent only a particular developmental period of organism in which it is contracted to a

thin thread. For instance, the cells determined to develop into eye are glued to the space-time sheet representing future eye and replication products belong also to this space-time sheet. Clearly, the gluing to the space-time sheet of the future expression domain would generate the needed long range correlation between cells in the expression domain. It must be emphasized that self-organization should play key role in this process: for instance, liquid crystal nature of the living matter should determine morphology to a high extent.

3. What makes differentiation and control of the morphogenesis possible?
   Differentiation must be explainable as a selective activation of transcription and although a local process, involves also top-down control making possible a precise timing. Concentration gradients for the transcription factors, that is proteins controlling transcription, are certainly crucial in this respect. When the concentration of the protein falls below a critical value, the truth value of a statement representing input to some gene program modules changes. This leads obviously to spatial patterns of gene expression resulting from branching of gene programs. For instance, the development of organs should result as a combination of genetic control of this kind plus self-organization. Join along boundaries bonds between gene space-time sheets and larger space-time sheets or genes and control regions of chromosome make possible quantum control of genetic expression based on phase gradients of the super conducting order parameters and resonant Josephson frequencies which correspond to magnetic transition frequencies of genes, control regions or related substructures. It could also be that the # contacts (wormhole contacts) from genes to various space-time sheets representing body parts provide the interaction with the classical fields of the macroscopic space-time sheets representing body arts and controlling the activity of a particular gene. In any case, the fact is that the action mechanisms of transcription factor proteins in eukaryotes are not understood. The mechanism is not purely chemical one since transcription factors are often located quite far from the promoter region. Electromagnetic oscillations with resonant frequencies could be in question. In absence/presence of oscillation gene is activated.

# 2 Background

The foundations of genetics were discovered by George Mendel in 1866, but remained generally unknown until 1900. During the first half of nineteenth century it was gradually realized that genes play major roles in the functioning and evolution of organisms. The discovery of DNA revealed the principles of heredity and how genes store hereditary information and transmit it from generation to next. Hereditary information is contained within the nucleotide sequence of DNA.

Organization, expression and evolution of the hereditary information are the main aspects of genetics. Hereditary information is organized into chromosomes consisting of DNA sequences. It is expressed via transcription to mRNA followed by a translation to protein. The evolution of the hereditary information involves basically sexual breeding in one chromosome from the chromosome pairs of both parents combine to form chromosome pair. Also recombination of the members of the chromosome pairs is possible during meiosis. Also other mechanisms, such as fusion or fission of chromosomes and modification of DNA sequences, are possible. There are excellent books about topics [4] but for the convenience of the reader the basics of genetics are very briefly summarized in the following.

## 2.1 DNA and RNA

DNA add RNA provide a manner to store and organize genetic information [4] .

1. Genetic information is stored in nucleic acids, which are long sequences of nucleotide serving as letters of genetic code: three nucleosides form single world of code. There are four different nucleotides so that the number of different words is 64.

2. Nucleotide consists of three basic units joined by covalent bonds: nucleotide= nucleoside+sugar+$5'$-phosphate. The units are sugar, which is deoxiribose in case of DNA and ribose in case of RNA, phosphate and nucleoside (nucleic acid). Nucleosides are the information carrying part of DNA and RNA.

3. DNA and RNA sequences contain 4 different nucleosides. In case of DNA they correspond to C(ytocine), T(ymine), A(denine) and T(ymine). In case of RNA T is replaced by U(racil). U, T and C are purines containing one carbon ring and A and G are pyrimidines containing two carbon rings.

4. DNA molecules/nucleic acids/polynucleotides are formed as very long sequences of nucleotides bound together by phospho-diester bonds.

DNA double helix consists of two DNA strands , which are conjugates of each other, conjugation being defined as $A \leftrightarrow T$, $C \leftrightarrow G$. The helices are bound by hydrogen bonds between A and T and C and G respectively.

Sequences of DNA triplets form genes, which represent basic units of hereditary information revealed as traits of the organism. Each gene involves also additional DNA sequences serving as control structures in the transcription of gene to mRNA. In prokaryotes there is only single chromosome in the form of a circular double strand. In eukaryotes the chromosomes are located in nucleus and appear in homologous pairs. Eukaryotic chromosome is a complicated helical structure resembling beads in thread formed by DNA. DNA is wound around nucleosomes with diameter $d \simeq 10$ nanometers. Nucleosomes consist of octamer formed from 4 different histones. Chromosome structure will be considered in more detail later.

RNA appears both inside nucleus and cell. There are several types of RNA.

1. Messenger RNA (mRNA) is the outcome of transcription of DNA inside nucleus and is translated to proteins outside the nucleus.

2. Transfer RNA (tRNA) is involved in the translation of mRNA to protein: tRNA molecules bind specific aminoacids and glue them to specific mRNA triplets in a manner dictated by genetic code. rRNA appears as a building block protein of ribosomes playing the role of reading head in the translation of mRNA to proteins.

3. In case of eukaryotes transcription involves intermediate state in which DNA is transcribed to hnRNA which contains also the transcriptions of introns ("junk DNA"), which are split in so called splicing process cutting away intron RNA to form RNA-protein complexes which remain inside nucleus.

## 2.2 Proteins

Proteins are in a vital role in organisms. The diversity and complexity of life is largely due to the diversity and complexity of proteins. Some proteins act as transcription factors controlling genetic expression. Some proteins are used by cells in chemical communication between cells: hormones serve as signalling proteins; various receptor proteins serve as receptors of chemical signals and hormone-receptor complexes serve as transcription factors. Neural transmitters appear in the synaptic communication between neurons. Some proteins act as enzymes catalyzing biochemical reactions. Other proteins serve as structural building blocks, either by themselves or in association with nucleic acids (nucleoproteins), polysaccharides (glycoproteins) or lipids (lipoproteins). Some proteins, such as myoglobins and hemoglobins are associated with metal-containing organic molecules.

Proteins consists of polypeptides, which are polymers of 20 different aminoacids. Genetic code assigns unique polypeptide to a given gene. With single exception aminoacids share the same basic structure. Hydrogen atom H, carboxyl group COOH and amino group $NH_2$ and radical R linked to carbon atom. $R$ determines exclusively the chemical properties of protein. 8 aminoacids are nonpolar (hydrophobic) and

12 of them are polar (hydrophilic). Of the twelve polar aminoacids 7 are neutral, 3 are basic (tending to become positively charged) and 2 and acidic (tending to become negatively charged) under physiological conditions. Carboxyl and amino groups tend to become ionized at physiological pH; -COOH group tends to lose its proton and $NH_2$ group tends to gain a proton.

In polypeptides, which are products of gene translation, aminoacids are linked to each other by peptide bonds formed when $NH_2$ group of one aminoacid and $COOH$ group of next aminoacid are linked ($H_2O$ molecule is snipped away in this process). Polypeptide chains spontaneously adopt so called secondary structure determined by the nature of the $R$ groups along the backbone. Backbone forms alpha helix, a coil containg 3.6 aminoacid redidues per turn. Another secondary structure is the beta pleated sheet configuration consisting of rows of polypeptide chains hydrogen bonded with each other. Polypeptide can also adopt the form of a random coil. Proline, because of its unique structure, causes a kink in the polypeptide backbone. Polypeptides have also tertiary structure. How the tertiary structure is determined by the chemistry of aminoacids is poorly understood. One of the big problems of biology is to understand who protein is able to fold to such a unique configuration. TGD suggests that tertiary structure might not be determined solely by the standard chemistry and that many-sheeted nature of protein might be crucial in determining the final result of the folding. There is also quaternary structure associated with proteins formed by polypeptide sequences. The formation of higher level structures, such as micro-tubules, micro-filaments, cell membranes and collagen fibers involves self-organization and living matter seems to behave as a liquid crystal whose basic properties depend only on very general properties of protein.

## 2.3 Replication, transcription, translation

Information processing in living matter involves three basic processes: replication, transcription and translation. Replication of DNA means replication of DNA double helices and is essentially copying of genetic information. Replication involves unwinding of the parental strands of DNA double helix. They serve as templates on which the growing complementary daughter strands are synthesized. The direction of the synthesis is opposite for the two strands and only the second (leading) strand can be synthetized continuosly whereas the synthesis of the second strand occurs discontinuously and results in disjoint pieces of DNA containing approximately 1000 nucleotide pairs (Okazaki fragments of length about 34 nanometers), which later combine to form connected DNA strand.

DNA can be transcribed to mRNA molecules (messenger RNA) translated to proteins; to tRNA (transfer RNA), which is the RNA molecule affecting the coding of RNA triplets to aminoacids and to rRNA, which is the building block of the machinery affecting the translation. In case of prokaryotes the transcription of DNA to mRNA occurs directly. The rules for the transcription are

$$\begin{aligned} A \to U \ , \quad T \to A \ , \\ C \to G \ , \quad G \to C \ . \end{aligned}$$

In case of eukaryotes the transcription involves two steps since eukaryote genes in general decompose into exons translated to protein plus introns. First the entire gene is transcribed to hnRNA sequence. After this so called splicing occurs and gives rise to mRNA, which corresponds to the DNA sequence formed by the exons. In the splicing process intron sequences are split off and wind around specific proteins which do not leave the nucleus. There are different pathways for slicing meaning that the decomposition to exons and introns is not unique. Dynamical exon-intron decomposition is essential for the working of immune system.

Transcription is a complicated process involving the action of several enzymes. RNA polymerase I is involved in the transciption of large rRNA molecules, RNA polymerase II with the transcription of hnRNA, RNA polymerase III with transcription of small 5S-rRNA molecules and tRNA molecules. Usually so called heavy strand is transcribed. Light strand can be transcribed to some tRNA molecules at least. Gene is preceded by AUG triplet. In eukaryote cells RNA polymerase II copies sequences containing

6000-8000, sometimes even 20.000 nucleotides. The average length of mRNA sequence is 1500 nucleotides and the aminoacid corresponds to a sequence of average length of 1200 nucleotides.

RNA II polymerase binds to the promotor region preceding the gene. Promotor region contains at least two binding sites, so called TATA block and CCAT sequence regognized by RNA polymerase. Between promotor site and gene are operator site in which repressor enzymes bind and make translation impossible. TAC sequence denotes the beginning of that part of gene which is translated to protein (apart from introns). At the end of the gene there is rather long $A \cdots AAA$ control sequence preceided by TGA sequence signifying the end of the part of the gene to be translated. Introns which are not translated begin with AC and end with CA.

The translation of mRNA to polypeptide occurs outside the nucleus. Translation involves tRNA molecules, which are about 80 nucleotides long. Each tRNA contains a specific triplet which is anticodeword for the corresponding codeword in mRNA and binds only to this codeword in translation process. Each tRNA molecule binds with a specific aminoacid molecule and each aminoacid has at least one tRNA binding to it. The allowed bindings of tRNA and aminoacid molecules define genetic code. In translation tRNA carrying aminoacid attaches to an mRNA codeword to its own anticodeword and the aminoacid forms a peptide bond with the polypeptide sequence already translated at rRNA.

Genetic code assigns to 64 RNA triplets 20 aminoacids so that there is a considerable degeneracy involved. The largest number of DNA codewords mapped to same aminoacid is six. Three codewords are interpreted as stoppping sign for the translation. Genetic code is universal for the nuclear DNA of all eukaryotes and prokaryotes. The mitochondrial genetic codes of various eukaryotes however differ slightly from the universal genetic code. For instance, 4 DNA triplets can correspond to stopping sign.

Replication, transcription and translation are not the only information transfer processes occurring in living matter.

1. Reverse transcription $RNA \rightarrow DNA$ is known to occur in some cases and is also involved with the homing phenomonen of introns. Reverse transcription might have led from a system of RNA and proteins to system involving DNA sequences and primitive form of genetic code. The simplest starting system of this kind would consist of DNA coding RNA coding a protein which catalyzes both transcription and reverse transcription. This kind of system might have gradually evolved to a more complex DNA sequences.

2. RNA replication can occur in cells infected by viruses. What happens is that viral RNA strand which can be either single or double stranded, is replicated to its complement which in turn serves as a template for the synthesis of progeny RNA molecules.

3. Direct translation of DNA to protein without transcription has been observed only in vitro. This process probably never occurs in living cells.

## 2.4 Introns, pseudogenes, repetitive DNA, silent DNA

The genes in nuclei of the eukaryote cells contain introns, sequences consisting of 10-1000 nuclotides interspersed with the exon parts of DNA which is translated to a protein coded by gene [2] . Molecular Darwinist could compare introns with the commercials appearing between TV program or simply as selfish DNA. One could see them also unused parts of a computer program separated from the program code by comment signs in front of each line corresponding now to DNA nucleotide. The latter metaphor is consistent with the observation that intron can begin even in the middle of DNA triplet and that the transcription to mRNA is not unique so that same gene can give rise to several proteins. The content of intron sequences seem to be unrelated to the exon sequences: as if two separate interspersed computer codes would be in question.

Only one prokaryote cell, photosynthetic cyanobacterium Fischerella, is known to contain introns [2] . Usually also the genes of cell organelles (such as mitochondria of human cell) contain only very few introns. Fungi are however an exception in this respect [4] . The higher the evolutionary level of the

eukaryote cell, the higher the fraction of introns in the genome is. For humane genome the fraction of exons is about one per cent. During transcription both introns and exons are transcribed to hnRNA, intron sections are snipped away in a process called splicing and the resulting mRNA for the protein coded by exons is transferred from the nucleus and translated to a protein coded by the gene. It is possible to snip off the introns from genome but the mRNA coded by these genes is not transferred from nucleus, which suggests that introns have some role in genetic program. The addition of introns does not seem to have any dramatic effects on the genetic program.

Introns are a headache of molecular Darwinism. The nickname "junk DNA" tells the basic attitude towards introns. Introns represent selfish DNA living as parasites of the genome. There are two opposite schools concerning how introns have appeared.

1. The first school claims that introns came early. Somewhat surprisinly, this school sees bacteria as results of a long evolution which has gradually snipped off the introns from a primitive cell in order to achieve maximal rate of DNA transcription. One can of course wonder why the same thing has not happened to the cell nuclei also.

2. Second school tells that introns came late: this view conforms with the observations about the fraction of introns in genome. Introns seem to start from preferred sites and exons seem often to correspond to a modular decomposition of the protein they code. On basis of this it has been also proposed that introns separate modular parts of proteins from each other. The facts that introns can appear in the middle of protein module and even split single DNA triplet are not however consistent with this interpretation.

One can criticize the identification of introns as junk DNA.

1. It is difficult to see how human genome containing so high per cent of junk DNA could work with such a fantastic precision while viruses, second form of junk DNA, are often lethal. There are several pathways for slicing. Exon-intron transformation has been found to occur: exon and intron parts of gene simply change their roles [2, 7] ! This suggest that exon-intron property is additional dynamical degree of freedom in genone and might have deep meaning. Exon↔exon transformation is indeed crucial for the working of immune system.

2. mRNA produced by intronless gene does not get out of nucleus. It seems that the presence of introns somehow initiates a module of genetic program taking care that protein mRNA gets out of the nucleus. Introns seem thus to be necessary for the functioning of the cell and could be in some sense regarded as an output of gene interpreted as a genetic subprogram. Note however that intron mRNA which winds around spherical proteins in the process of splicing, have not been reported to serve as transcription factors.

3. The positions of the intron sequences in similar genes are not same for various species. There are wandering introns which can move even from cell to another one. There is a phenomenon called homing [2, 6] : the RNA coded by intron inserts itself into DNA sequence and builds by inverse transcription its complement in complementary DNA strand. Retrohoming in turn means that introns can carry and install long pieces of RNA to DNA sequences to DNA [5] . This suggests that introns might provide a new mechanism for the evolution of the genome and provide a mechanism for modifying the program code of genetic programs. It is also known that there are long range correlations (in scale of one micro-meter) in genes containing introns [3] . This suggests that introns are essential element in the organization of DNA to larger structures.

All these properties of introns suggest that their role in genetic program is badly misunderstood in the framework provided by molecular Darwinism and the basic dogmas of genetics.

Besides introns there are pseudogenes of various types, which by definition code no proteins. For instance, eukaryote genes from which introns have been snipped off, behave as pseudogenes. Pseudogenes

can also contain "programming errors": for instance, the DNA triplet signifying the beginning of gene has changed. Genetic program metaphor suggests interpretation of pseydogenes as unused program modules. The idea about two interspersed program codes could explain the program errors as only apparent program errors. Of course, every experienced computer programmer would suggests the possibility of also genuine program errors! Also the interpretation as control structure affecting transcription via long range interactions rather than via chemical contact interactions might make sense. It is indeed known that so called enhancers and silencers act as transcription factors in this manner.

Genetic code contains large amounts of repetitive DNA.

1. Five per cent of genome of the eukaryotes consists of highly repetitive DNA consisting of 5-300 nucleotides (even $10^6$ copies are possible). In particular satellite DNA, containing less than 10 nucleotides belongs to this class. This DNA are active during mitosis and meiosis [4] .

2. 30 per cent of DNA is moderately repetitive. The first class corresponds to rRNA, 5SRNA, tRNA and histogenes (10-100 copies). These genes are concentrated in certain chromosomes. In case of genes coding rRNA, tRNA the repetition of genes is understandable since translation making possible large number of aminoacid copies does not occur. The fact is however that also genes coding proteins appear as very many copies and there is no obvious explanation for this. So called SINE segments have length not longer than $10^3$ np and are interspersed through the entire genome as $10^4 - 10^5$ copies. LINE-segements consist about $3 \times 10^3$ np: there are about $10^4$ copies are interspersed through the entire genome. Part of these sequences are transposons (see below).

3. 65 per cent of DNA are present in only few (1-15) copies. Both exons and introns belong to this group of DNA and exons form only one percent of human genome.

4. The control regions between genes are rather long and seem to contain DNA with no obvious function. Also second strand of DNA can be regarded as silent DNA since its presence is not absolutely necessary for the storage of genetic information. The question is whether this silent DNA has some hitherto unidentified function.

The genome of both prokaryotes and eukaryotes contains transposons, which are movable DNA sequences able to insert themselves to DNA with the help of insertion sequences. Insertion sequences are short (less than 2000 nucleotides) and do not code proteins. Insertion sequences can carry also promotor and repressor sequences with them. Transposons could be important for evolution.

## 2.5 Is Central Dogma an absolute truth?

The Central Dogma of molecular biology states that each gene corresponds to a unique polypeptid. There are several observations challenging Central Dogma.

1. It is known that many alternate pathways of transcript splicing are possible and give rise to different protein outcomes called isoforms. This would suggest that transformation of some introns to exons and vice versa occurs routinely in gene expression. Using computer program analogy, this transformation would mean that the program part represented by introns becomes active and the part represented by exons becomes passive.

2. The phenomenon of superimposed genes [4] . There are genes nested inside genes and translation can start also in the middle of gene producing shorter protein than the gene usually. These phenomena were first observed for bacteriophage $\phi X174$, whose genome is known in its entirety. It is known that gene is transcribed as a whole and that different proteins result from frame shift. Gene can also overlap the DNA sequences formed by two subsequent genes as first observed in bacteriophage $G4$. These observations suggest that the standard notion of gene fails somehow.

3. It is known that also the "nonsense" strand of DNA can serve as template for transcription [4] .

## 2.6 Is life nothing but biochemistry?

It is not at all obvious whether the hypothesis "life is nothing but biochemistry" holds true.

1. It is not known whether protein folding is coded into the chemistry of DNA. The problem is mathematically unattractable due to the occurrence of combinatorial explosion. It seems more probable that folding might be self-organization type phenomenon and thus affected by the conditions of environment: protein development can be regarded as hopping in spin glass type energy landscape leading to some deep valley of free energy valley. TGD suggest that folding is the quantum analog of this kind of process. In particular, p-adic length scale hierarchy and many-sheeted space-time concept suggest that one cannot understand protein folding in terms of DNA chemistry alone.

2. DNA is essentially one-dimensional structure. This suggests that gene codes only one-dimensional skeleton of its expression domain and that self-organization by quantum jumps could take care of the rest. Indeed, the work of Mae-Wan Ho [9] shows that living organisms are liquid crystals which can be regarded as one-dimensional crystals and two-dimensional liquids, whose properties can be characterized by some global parameters. Perhaps genes code the properties of various layers of the liquid crystal. One of the basic characteristics of liquid crystals is self-assembly and de-assembly. Depending on pH, ionic concentrations, temperature, electric fields,... liquid crystals organize to micelle like structures (cell membranes, collagen fibers,....) and effectively one-dimensional layered structures [1] .

3. One can wonder how morphology is coded in DNA and how it is decoded from DNA. It is not at all obvious that DNA chemistry, which is purely local, is enough to code morphology.

4. So called enhancers and silencers are transcription factors, which encourage or disencourage gene expression in eukaryotes. The position of these proteins or orientation in DNA does not seem to be important [4] . For instance, they can bind to introns and the distance of the binding site from gene promotor regions can be thousands of nucleotide pairs. This would suggest that the mechanisms of enhancing and silencing are not purely chemical if chemical at all. This would suggest the generalization of the notions of gene expression and transcription factor. Chemical expression takes place very slowly. Non-chemical expression modes yielding nonchemical transcription factors could make possible very fast running of genetic programs and there could be even connection between many-sheeted genome and nerve pulse activity.

5. The naive expectation is that the size of the genome should correlate with the evolutionary stage of the species. Eukaryotes indeed have genome which is typically $10^3$ times longer than prokaroyote genome. The table below however shows that the total length of genome does not correlate with the complexity of the organism faithfully. The genome of plants is typically 10-100 times longer than human genome. The genome of amoeba is by two orders of magnitude longer than that of human! The genomes of monkeys and men are almost identical. This suggests that there might be some unindentified degree of freedom associated with DNA which explains these differences.

| Organism | Human | Mus musculus | Amoeba | Marbled lungfish |
|---|---|---|---|---|
| $N(DNA)/10^9$ | 3 | 3 | 670 | 139 |
| Organism | Salamander | Onion | Trumpet lily | |
| $N(DNA)/10^9$ | 81 | 18 | 90 | |

Table 1. The amount of total genome measured as the number of DNA triplets.

# 3 Many-sheeted DNA

The notion of many-sheeted DNA suggest a profoundly new manner to understand how the morphology of the organism is coded to and decoded from DNA. p-Adic length scale hypothesis leads to quantitative predictions for the number of levels of genetic program as function of a suitably defined size of the organ. The proposed model for introns inspires the interpretation of gene as a representation for Boolean algebra and to the proposal that genes realize not necessarily conscious-to-us Boolean mind at the basic level. Many-sheeted DNA suggests also new forms of gene expression and of control of gene expression. For instance, nerve pulse patterns could affect also genetic program of postsynaptic cell via the classical em and $Z^0$ field patterns associated with them and genes could affect cell membrane via conformational waves propagating along micro-tubules connecting nucleus to cell membrane.

## 3.1 Many-sheeted DNA as hierarchy of genetic programs

Many-sheeted DNA allows to realize genetic subprogram hierarchy in an elegant manner. Many-sheeted DNA and proteins are like a hierarchy of ordinary DNA and proteins effectively living in different space-times corresponding to body parts. One can consider the possibility that subprograms correspond to p-adic space-time sheets and subprogram hierarchy corresponds to the hierarchy of p-adic space-time sheets. The gene program in a given length scale would selectively activate programs in shorter length scale, etc.. DNA sequences with the same chemical structure correspond to different genetic programs since the many-sheeted structure of DNA affects its functioning. Analogous conclusion is true about proteins.

One can assign to gene a unique p-adic prime as the prime characterizing the largest p-adic sheet at which gene has # contacts. The number of levels in subprogram hierarchy could be deduced from the size of the organism. Gene can have # contacts to several space-time sheets characterized by p-adic primes $p \simeq 2^k$, $k$ power of prime. Denote by $k_G$ the largest value of $k$ associated with gene. $k_G$ characterizes the position of gene in subprogram hierarchy. Gene can have # contacts with space-time sheets $k < k_G$ also. Gene can be characterized by the p-adic $k_G$ labelling the largest space-time sheet to which it has # contacts. "Comment sign" marking each nucleotide of intron could correspond to a direction of classical field at some space-time sheet characterized by p-adic prime $p \simeq 2^k$, $k = k_I$. The only sensible assumption seems to be $k_I = k_G$.

The other # contacts of gene must be assumed to be on space-time sheets with $k < k_G = k_I$. This implies that given program can call only programs which are in the lower level of the hierarchy. This would suggest that programs belonging at the lower level of hierarchy cannot call program at higher level. Does this imply that growth process in which larger and larger space-time sheets are activated can only occur by self-organization? This would mean that DNA space-time sheets with increasing value of $k_G$ expand in phase transition like manner and fuse to form space-time sheets corresponding to various body parts. On the other hand, it is not at all obvious that growth process could not start from higher level and lead to gradual differentation at lower levels. In fact, embryogenesis seems to occur in this manner [4] .

Also proteins can be classified by the the number $k_P$ characterizing the largest space-time sheet to which protein has # contacts. Proteins must mediate program calls to gene modules $G_1$ with various values of $k_{G_1} < k_G$. This suggests that protein activating gene characterized by $k_{G_1}$ must have same $k_P = k_{G_1}$. This would automatically guarantee that chemically identical proteins activate only the genes belonging to the level of the fractal hierarchy they represent.

The notion of many-sheeted DNA has immediate applications.

1. Many-sheeted DNA provides a possible explanation for why DNA triplets act as codewords of the genetic code. If members of each DNA triplet are glued to space-time sheet containing only # contacts from the nucleotides of the triplet, codewords have a clear geometrical meaning.

2. The notions of many-sheeted DNA and many-sheeted protein suggests also an explanation for how enhancers and silencers are able to regulate gene expression. Interaction with classical em or $Z^0$ fields via wormhole contacts would provide a nonchemical interaction mechanism. Second mechanism is based on Josephson currents running along join along boundaries contacts. Since an interaction with much larger length scale is involved, these interaction mechanisms are not too sensitive to the position of the transcription factor and the distance of the binding site from gene promotor regions can be thousands of nucleotide pairs. This mechanism explains also the observe issue specificity of some transcription factors. Proteins with same chemical structure can be quite different trascription factors if they have contacts to different space-time sheets.

## 3.2 Possible answers to the basic questions

Many-sheeted DNA suggests stupifyingly simple coding of body's morphology. The genes would be obtained by simply contracting the many-sheeted space-time representing expression domains of genes to one-dimensional structure. Decoding of the morphology means the growth of this structures to their orginal size. Of course. this hypothesis is oversimplified but its extreme simplicity makes it worth of testing.

### 3.2.1 How the structure of expression domain of the gene is coded in the structure of gene?

The p-adic length scale of the gene correlates trivially with the p-adic length scale of the protein coded by it. Already protein folding implies that the correlation with the size of the structure coded by DNA is not so straightforward. Furthermore, proteins are not mere building blocks but can have quite abstract functions like regulating gene expression of genes.

Consider now various aspects of the idea that expression the domain of gene is coded into the structure of gene and this that correspondence could be also realized at functional level.

1. The first thing that comes into mind is that the p-adic length scale of the gene correlates with the p-adic prime of the space-time sheet which corresponds to the expression domain of the gene during early phases of the embryogenesis. Gene clusters, say Hox cluster, would represent kind of a miniature of the body and every gene of Hox cluster would give rise to a space-time sheet which would be a scaled down model of the expression domain of the gene. Thus the expression domains of various genes in the genome could correspond to the extended space-time sheets at the level of the genome and the topology of these genome level expression domains, in particular, their ordering, would be consistent with that for the actual expression domains. Expression domain corresponds most naturally to a join along boundaries condensate generated by the formation of the join along boundaries bonds between the extended space-time sheets associated with the genes. This means that the p-adic prime of the expression domain can be much smaller than one could conclude it to be on basis of its size.

2. One could test the hypothesis that the total length of the region occupied by gene and by the DNA controlling its activity in the genome could correlate with the size of its expression domain at the stage of the development when the gene is expressed. Note that many genes affecting morphogenesis are expressed in a very early stage: many of them in the embryonic stage when no cell formation has yet occurred. This stage corresponds to the p-adic length scale of a fertilized cell about $10^{-4}$ meters. Of course, the correlation between the content of the gene program and the size of its expression domain, is not necessary and might be even un-desirable.

3. Fractality suggests that the communication by expression factor proteins at the level of genome might mimick the hormonal communication occurring at the level of the entire organism. This could mean that the hormonal communication between the expression domains of two genes is

equivalent with the presence of a transcription factor communication between corresponding genes at the level of nucleus. Hormonal communication between cells involves the formation of hormone-receptor complex acting as a transcription factor.

The length of human genes ranges to thousands of nucleotides. This would mean that the longest p-adic length scales of human gene would correspond to $L(173) \sim 16$ micro-meters. The total length of a human chromosome is about $75 \times 10^6$ DNA triplets. The corresponding p-adic length scale is $L(193) \sim 2$ cm. The next length scales correspond to the pair $(197, 199)$ and correspond roughly to the size of brain hemisphere and brain. The total length of DNA in chromosomes is $48 \times L(193) \sim 1$ meter, the size scale of human body.

Many-sheeted space-time concept suggests that genes actually correspond to DNA sequences glued to a larger space-time sheet defining the gene. Hox clusters could be one example of this. The geometry of the organism might be coded to these secondary, tertiary, etc. space-time sheet structures of the DNA sequence guaranteing the coding the topology of the body plan to the topology of the multi-sheeted DNA. These structures are be labelled by p-adic primes and their number would be quite limited.

The linearity of DNA suggests that also the plan of the expression domain should be essentially linear such that each cross section of each module of the expression domain is essentially homogenous phase and its structure is determined by a self organization process constrained by the p-adic length scale hypothesis rather than purely genetically. According to Mae-Wan [9, 10] living systems are liquid crystals and the basic characteristic of the liquid crystals is that they have crystal like structure in one dimension and are liquids in transversal dimensions [1] forming. thus layer-like structures. This suggests that p-adic self-organization determines the size of the transversal layer and that DNA only codes some general properties of the liquid phase for a given layer.

The sizes for the expression domains of the genes should form a hierarchy. Effective expression domain can be much larger than the p-adic length scale characterizing it since join along boundaries condensates are possible. For instance, the modularization of the genetic programs of plants is perhaps stopped at the level $k = 167$ so that expression domains for plant cells could be regarded as join along boundaries concept of of $k = 167$ plant cells. At the level of organism this perhaps corresponds to the emergence of cell walls hindering the formation of higher level structures formed from cells: plant could perhaps be regarded as a large join along boundaries condensate of $k = 167$ plant cells surrounded by a wall. Besides the length of the genome, the number of the p-adic hierarchy levels in the space-time sheet hierarchy of DNA is a natural candidate for a measure of the complexity of the organism.

### 3.2.2 How the information about morphology is expressed?

One of the fundamental questions of the developmental biology is how the information of genes stored into DNA is translated to the geometry and topology of the organism. The idea of many-sheeted DNA suggests an immediate answer to this question. Expression is 'nothing but' the reversal of the coding. The expression domain of the gene contracted effectively to one-dimensional DNA-thread grows back to the expression domain with non-uniqueness and flexibility brought in by self-organization depending on external parameters. This means that various space-time sheets associated with DNA grow during grow to space-time sheets representing actual organs. This process involves the formation of join along boundaries bonds between growing space-time sheets associated with various DNA molecules so that coherent macroscopic quantum phases become possible.

One can ask how the growth plan is coded into DNA. Or how much of it is coded into the chemistry of DNA? The idea that DNA is essentially body contracted to a thin thread suggests that the chemical control of DNA is restricted to the local properties of tissues. The space-time sheets of replicating DNA at various body parts simply grow and fuse to form join along boundaries condensates growing and giving rise to various organs. The replication of DNA would in turn be quantum self-organization process involving essentially self-hierarchy starting from atomic level and ending up the level of entire organism.

#### 3.2.3 What makes cell differentiation possible?

Cell differentiation is one of the great mysteries of biology. It is known that only part of DNA is active in a cell located in a given part of body and that selective activation of the genome gives rise to differentiation. The problem is to understand the mechanism of activation. Especially difficult challenge for the view about life as mere chemistry is the interaction between large length scales with gene level making possible precise timing of genetic activity.

In TGD framework cell differentiation should correspond to a selection of branch in the the flow diagram describing genetic program. This occurs during the growth since the concentrations of the proteins representing the inputs of the gene programs evolve during the growth and generate also spatial gradients. Therefore different branches of the genetic program are activated in different parts of the developing organism. Also the genes associated with space-time sheet of increasing size are activated during growth and this brings in new and higher control levels.

Very probably the mechanism involves interaction between microscopic degrees of freedom for DNA and between macroscopic degrees of freedom representing body part where DNA resides. The control and coordination based on Josephson currents between gene space-time sheets and larger space-time sheets is very probably involved as is suggested by the general time scales of genetic activity. Also the interaction with the classical fields of the space-time sheet of the body part to which DNA has wormhole contacts provides an obvious mechanism of activation. The frequencies of the coherent oscillations of em fields involved could be important in both interaction mechanisms. This kind of interactions with larger space-time sheets makes possible to understand induction phenomenon, which corresponds signalling between cells and entire cells groups. This kind of signalling could be crucially important for morphogenesis. Many-sheeted space-time thus provides explanation for the ability of cells to form organs. The notion of cell cohesion is introduced to explain this: the cohesion would correspond to the formation of join along boundaries condensate of extended gene space-time sheets.

### 3.3 What is the number of the levels in program hierarchy?

The obvious idea is that the size of the organism determines the largest p-adic prime contributing to the program hierarchy. It is however not obvious whether to define the size of organism as the 'physical', visible size or as electromagnetic size, which is well defined notion in TGD framework.

#### 3.3.1 Does the visible size of the organism determine the number of hierarchy levels?

The simplest working hypothesis is that the number of the levels in the program hierarchy is the number of p-adic length scales between atomic length scale and body size. The larger the visible size of the organism, the larger the number of the levels in the genetic program hierarchy, if this hypothesis is correct. This number is testable characteristic of species and could be valuable guide in attempts to understand how genetic code functions. One can identify the hierarchical level of the gene by looking how many genes it activates before building block protein is coded. It must be however emphasized that visible size need not be a correct criterion: the point is that join along boundaries condensates are possible and give rise to a much larger body size than one might conclude from the value of largest p-adic prime involved.

It is instructive to look the numbers of hierarchy levels in some specific examples assuming that the visible size of the organism determines the number of hierarchy levels. It is assumed that $k = 139$ is the first level which counts as a hierarchy level.

1. Viruses could have 4 hierarchy levels if $k = 139, 149, 151, 157$. Proteins, lipid layers of cell membrane and cell membrane and genes coding building block proteins. It could be that only k=149 is present for the simplest viruses since the formation of the envelope is self-organization process.

2. Bacteria should have 5 levels. $k = 139, 149, 151, 157, 163$.

3. Home fly should have 12 levels since its size is below $L(197) \simeq 1.6$ cm.

4. Animals with size between $L(199) \simeq 16$ cm and $L(211) \simeq 10$ m have 15 hierarchy levels. Note the large gap between $L(199)$ and $L(211) = 64L(199)$.

5. The next level corresponds to the level of dinosauri and whales having sixteen levels unless they correspond to join along boundaries condensates formed from smaller structures which is quite possible. The next level is $L(223)$ and corresponds to size of 640 m!

### 3.3.2 Does the electromagnetic size of of organism determine the number of hierarchy levels?

There is a large gap between $L(199)$ and $L(211)$ and the next twin length scale corresponds to a length scale of one kilometer. This suggests that new levels of hierarchy possibly emerged after $L(199)$ cannot correspond to the physical growth of body. Mere large size does not guarantee intelligence. Furthermore, if the visible size of the organism determines the number of the hierarchy levels, then dinosauri would have been in a well defined sense more intelligent animals than we! These arguments suggest that the visible size of the organism need not determine the number of genetic program levels.

1. It could be that DNA codes and even controls also the electromagnetic structure of the organism realized as topologically quantized electromagnetic field, "aura", characterizing the organism.

2. An alternative option inspired by the notion of memetic code, which is next level in the hierarchy of genetic codes predicted by the TGD inspired simple model of abstraction process, is that there are higher hierarchy levels present but they are not controlled by the genetic program but call it as a subprogram.

A natural working hypothesis is that EEG correlates with the electromagnetic size of the organism. EEG has emerged rather lately in the evolution and is possessed only by vertebrates. In case of humans it becomes fully developed only at the age of 18. Meditation in general tends to increase the amplitudes of low frequency waves with 8 Hz (alpha wave s) and also waves with lower frequencies (theta wave s). This suggests that growth in electromagnetic degrees of freedom can continue all the lifetime and could be identified as what is called "spiritual growth". It could continue also after the physical death so that the protein based state of life would be only a part of much longer lasting process of self-organization analogous to the development of butterfly. Indeed, in TGD based picture about geometric time the death of the physical body does not mean the end of life.

Schumann resonances are resonances of em fields in the wave cavity defined by the 80 km thick layer between Earth's surface and ionosphere. The frequency range in question correspond to the frequency range of EEG. A hypothesis worth of considering is that human body generates via Schumann resonances topological field quanta, which define electromagnetic sub-selves having the size of Earth. One could even consider the possibility that the highest value of $k_G$ depends on individual and people having tendency to have religious and mystical experiences have exceptionally large value of $k_G$.

The length scale corresponding to alpha waves is $3.8 \times 10^7$ meters and corresponds is roughly 3.75 times the length scale $L(251)$. If levels up to $L(257)$ are present in the human genome then the number of hierarchy levels is 22, not too large number. $L(251) \sim 10^7$ m corresponds to a frequency of 37.5 Hz and is quite near to the 40 Hz frequency claimed by Koch and Crick to be crucial for the visual consciousness! The frequency associated with $k = 257$ corresponds to the frequency of 5 Hz, which also belongs to EEG.

The electromagnetic size of the organ increases rapidly with the number of levels present in the hierarchy as the following table demonstrates.

| k | 227 | 229 | 233 | 239 | 241 |
|---|---|---|---|---|---|
| $L_p/m$ | $2.5E+3$ | $5E+3$ | $2E+4$ | $1.6E+5$ | $3.2E+5$ |
| k | 251 | 257 | 263 | 269 | 271 |
| $L_p/m$ | $E+7$ | $8E+7$ | $6.4E+8$ | $5E+9$ | $E+10$ |

Table 2. Table of p-adic length scales above $L(211) \simeq 10$ meters. $L(151) = 10^{-8}$ meters is assumed.

There are even more explicit observations about the importance of ELF em fields for the functioning of living matter and these observations finally led to a breakthrough in TGD based model of conscious brain. The observations about the special effects of ELF em fields on brain at cyclotron frequencies of ions $Na^+, Cl^-, K^+$ and $Ca^{++}$ in endomagnetic fields $B_{end} = 2B_E/5 = .2$ Gauss were made already at 1983 [12] . These experiments suggest that these ions/their Cooper pairs form are confined in the magnetic field of Earth and form bound states with macroscopic size of order cell size and with extremely small binding energy corresponding to frequency of order 10 Hz. This is impossible in the standard physics framework but can be understood as resulting from the dropping of ions and electrons from the atomic space-time sheet to the space-time sheet of the cell where the density of the matter is very low.

Also electron Cooper pairs of high $T_c$ electronic super conductor as well as Cooper pairs of neutrino super conductor are important. Besides magnetic cyclotron frequencies $Z^0$ magnetic cyclotron frequencies and wormhole cyclotron frequencies make sense: $Z^0$ currents for ions indeed induce automatically also ionic currents.

One can argue that there is very cold, dry and silent at the cellular space-time sheets and this makes possible macroscopic quantum phases formed by Cooper pairs of ions $Na^+, Cl^-, K^+$ and electron as well as well as $Ca^{++}$ ions. Later the argument was modifiedthe large values of Planck constant [14, 13] imply that cyclotron energy scale is above thermal energy at room temperature even if thermal equilibrium of dark space-time sheets with ordinary ones is allowed. Also other ions are possible but these ions are especially important for nerve pulse generation. These super conductors must be effectively one-dimensional (otherwise gap energy is extremely small) and the needed confinement in the transversal degrees of freedom is caused by the presence of $B_{end}$ which could be in TGD framework interpreted as the dark companion of the Earth's magnetic field responsible for controlling biomatter possibly also associated with the personal magnetic body. One could regard these super conductors as associated with the flux quanta of $B_{end}$ having radius 25 $\mu$m (the size of a large neuron) by flux quantization and serving as templates for the formation of biostructures.

When the Josephson frequency (potential difference) associated with the weakly coupled super conductors of this kind corresponds to a magnetic transition frequency, quantum jumps between states of either super conductor occur and change the charge distributions and hence potential differences associated with other Josephson junctions associated with either super conductor. Quantum jumps can lead to 'wake-up' of either or both super-conductor sub-self giving rise to a mental image. Also emission of ELF photons with resonance frequency is involved. The topological field quanta associated with these photons have typically size of order Earth's circumference. The fact that multiples of the cyclotron frequencies correspond directly to the most important frequencies of EEG and also to some important Schumann frequencies suggests very strongly that the 'ELF selves' associated with these topological field quanta represent also selves in our self hierarchy. This leads to a general model for quantum control and for how the space-time sheets representing the self-hierarchy are coupled by join along boundaries bonds serving as Josephson junctions, to a detailed model for the quantum correlates of the sensory qualia and to a model of Boolean mind. ELF selves are a crucial factor of all these models [15, 16] .

The work of Michael Persinger shows that ELF em fields and ELF modulated em fields, affect also gene expression [11] . Thus it seems that ELF levels, rather than being controlled by gene level, actually control and coordinate gene level rather via the formation of join along boundaries bonds between gene space-time sheets and ELF space-time sheet. Whether gene level actually *codes* also ELF levels of the organism is an interesting question. The idea about genome as the entire many -sheeted organism contracted to a thin thread would support this view. On the other hand, the notion of the memetic code identified as the next level of abstraction hierarchy suggests that ELF level corresponds to something genuinely new not reducible to gene level. ELF level could be even seen as a different life form next to the biological life living in symbiosis with biological life. One must also remember that higher levels could couple with gene level only via join along boundaries contacts and that the development of organism could be seen as a 'social' process in the sense that growing organism gradually builds join along boundaries contacts

to the space-time sheets representing higher level selves.

Whether the number of the hierarchy levels in the genetic program hierarchy is larger than the visible size of organism, might be perhaps tested sooner or later by deciphering the number of hierarchy levels in the genetic program. To check the hypothesis about EEG, it is enough to study simplest verterbrates possessing EEG. The identification the levels of various genes in program hierarchy would mean a tremendous boost in the understanding of genetic code and dramatic change in world view.

## 3.4 Band structure of chromosomes as an evidence for many-sheeted DNA?

In prokaryotes DNA is arranged in single chromosome forming closed circular double strand whereas in eukaryotes DNA genome is organized into chromosome pairs. Chromosome is believed to correspond to single DNA thread which has beads in thread structure. Beads are spherical nucleosomes of diameter $10^{-8}$ meters ($L(151)$!) consisting of histones of 4 different types forming histone octamer. DNA is wound very tightly around nucleosomes, there is about 70 nanometers (slightly less than $L(157)$ of DNA per nucleosome. chromosome forms a helical coil with diameter found to be 30 nm. In interphase chromosomes are coiled once more to a hollow tube of diameter 200 nm (slightly less than $L(167)$) a helix of thickness about $10^{-7}$ meters. The transition from interphase chromosome to metaphase chromatid is accompanied by a winding to a helical coil of diameter about 600 nm (slightly more than $L(169)$). A possible interpretation of these transformations is as generation of new space-time sheets.

Chromosome banding was discovered already in eighteenth century by Metzner. Chromosome banding characterizes both the chromosome and the method used to produced the banding structure and there are many methods for revealing the band structure. Increasing resolution implies the division of band structures to smaller structures in fractal like manner. The band structures can be divided into two classes.

1. The highly localized heterochromatic bands, nucleolar organizers and kinetochores appear in all organisms. The latter two structures seem to reflect the purely geometrical organization, "packing", of genome rather than the internal organization of genome. The main features of heterochromatic banding are its universality, diversity and variability. Heterochromatic banding is present in all eukaryotes and can differ widely for closely related species and be very similar to widely different species. Heterochromatin seems to correspond to highly repetitive short DNA sequences of 10 nucleotid pairs ($10^6$ copies) located near the centromere of the chromosome. This DNA is not transcribed to DNA. Pairs are often duplicated and duplication leads to various physiological defects. Soma cells of some organisms appear to have ability to get rid of of heterochromatin whereas it is present in germ cells. These facts suggest that the regions of chromosome near its center regulate gene expression and that highly repetitive DNA sequences represent sites for genes at which repressor proteins bind. Abnormally large duplication of repressor sites would lead to stronger repression is more effective and could lead to abnormal development.

2. The chromosomes of the eukaryotes contain also non-localized bands called euchromatic bands. Patterns of euchromatic bands resemble closely to the patters of DNA replication and patterns correlate very strongly with species. Thus euchromatic bands correspond to active RNA. The moderately repetitive DNA which is transcribed corresponds corresponds to euchromatin. It is known that there are several types of euchromatic banding. Banding patterns can be used as diagnostic tools to identify various chromosome fusions and splittings. Various bandings are of enormous value in providing manner to locate genes in genome.

In TGD framework a natural interpretation of various types euchromatic banding provide evidence for the many-sheeted DNA. Thus euchromatic banding should reflect the modular structure of the genetic program as well as the interspersing of control regions and transcribed regions of genes corresponding to the basic structure "If A then B" of the gene.

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