Matrix genetics, part 1: permutations of positions in triplets and symmetries of genetic matrices

Sergey V. Petoukhov

Department of Biomechanics, Mechanical Engineering Research Institute of the Russian Academy of Sciences
s*petoukhov@gmail.com*, *petoukhov@imash.ru*, *http://symmetry.hu/isabm/petoukhov.html*

Abstract: The Kronecker family of the genetic matrices is investigated, which is based on the genetic matrix [C T; A G], where C, T, A, G are the letters of the genetic alphabet. The matrix [C T; A G] in the second Kronecker power is the (4*4)-matrix of 16 duplets. The matrix [C T; A G] in the third Kronecker power is the (8*8)-matrix of 64 triplets. It is significant that peculiarities of the degeneracy of the genetic code are reflected in the symmetrical black-and-white mosaic of these genetic matrices. The article represents interesting mathematical properties of these mosaic matrices, which are connected with positional permutations inside duplets and triplets; with projector operators; with unitary matrices and cyclic groups, etc. Fractal genetic nets are proposed as a new effective tool to study long nucleotide sequences. Some results about revealing new symmetry principles of long nucleotide sequences are described.

Contents

1 Introduction

An investigation of structural analogies between computer informatics and genetic informatics is one of the important tasks of modern science in a connection with a creation of DNA-computers and with a development of bioinformatics. Information is stored in computers in a form of matrices. The author considers matrix presentations of natural ensembles of elements of the genetic code. Such matrix approach reveals new structural aspects of the genetic system and proposes new possibilities to understand the question, why the nature has chosen such special system of genetic elements from huge number of other possible systems. It is important because the modern science does not know why the alphabet of genetic language has four letters (it could have any other number of letters in principle) and why just these four nitrogenous bases are chosen as elements of the genetic alphabet from billions possible chemical compounds.

This article is devoted to analysis of ensembles of molecular structures of the genetic code from the viewpoint of matrix methods of computer informatics. The used symbols A, C, G, T mean adenine, cytosine, guanine and thymine that are elements of the genetic alphabet in DNA (thymine T is replaced by uracil U in RNA). This version of the article uses the symbol T instead of the symbol U in previous versions. Also the genetic matrix [C T; A G] is used instead of the related genetic matrix [C A; U G] in previous versions (the using of the matrix [C T; A G] allows showing a connection of the genetic system with well-known types of hypercomplex numbers more easily). New essential materials are added about fractal genetic nets and Symmetry Principles of long DNA-sequences.

2 The natural system of binary numeration of multiplets in the genetic matrices

The Kronecker family of genomatrices $P^{(n)} = [C\ T;\ A\ G]^{(n)}$ gives complete sets of genetic multiplets in the universal mathematical form based on the square matrix of the genetic alphabet. Each genomatrix $P^{(n)} = [C\ T;\ A\ G]^{(n)}$ contains a complete set of n-plets as its matrix elements. For example, the (8*8)-genomatrix $P^{(3)} = [C\ T;\ A\ G]^{(3)}$ contains all 64 triplets, which encode 20 amino acids and stop-signals (Figure 1). The set of the letters A, C, G, T of the genetic alphabet is not an arbitrary one, but it bears an important system of binary-opposite attributes. The system of such attributes parts the four-letter alphabet into three various pairs of letters, which are equivalent from a viewpoint of one of these attributes or its absence: 1) C=T, A=G (according to binary-opposite attributes: "pyrimidine" or "purine"); 2) A=C, G=T (according to attributes: "keto" or "amino" [Waterman, 1999, § 6.3]; 3) C=G, A=T (according to attributes: three or two hydrogen bonds are materialized in these complementary pairs).

Let us number these binary-opposite attributes by numbers N = 1, 2, 3 and ascribe to each of the four letters A, C, G, T the symbol "1_N" , if a letter has one of two attributes marked by number "N", and the symbol "0_N", if this letter has the opposite attribute marked by the same number N (see details on Figure 2). In that way we receive representation of the four-letter alphabet in the system of its three "binary sub-alphabets to attributes".

$$P = \begin{array}{c|c|c} & 1 & 0 \\ \hline 1 & C\ 11(3) & T\ 10(2) \\ \hline 0 & A\ 01(1) & G\ 00(0) \end{array} \quad ; \quad P^{(2)} =$$

	11 (3)	10 (2)	01 (1)	00 (0)
11(3)	CC 1111 *(15)*	CT 1110 *(14)*	TC 1101 *(13)*	TT 1100 *(12)*
10(2)	CA 1011 *(11)*	CG 1010 *(10)*	TA 1001 *(9)*	TG 1000 *(8)*
01(1)	AC 0111 *(7)*	AT 0110 *(6)*	GC 0101 *(5)*	GT 0100 *(4)*
00(0)	AA 0011 *(3)*	AG 0010 *(2)*	GA 0001 *(1)*	GG 0000 *(0)*

$$P^{(3)}=$$

	111 (7)	110 (6)	101 (5)	100 (4)	011 (3)	010 (2)	001 (1)	000 (0)
111 (7)	CCC 111111 (63)	CCT 111110 (62)	CTC 111101 (61)	CTT 111100 (60)	TCC 111011 (59)	TCT 111010 (58)	TTC 111001 (57)	TTT 111000 (56)
110 (6)	CCA 110111 (55)	CCG 110110 (54)	CTA 110101 (53)	CTG 110100 (52)	TCA 110011 (51)	TCG 110010 (50)	TTA 110001 (49)	TTG 110000 (48)
101 (5)	CAC 101111 (47)	CAT 101110 (46)	CGC 101101 (45)	CGT 101100 (44)	TAC 101011 (43)	TAT 101010 (42)	TGC 101001 (41)	TGT 101000 (40)
100 (4)	CAA 100111 (39)	CAG 100110 (38)	CGA 100101 (37)	CGG 100100 (36)	TAA 100011 (35)	TAG 100010 (34)	TGA 100001 (33)	TGG 100000 (32)
011 (3)	ACC 011111 (31)	ACT 011110 (30)	ATC 011101 (29)	ATT 011100 (28)	GCC 011011 (27)	GCT 011010 (26)	GTC 011001 (25)	GTT 011000 (24)
010 (2)	ACA 010111 (23)	ACG 010110 (22)	ATA 010101 (21)	ATG 010100 (20)	GCA 010011 (19)	GCG 010010 (18)	GTA 010001 (17)	GTG 010000 (16)
001 (1)	AAC 001111 (15)	AAT 001110 (14)	AGC 001101 (13)	AGT 001100 (12)	GAC 001011 (11)	GAT 001010 (10)	GGC 001001 (9)	GGT 001000 (8)
000 (0)	AAA 000111 (7)	AAG 000110 (6)	AGA 000101 (5)	AGG 000100 (4)	GAA 000011 (3)	GAG 000010 (2)	GGA 000001 (1)	GGG 000000 (0)

Figure 1. The beginning of the Kronecker family of symbolic genomatrices $P^{(n)}=[C\ T;\ A\ G]^{(n)}$ for n = 1, 2, 3. Each genomatrix $[C\ T;\ A\ G]^{(n)}$ has individual binary numeration for each column, each row and each n-plet due to the sub-alphabets of the genetic alphabet (see explanations in text).The decimal equivalents of these binary numbers are shown in brackets.

	Symbols of genetic "letter" from a viewpoint of a kind of binary-opposite attributes	C	A	G	T	
N=1	1_1 – pyrimidine 0_1 – purine	1_1	0_1	0_1	1_1	
N=2	1_2 – amino 0_2 – keto	1_2	1_2	0_2	0_2	
N=3	1_3 – a letter with three hydrogen bonds 0_3 – a letter with two hydrogen bonds	1_3	0_3	1_3	0_3	

Figure 2. Three binary sub-alphabets according to three kinds of binary-opposite attributes in the set of the nitrogenous bases C, A, G, T

The four-letter alphabet of the genetic code is curtailed into the two-letter alphabet on the basis of each kind of the attributes. For example, from the viewpoint of the first kind of binary-opposite attributes (N=1) we have the alphabet from two letters 0_1 and 1_1 (instead of the four-letter alphabet), which can be named "the binary sub-alphabet to first kind of binary attributes". The binary sub-alphabets of the genetic alphabet are the basis for the special system of numerations of each n-plet, each column and each row of the genomatrices $P^{(n)}$. Let us describe this system.

A binary numeration of columns and rows of the matrix $P^{(n)} = [C\ T;\ A\ G]^{(n)}$ (see Figure 1) is connected with binary symbols of letters C, A, G, T in the binary sub-alphabets №№ 1 and 2

(N=1 and N=2) respectively. More precisely, to get number of a column of the matrix [C T; A G]$^{(n)}$, one should take a sequence of letters of any n-plet from this column and write the corresponding sequence of the binary symbols of these letters from the viewpoint of the binary sub-alphabet № 1. This binary sequence is binary number of this column (all n-plets of this column are equivalent to each other from the viewpoint of binary sub-alphabet № 1). For example, let's consider the matrix [C T; A G]$^{(3)}$ and its column with a triplet CAT (Figure 1). From the viewpoint of the binary sub-alphabet № 1 (where C=T=1 and A=0), the sequence of letters CAT is equivalent to the binary sequence 101. This binary number 101 is the numeration number of the whole column because all triplets of this column have the same binary sequence 101 from the viewpoint of binary sub-alphabet № 1.

The binary number of a row of the matrix [C T; A G]$^{(n)}$ is constructed in a similar algorithmic way by interpretation of any n-plet of this row from the viewpoint of the binary sub-alphabet № 2. For example, let us consider the same triplet CAT in the matrix [C T; A G]$^{(3)}$. From the viewpoint of the binary sub-alphabet № 2 (where C=A=1 and T=0), the sequence of letters CAT is equivalent to the binary sequence _110_. This binary number _110_ is the numeration number of the matrix row with the triplet CAT because all triplets of this column have the same binary sequence _110_ from the viewpoint of binary sub-alphabet № 1.

Any matrix [C T; A G]$^{(n)}$ has a binary coordination number for each of its n-plets. All sets of its n-plets have a series of binary coordination numbers algorithmically, which are equivalent to a series of integers 0, 1, 2 ,…, (4^n-1) in decimal numeration system. Such coordination number of each n-plet is constructed by means of combination of binary numbers of its row and its column into the single whole in a form of 2n-digit binary number. The first half of such coordination number coincides with binary number of the matrix row of this n-plet, and the second half coincides with binary number of its column. For example, the considered triplet CAT has the individual coordinate 110101 in the matrix [C T; A G]$^{(3)}$ (Figure 1). At translation of such 2n-digit binary numbers into the decimal numeration system, all n-plets receive their individual decimal numbers from the series of integers 0, 1, 2 ,…, (4^n-1). All n-plets are disposed in the genomatrices regularly in a form of sequences with the monotonous change of coordinates of n-plets. For example, all triplets in the genomatrix [C T; A G]$^{(3)}$ have their natural ordering in accordance with the monotonous sequence of their coordinates 0, 1, 2,…, 63. Such natural numerations of well-ordered n-plets are useful for investigation of rules of symmetric relations among elements of various dialects of the genetic code. In this way we obtain the opportunity to work with numbers in genetic codes. In other words, we digitize elements of the genetic code.

One can replace each triplet of the genomatrix [C T; A G]$^{(3)}$ by its 6-digit binary coordinate (Figure 1). It is interesting, that such variant of the genomatrix P$^{(3)}$ is famous for a few thousand years: it is identical to the famous matrix of 64 hexagrams in Fu-Xi's order from the ancient Chinese "The Book of Changes" ("I Ching"). This matrix of 64 hexagrams was declared by ancient Chinese as the universal natural archetype [Petoukhov, 2001a,b; 2005; 2008b]. Each hexagram in the Chinese matrix is arranged by two independent trigrams, which symbolize its row and its column. But each element of the genomatrix [C T; A G]$^{(3)}$ is also connected with a binary hexagram arranged by two independent trigrams, which symbolize its row and its column. The creator of the first computer G.Leibniz was amazed by this Chinese matrix, when he became acquainted with it, because he considered himself as the originator of the binary numeration system, which was presented in this ancient matrix already. He saw in peculiarities of this matrix many materials for his ideas of a universal language and binary systems. "Leibniz has seen in this similarity the evidence of the pre-established harmony and unity of the divine plan for all epochs and for all people" [Schutskiy, 1997, c. 12]. Thereby our matrix approach to the genetic code ("matrix genetics") leads us additionally to historical analogies and to the problem of a connection of times. One can add that molecular genetics is interested for a few decades already to investigate analogies between the genetic code and the system of "I Ching" [Stent, 1969; Jacob, 1974, 1977; and others]. Modern physics pays attention to "I Ching" also [Capra, 2000].

3 Realignments of the genomatrix [C A; T G]$^{(3)}$ by permutations of positions in triplets

Now we continue the analysis of matrix presentations of the genetic code {see [Petoukhov, arXiv:0802.3366 (q-Bio.Qm)]}. Modern science recognizes many variants (or dialects) of the genetic code, data about which are shown on the NCBI's website http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi. 17 variants (or dialects) of the genetic code exist which differ one from another by some details of correspondences between triplets and objects encoded by them. Most of these dialects (including the so called Standard Code and the Vertebrate Mitochondrial Code) have the following general scheme of their degeneracy where 32 "black" triplets with "strong roots" and 32 "white" triplets with "weak" roots exist.

In this general or basic scheme, the set of 64 triplets contains 16 subfamilies of triplets, every one of which contains 4 triplets with the same two letters on the first positions of each triplet (an example of such subsets is the case of the four triplets CAC, CAA, CAT, CAG with the same two letters CA on their first positions). We shall name such subfamilies as the subfamilies of *NN*-triplets. In the described basic scheme of degeneracy, the set of these 16 subfamilies of *NN*-triplets is divided into two equal subsets from the viewpoint of degeneration properties of the code (Figure 3). The first subset contains 8 subfamilies of so called "two-position" *NN*-triplets, a coding value of which is independent of a letter on their third position. An example of such subfamilies is the four triplets CGC, CGA, CGT, CGC (Figure 3), all of which encode the same amino acid Arg, though they have different letters on their third postion. All members of such subfamilies of *NN*-triplets are marked by black color in Figures 3 and 4.

The second subset contains 8 subfamilies of "three-position" NN-triplets, the coding value of which depends on a letter on their third position. An example of such subfamilies in Figure 3 is the four triplets CAC, CAA, CAT, CAC, two of which (CAC, CAT) encode the amino acid His and the other two (CAA, CAG) encode another amino acid Gln. All members of such subfamilies of NN-triplets are marked by the white color in the genomatrix $P^{(3)} =$ [C T; A G]$^{(3)}$ on Figure 4. So the genomatrix [C T; A G]$^{(3)}$ has 32 black triplets and 32 white triplets. Each subfamily of four NN-triplet is disposed in an appropriate (2x2)-subquadrant of the genomatrix [C T; A G]$^{(3)}$ due to the Kronecker algorithm of construction of the genomatrix [C T; A G]$^{(3)}$ of triplets from the alphabet genomatrix P = [C T; A G] (Figure 1).

Here one should recall the work by Rumer [Rumer, 1968] where a combination of letters on the two first positions of each triplet was named as a "root" of this triplet. A set of 64 triplets contains 16 possible variants of such roots. Taking into account properties of triplets, Rumer has divided the set of 16 possible roots into two subsets with eight roots in each. Roots CC, CT, CG, AC, TC, GC, GT, GG form the first of such octets. They were named by Rumer "strong roots". The other eight roots CA, AA, AT, AG, TA, TT, TG, GA form the second octet and they were named weak roots. When Rumer published his works, the Vertebrate Mitochondrial code and some of the other code dialects were unknown. But one can check easily that the set of 32 black (white) triplets, which we show on Figure 3 for cases of the Standard code and the Vertebrate Mitochondrial Code, is identical to the set of 32 triplets with strong (weak) roots described by Rumer. So, using notions proposed by Rumer, the black triplets can be named as triplets with the strong roots and the white triplets can be named as triplets with the weak roots. Rumer believed that this symmetrical division into two binary-oppositional categories of roots is very important for understanding the nature of the genetic code systems.

One can check easily on the basis of data from the NCBI's website (http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi) that the following 11 dialects of the genetic code have the same basic scheme of degeneracy with 32 black triplets and with 32 white triplets: 1) the Standard Code; 2) the Vertebrate Mitochondrial Code; 3) the Yeast Mitochondrial Code; 4) the Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code; 5) the Ciliate, Dasycladacean and Hexamita Nuclear Code; 6) the Euplotid Nuclear Code; 7) the Bacterial and Plant Plastid Code; 8) the Ascidian

Mitochondrial Code; 9) the Blepharisma Nuclear Code; 10) the Thraustochytrium Mitochondrial Code; 11) the Chlorophycean Mitochondrial Code. In this article we will consider this basic scheme of the degeneracy which is presented by means of a black-and-white mosaics in a family of genetic matrices ($P^{(3)} = [C\ T;\ A\ G]^{(3)}$, etc.) on Figure 4.

One can mentioned that the other 6 dialects of the genetic code have only small differences from the described basic scheme of degeneracy: the Invertebrate Mitochondrial Code; the Echinoderm and Flatworm Mitochondrial Code; the Alternative Yeast Nuclear Code; The Alternative Flatworm Mitochondrial Code; the Trematode Mitochondrial Code; the Scenedesmus obliquus mitochondrial Code.

According to general traditions, the theory of symmetry studies initially those natural objects that possess the most symmetrical character, and then it constructs a theory for cases of violations of this symmetry in other kindred objects. For this reason one should pay special attention to the Vertebrate Mitochondrial code which is the most symmetrical code among dialects of the genetic code and which corresponds to the basic scheme of the degeneracy. One can mention additionally that some authors consider this dialect not only as the most "perfect" but also as the most ancient dialect [Frank-Kamenetskiy, 1988], but this last aspect is a debatable one. Figure 3 shows the correspondence between the set of 64 triplets and the set of 20 amino acids with stop-signals (Stop) of protein synthesis in the Standard Code and in the Vertebrate Mitochondrial Code.

THE STANDARD CODE	
8 subfamilies of the "two-position NN-triplets" ("black triplets") and the amino acids, which are encoded by them	8 subfamilies of the "three-position NN-triplets" („white triplets") and the amino acids, which are encoded by them
CCC, CCT, CCA, CCG➔ Pro	CAC, CAT, CAA, CAG ➔ His, His, Gln, Gln
CTC, CTT, CTA, CTG➔ Leu	AAC, AAT, AAA, AAG ➔ Asn, Asn, Lys, Lys
CGC, CGT, CGA, CGG➔ Arg	ATC, ATT, ATA, ATG ➔ Ile, Ile, Ile, Met
ACC, ACT, ACA, ACG➔ Thr	AGC, AGT, AGA, AGG ➔ Ser, Ser, Arg, Arg
TCC, TCT, TCA, TCG➔ Ser	TAC, TAT, TAA, TAG ➔ Tyr, Tyr, Stop, Stop
GCC, GCT, GCA, GCG➔ Ala	TTC, TTT, TTA, TTG ➔ Phe, Phe, Leu, Leu
GTC, GTT, GTA, GTG➔ Val	TGC, TGT, TGA, TGG ➔ Cys, Cys, Stop, Trp
GGC, GGT, GGA, GGG➔ Gly	GAC, GAT, GAA, GAG ➔ Asp, Asp, Glu, Glu

THE VERTEBRATE MITOCHONDRIAL CODE	
8 subfamilies of the "two-position NN-triplets" ("black triplets") and the amino acids, which are encoded by them	8 subfamilies of the "three-position NN-triplets" („white triplets") and the amino acids, which are encoded by them
CCC, CCT, CCA, CCG➔ Pro	CAC, CAT, CAA, CAG ➔ His, His, Gln, Gln
CTC, CTT, CTA, CCG➔ Leu	AAC, AAT, AAA, AAG ➔ Asn, Asn, Lys, Lys
CGC, CGT, CGA, CGG➔ Arg	ATC, ATT, ATA, ATG ➔ Ile, Ile, Met, Met
ACC, ACT, ACA, ACG➔ Thr	AGC, AGT, AGA, AGG➔ Ser, Ser, Stop, Stop
TCC, TCT, TCA, TCG➔ Ser	TAC, TAT, TAA, TAG ➔ Tyr, Tyr, Stop, Stop
GCC, GCT, GCA, GCG➔ Ala	TTC, TTT, TTA, TTG ➔ Phe, Phe, Leu, Leu
GTC, GTT, GTA, GTG➔ Val	TGC, TGT, TGA, TGG ➔ Cys, Cys, Trp, Trp
GGC, GGT, GGA, GGG➔ Gly	GAC, GAT, GAA, GAG ➔ Asp, Asp, Glu, Glu

Figure 3. Two examples of the basic scheme of the genetic code degeneracy with 32 "black" triplets and 32 "white" triplets. Top: the case of the Standard Code. Bottom: the case of the Vertebrate Mitochondrial Code. Yellow color highlights the triplets which changed their code meanings in relation to the Standard Code. All initial data are taken from the NCBI's web-site *http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi*.

The author has revealed that the disposition of the black and white triplets in the genomatrix $P^{(3)} = [C\ T;\ A\ G]^{(3)}$ for this basic scheme of the genetic code degeneracy gives the very symmetrical black-and-white mosaic of the code degeneracy (Figure 4), though the most

variants of their possible dispositions give quite asymmetric mosaics [Petoukhov, arXiv:0802.3366 (q-bio.QM)].

It is much unexpected that any kind of permutation of positions in triplets, which is accomplished in all 64 triplets simultaneously, leads to the transformed genomatrix, which possesses a symmetrical mosaic of degeneracy also. The six kinds of sequences of positions in triplets exist: 1-2-3, 2-3-1, 3-1-2, 1-3-2, 2-1-3, 3-2-1. It is obvious that if one changes the positional sequence 1-2-3 in triplets, for example, by the sequence 2-3-1, the most triplets change their disposition in the genomatrix. And the initial genomatrix is reconstructed cardinally into the new mosaic matrix. For instance, in the result of such permutation the black triplet CGA is replaced in its matrix cell by the white triplet GAC, etc. Let us denote the six genomatrices, which correspond to the mentioned kinds of positional sequences in triplets, by the symbols $P^{CTAG}_{123}{}^{(3)}(=P^{(3)}=[C\ T;\ A\ G]^{(3)})$, $P^{CTAG}_{231}{}^{(3)}$, $P^{CTAG}_{312}{}^{(3)}$, $P^{CTAG}_{132}{}^{(3)}$, $P^{CTAG}_{213}{}^{(3)}$, $P^{CTAG}_{321}{}^{(3)}$. Here the bottom indexes show the appropriate positional sequences in triplets; the upper index shows the kind of basic genomatrix [C T; A G] of the Kronecker family (later we shall consider other cases of such basic genomatrices). Figure 4 demonstrates these six genomatrices.

CCC	CCT	CTC	CTT	TCC	TCT	TTC	TTT
CCA	CCG	CTA	CTG	TCA	TCG	TTA	TTG
CAC	CAT	CGC	CGT	TAC	TAT	TGC	TGT
CAA	CAG	CGA	CGG	TAA	TAG	TGA	TGG
ACC	ACT	ATC	ATT	GCC	GCT	GTC	GTT
ACA	ACG	ATA	ATG	GCA	GCG	GTA	GTG
AAC	AAT	AGC	AGT	GAC	GAT	GGC	GGT
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG

CCC	CTC	TCC	TTC	CCT	CTT	TCT	TTT
CAC	CGC	TAC	TGC	CAT	CGT	TAT	TGT
ACC	ATC	GCC	GTC	ACT	ATT	GCT	GTT
AAC	AGC	GAC	GGC	AAT	AGT	GAT	GGT
CCA	CTA	TCA	TTA	CCG	CTG	TCG	TTG
CAA	CGA	TAA	TGA	CAG	CGG	TAG	TGG
ACA	ATA	GCA	GTA	ACG	ATG	GCG	GTG
AAA	AGA	GAA	GGA	AAG	AGG	GAG	GGG

CCC	CCT	TCC	TCT	CTC	CTT	TTC	TTT
CCA	CCG	TCA	TCG	CTA	CTG	TTA	TTG
ACC	ACT	GCC	GCT	ATC	ATT	GTC	GTT
ACA	ACG	GCA	GCG	ATA	ATG	GTA	GTG
CAC	CAT	TAC	TAT	CGC	CGT	TGC	TGT
CAA	CAG	TAA	TAG	CGA	CGG	TGA	TGC
AAC	AAT	GAC	GAT	AGC	AGT	GGC	GGT
AAA	AAG	GAA	GAG	AGA	AGG	GGA	GGG

CCC	TCC	CTC	TTC	CCT	TCT	CTT	TTT
ACC	GCC	ATC	GTC	ACT	GCT	ATT	GTT
CAC	TAC	CGC	TGC	CAT	TAT	CGT	TGT
AAC	GAC	AGC	GGC	AAT	GAT	AGT	GGT
CCA	TCA	CTA	TTA	CCG	TCG	CTG	TTG
ACA	GCA	ATA	GTA	ACG	GCG	ATG	GTG
CAA	TAA	CGA	TGA	CAG	TAG	CGG	TGG
AAA	GAA	AGA	GGA	AAG	GAG	AGG	GGG

CCC	TCC	CCT	TCT	CTC	TTC	CTT	TTT
ACC	GCC	ACT	GCT	ATC	GTC	ATT	GTT
CCA	TCA	CCG	TCG	CTA	TTA	CTG	TTG
ACA	GCA	ACG	GCG	ATA	GTA	ATG	GTG
CAC	TAC	CAT	TAT	CGC	TGC	CGT	TGT
AAC	GAC	AAT	GAT	AGC	GGC	AGT	GGT
CAA	TAA	CAG	TAG	CGA	TGA	CGG	TGG
AAA	GAA	AAG	GAG	AGA	GGA	AGG	GGG

CCC	CTC	CCT	CTT	TCC	TTC	TCT	TTT
CAC	CGC	CAT	CGT	TAC	TGC	TAT	TGT
CCA	CTA	CCG	CTG	TCA	TTA	TCG	TTG
CAA	CGA	CAG	CGG	TAA	TGA	TAG	TGG
ACC	ATC	ACT	ATT	GCC	GTC	GCT	GTT
AAC	AGC	AAT	AGT	GAC	GGC	GAT	GGT
ACA	ATA	ACG	ATG	GCA	GTA	GCG	GTG
AAA	AGA	AAG	AGG	GAA	GGA	GAG	GGG

Figure 4. The genomatrices $P^{CTAG}_{123}{}^{(3)}$ (or $P^{(3)}$ in Figure 1), $P^{CTAG}_{231}{}^{(3)}$, $P^{CTAG}_{213}{}^{(3)}$, $P^{CTAG}_{321}{}^{(3)}$, $P^{CTAG}_{312}{}^{(3)}$, $P^{CTAG}_{132}{}^{(3)}$. Each matrix cell has a triplet and an amino acid (or stop-signal) coded by this triplet. The black-and-white mosaic presents a specificity of the basic scheme of the genetic code degeneracy.

It should be mentioned that the quantity of variants of possible dispositions of 64 genetic triplets in 64 cells of the genomatrix $[C\ T;\ A\ G]^{(3)}$ is equal to the huge number $64! \sim 10^{89}$; the most of these variants have not symmetries in a disposition of these black triplets and white triplets in (8*8)-matrix, of course. But each of these six genomatrices has a symmetric character unexpectedly (Figure 4). For example, the first genomatrix $P^{CTAG}_{123}{}^{(3)} = [C\ T;\ A\ G]^{(3)}$ has the following symmetric features:

1. The upper and lower halves of this matrix are mirror-antisymmetric to each other by its colors: any pair of cells, disposed by the mirror-symmetric manner in these halves, has opposite colors.
2. Diagonal quadrants of the matrix are identical to each other from the viewpoint of their mosaics.
3. The adjacent columns 0-1, 2-3, 4-5, 6-7 are identical to each other from the viewpoint of the mosaic and of the disposition of the same amino acids in their proper cells.
4. Mosaics of all columns of the (8x8)-genomatrix and of its (4x4)-quadrants have a meander-line character, which is connected with Rademacher functions from theory of digital signal processing.
5. The turning of the genomatrix $P^{CTAG}_{123}{}^{(3)}$ into a cylinder with an agglutination of its upper and lower borders reveals a symmetric pattern of cyclic shifts. This pattern is demonstrated more clearly by the tessellation of a plane with this mosaic genomatrix $P^{CTAG}_{123}{}^{(3)}$ (Figure 5, left).

Each of the other 5 genomatrices on Figure 4 has symmetrical properties also, first of all, the following two properties:

1. The upper and lower halves of each matrix are mirror-antisymmetric to each other by its colors: any pair of cells, disposed by the mirror-symmetric manner in these halves, has opposite colors.
2. Mosaics of all columns of each (8x8)-genomatrix and of its (4x4)-quadrants have a meander-line character, which is connected with Rademacher functions from theory of digital signal processing.

4 The tessellation of a plane by the mosaics of the genetic matrices

The plane with the tessellation by the mosaic genomatrix $P^{CTAG}_{123}{}^{(3)} = [C\ T;\ A\ G]^{(3)}$ has the ornamental pattern with two pattern units. These two pattern units are identical in their forms, but they are inverse in their colors (black and white) and orientations (left and right). This pattern has the character of cyclic shifts that permits to think about a possible genetic meaning of cyclic codes, which play significant role in the theory of digital signal processing.
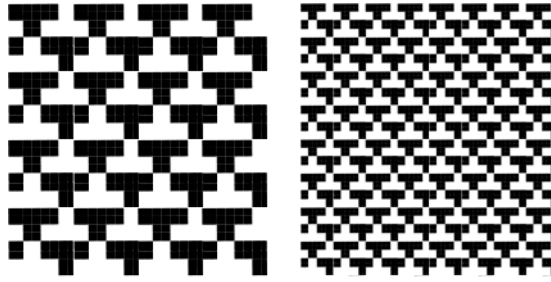
Figure 5. At the left: the tessellation of a plane by the mosaics of $P^{CTAG}_{123}{}^{(3)}$ from Figure 4.
At the right: the tessellation of a plane by the mosaics of $P^{CTAG}_{213}{}^{(3)}$ from Figure 4.

The second genomatrix $P^{CAUG}_{231}{}^{(3)}$ on Figure 4 is generated by the cyclic shift of positions in triplets (2-3-1 instead of 1-2-3). This genomatrix has the symmetric features also:

1. The upper and lower halves of this matrix are mirror-antisymmetric to each other by their colors.
2. All (4x4)-quadrants are identical to each other by their mosaics.
3. The left and the right halves of the genomatrix are identical to each other from the viewpoint of dispositions of all amino acids and stop-signals in the case of the vertebrate mitochondrial code from Fig.3.
4. The genomatrix has 4 pairs of identical columns again: 0-4, 1-5, 2-6, 3-7 that are not adjacent columns in this matrix.
5. All columns of the (8x8)-genomatrix and its (4x4)-quadrants have a meander-line character again, which is connected with Rademacher functions.

Note, that the mosaic of the initial (8x8)-genomatrix $P^{CTAG}_{123}{}^{(3)}$ is reproduced in (4x4)-quadrants of this $P^{CTAG}_{213}{}^{(3)}$ in a fractal manner: the coefficient of the fractal ranging of areas is equal to 4. The tessellations of a plane by the mosaics of $P^{CTAG}_{123}{}^{(3)}$ and of $P^{CTAG}_{213}{}^{(3)}$ demonstrate their fractal correspondence very clearly (Figure5). Such scale transformation of areas in the mosaics of the code degeneration will be named the "tetra-reproduction" transformation. The cyclic-generated genomatrix $P^{CTAG(3)}_{231}$ has the quantity of the pattern units 4 times more than the initial genomatrix $P^{CTAG(3)}_{123}$ due to this tetra-reproduction (Figures 4 and 5).This fact is interesting because an analogical tetra-reproduction (or a tetra-division) exists in the living nature always in a course of division of gametal cells, which are transmitters of genetic information. In this mysterious act of meiosis, one gamete is divided into four new gametes (this fact was mentioned specially by Schrodinger in his famous book [Schrodinger, 1955, §13]). The described tetra-reproduction of the mosaics of the genomatrices can be utilized, in particular, in formal models of meiosis. We will return to this reproduction property below in Section 9.

Presented materials of the matrix genetics lead us to questions of biological meaning. Really, we revealed unexpectedly that a simple algorithmic re-packing (re-arrangement) of elements in triplets by the cyclic shift is sufficient to receive new genomatrix with the fractal tetra-reproducing of mosaics of the code degeneration. It seems that a similar re-packing of molecular elements in biological object can be sufficient also to provide foundations of a process of tetra-reproducing in some cases, first of all, in the case of meiosis. These and other considerations permit us to put forward a hypothesis of molecular re-packing. According to this hypothesis, the mysterious process of meiosis is based on a mechanism of algorithmic re-arrangement of molecular elements of gametes with a participation of algorithms of cyclic and dyadic shifts. In our opinion, the principle of re-packing of biological molecules and of their ensembles is an important general principle of biological self-organization. It is interesting also that one can compare the tetra-division of material gametes with the tetra-division of the code genomatrices, which are information objects. These materials testify that meiosis is not an

accidental material process but it is coordinated with more ancient information structures of the genetic code in their matrix form.

Now let us additionally consider on Figure 4 the genomatrix $P^{CTAG}_{321}{}^{(3)}$ with the inverse order of positions in all triplets (3-2-1 instead of 1-2-3). One can compare its mosaic with the mosaic of the $P^{CTAG}_{213}{}^{(3)}$ based on the cyclic shift of positions in all triplets: 2-1-3 instead of 3-2-1. In this case the similar phenomenon of the tetra-reproduction of these mosaics becomes apparent again but with new pattern (Figure 6).
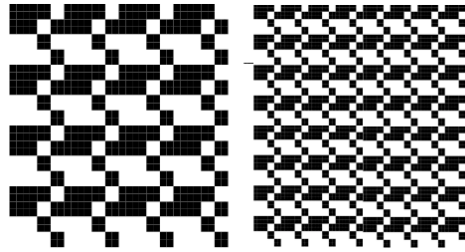
Figure 6. The tessellations of a plane by the mosaics of the genomatrices P^{CTAG}_{213} (at the left) and P^{CTAG}_{321} (on the right)

One can note also that all six genomatrices on Figure 4 are interconnected by special permutations of their columns and rows. The same genomatrices can be received from the initial genomatrix $P^{CTAG}_{123}{}^{(3)}$ by appropriate permutations of positions in binary 3-digit numeration of their columns and rows. In other words, the "local" permutations of positions in triplets give the same results as "global" permutations of positions in binary 3-digit numeration of columns and of rows. All six genomatrices on Figure 4 are connected with Hadamard matrices on the basis of the T-algorithm (its another name is the U-algorithm) described in [Petoukhov, 2005; 2008 a, b]. The presented permutations gave interesting results in their application to genomatrices. It seems that applications of similar permutations to genetic sequences of triplets can give interesting results also. Our study of properties of permutations in structural regularities of long nucleotide sequences is briefly described in the end of the article in a connection with fractal genetic nets.

5 The genetic encoding and a fast Fourier transformation

The revelation of the permutation group of the six symmetric genomatrices $P^{CTAG}_{123}{}^{(3)}$ (or $P^{(3)}$ in Figure 1), $P^{CTAG}_{231}{}^{(3)}$, $P^{CTAG}_{213}{}^{(3)}$, $P^{CTAG}_{321}{}^{(3)}$, $P^{CTAG}_{312}{}^{(3)}$, $P^{CTAG}_{132}{}^{(3)}$ seems to be the essential fact additionally because of heuristic associations with the mathematical theory of digital signal processing, where similar permutations are utilized for a long time as the useful tool. For example, the book [Ahmed, Rao, 1975, § 4.6] gives the example of the important role of the method of data permutation and of binary inversion for one of variants of the algorithm of a fast Fourier transformation. In this example the numeric sequence 0, 1, 2, 3, 4, 5, 6, 7 is reformed into the sequence 0, 4, 2, 6, 1, 5, 3, 7. But the same change of the numeration of the columns and the rows takes a place in our case (Figure 4) where the genomatrix P^{CTAG}_{123} is reformed into the genomatrix P^{CTAG}_{321} in the result of the inversion of the binary numeration of the columns and the rows (or of the inversion of the positions in the triplets). These and other facts permit to think that the genetic system has a connection with a fast Fourier transformation (or with a fast Hadamard transformation) [Petoukhov, 2006, 2008b].

6 The tetra-reproduction of the genomatrices in their binary presentation

Why the nature has chosen this variant of degeneration of genetic code, which gives such mosaics? Whether these six "triplets-permutations" genomatrices $P^{CTAG}_{123}{}^{(3)}$, $P^{CTAG}_{231}{}^{(3)}$, $P^{CTAG}_{213}{}^{(3)}$, $P^{CTAG}_{321}{}^{(3)}$, $P^{CTAG}_{312}{}^{(3)}$, $P^{CTAG}_{132}{}^{(3)}$ have such mutual mathematical property that can be associated with famous biological facts of genetic inheritance? Yes, such mutual property exists and it is connected with the tetra-reproduction by analogy with meiosis again. This

property is not-trivial one and it does not exist in the most variants of arbitrary dispositions of 32 black triplets and 32 white triplets in (8*8)-matrices.

We have mentioned already that each mosaic row of the considered genetic matrices (see Figure 4) corresponds to one of Rademacher functions ($r_n(t)$ = sign($\sin 2^n \pi t$), n = 1, 2, 3,…), which consists of components "+1" and "-1" only (see also [Petoukhov, arXiv:0802.3366v3]). Taking this fact into account, let us represent the black-and-white mosaic of each from the mentioned six genomatrices as a binary mosaic of numbers "+1" and "-1" by means of replacing black (white) color of each matrix cell by an element "+1" ("-1"). In such "Rademacher representation", the genomatrices $P^{CTAG}_{123}{}^{(3)}$, $P^{CTAG}_{231}{}^{(3)}$, $P^{CTAG}_{213}{}^{(3)}$, $P^{CTAG}_{321}{}^{(3)}$, $P^{CTAG}_{312}{}^{(3)}$, $P^{CTAG}_{132}{}^{(3)}$ are reformed into the genomatrices B_{123}, B_{231}, B_{312}, B_{132}, B_{213}, B_{321} (Figure 7). Unexpected mutual property of these six binary genomatrices on Figure 7 is the following one. The multiplication of each genomatrix with itself (the square of each genomatrix) gives a phenomenon of its tetra-reproduction: four duplicates of the genomatrix are appeared. Really the following formulas take place:

$$(B_{123})^2 = 4*B_{123}; \qquad (B_{231})^2 = 4*B_{231}; \qquad (B_{312})^2 = 4*B_{312}$$

$$(B_{132})^2 = 4*B_{132}; \qquad (B_{213})^2 = 4*B_{213}; \qquad (B_{321})^2 = 4*B_{321} \qquad (1)$$

This fact is interesting because the genetic code is destined by the nature for reproduction of biological structures, and matrices of the genetic code in their binary representation possess the non-trivial algebraic property of their own tetra-self-reproduction.

The set of these six binary genomatrices has many other interesting properties (for instance, $B_{123}*B_{321}+B_{123}*B_{132} = B_{123}{}^2$, etc.), which generate heuristic associations with genetic phenomena and which can be utilized to model the meiosis process of tetra-reproduction of gametal cells with a specific behavior of chromosomes. But these properties do not considered in this article.

It can be mentioned additionally that one can consider those "complementary" variants of the genomatrices $P^{CTAG}_{123}{}^{(3)}$ (or $P^{(3)}$ in Figure 1), $P^{CTAG}_{231}{}^{(3)}$, $P^{CTAG}_{213}{}^{(3)}$, $P^{CTAG}_{321}{}^{(3)}$, $P^{CTAG}_{312}{}^{(3)}$, $P^{CTAG}_{132}{}^{(3)}$, which are received by replacement of each triplet by its complementary triplet (the example of the complementary triplets is CAG and GTC). In each case the "complementary" matrix is identical to 180-degree turn of the initial matrix. The "complementary" genomatrices in similar binary presentations have the same properties of their tetra-reproduction [Petoukhov, 2008,b].
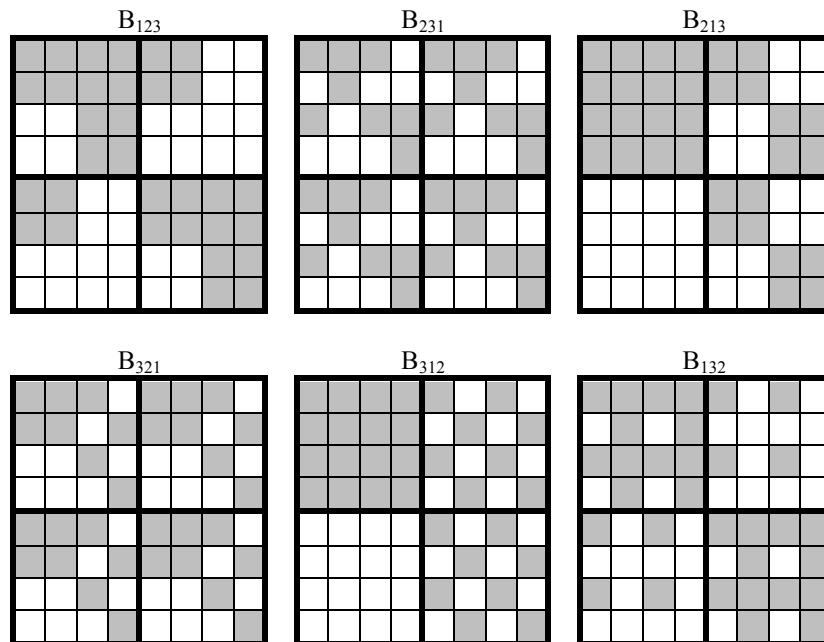

B_{123}   B_{231}   B_{213}
B_{321}   B_{312}   B_{132}

Figure 7. Binary numeric genomatrices, in which each black cell means the element "+1";
each white cell means the element "-1".

7 Projector operators in matrix presentations of the genetic code

The "Rademacher representation" of the genetic matrices on Figure 7 reveals also an unexpected connection of the genetic code structures with so called "projector operators", which are well-known in quantum mechanics, automatic control systems, etc. By definition, a linear operator P in a linear space is named a projector operator if it satisfies the following condition:

$$P^2 = P \qquad (2)$$

Let us consider matrices $Y_{123} = 4^{-1}*B_{123}$, $Y_{231} = 4^{-1}*B_{231}$, $Y_{312} = 4^{-1}*B_{312}$, $Y_{321} = 4^{-1}*B_{321}$, $Y_{213} = 4^{-1}*B_{213}$, $Y_{132} = 4^{-1}*B_{132}$. One can check that each of these matrices Y_k is a projector operator because it satisfies the condition (2). We will name projector operators, which are based on genetic matrices, as "genoprojector operators". Some of these genoprojectors are commutative, other ones are non-commutative. Some examples of commutative genoprojectors are the following: $Y_{312}*Y_{213}=Y_{213}*Y_{312}$, $Y_{123}*Y_{321}=Y_{321}*Y_{123}$, $Y_{231}*Y_{132}=Y_{132}*Y_{231}$. Of course, each of new matrices $Y_{123}*Y_{321}$, $Y_{231}*Y_{132}$, $Y_{312}*Y_{213}$ is a projector also.

By definition, two projectors P_1 and P_2 are named orthogonal if $P_1*P_2=0$. One can check that the three genoprojectors $Y_{312}*Y_{213}$, $Y_{123}*Y_{321}$, $Y_{231}*Y_{132}$ are orthogonal each to other.

Some other variants of genetic (8*8)-matrices of triplets in the similar „Rademacher representation" with the same general factor 4^{-1} are genoprojector operators also: [G A; T C][3], [G T; A C][3], [C A; T G][3]. These matrices contain C and G along their diagonals. All possible variants of permutations of positions of triplets (1-2-3, 2-3-1, etc) in these matrices lead to new genoprojector operators. But the genomatrices, which contain the letters C and G not along their diagonals, do not lead to projector operators: [C T; G A][3], [C G; A T][3], etc. The (8*8)-matrices of genoprojectors are connected with genetic 8-dimensional Yin-Yang algebras (or bipolar algebras) which were presented in our works [Petoukhov, arXiv:0803.3330 and arXiv:0805.4692; Petoukhov, 2008b; Petoukhov, He, 2009].

A similar situation is true for mosaic (4*4)-matrices of duplets where black (white) cells contain two first letters of the subsets of black (white) triplets (see Figure 8): [C A; T G][2], [G A; T C][2], [G T; A C][2], [C T; A G][2]. The similar numeric presentation of these genomatrices (where black cells and white cells contain elements „+1" and „-1" correspondingly, with the general factor 2^{-1} in this case) lead to new genoprojectors. The permutation of positions in all duplets (2-1 instead 1-2) lead to new genoprogectors again (these genoprojectors are non-commutative). But this is true only for genomatrices which contain C and G along their diagonals. Other genomatrices, which contain C and G not along their diagonals, do not lead to projector operators.

It is known that theory of projector operators has a set of interesting results and applications (see for example [Halmos, 1974; Messiah, 1999]). For example every family of commutative projectors generates algorithmically a Boolean algebra of projectors. Taking this into account, questions about a set of genoprojectors and corresponding Boolean algebras of genoprojectors should be studied systematically in theoretical and applied aspects including their biological meaning. The phenomenological fact of the connection of genetic code structures with special classes of projective operators allows developing new methods in bioinformatics and in technological fields of genetic algorithms on the base of the theory of projectors. Specifically we study applications of the theory of projectors for analysis of genetic sequences.
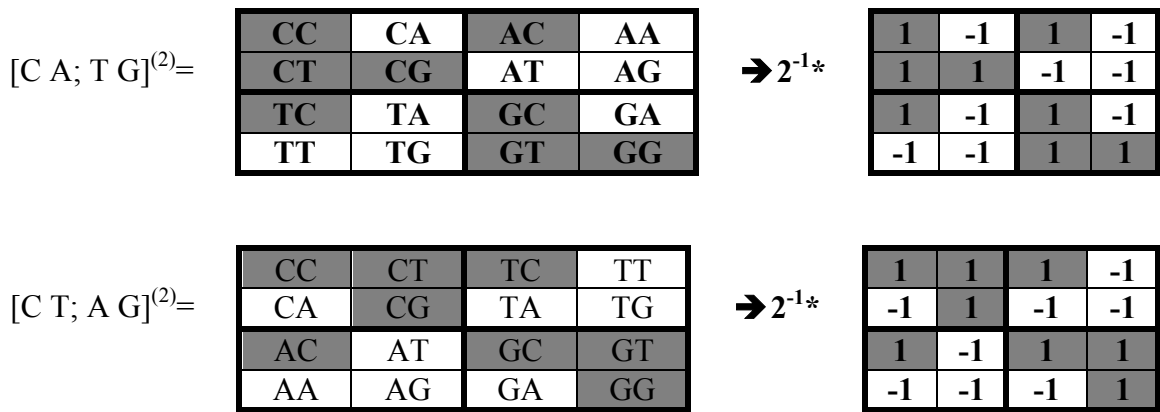
CC	CA	AC	AA		1	-1	1	-1
CT	CG	AT	AG	$\rightarrow 2^{-1}*$	1	1	-1	-1
TC	TA	GC	GA		1	-1	1	-1
TT	TG	GT	GG		-1	-1	1	1

$[C\ A;\ T\ G]^{(2)}=$ (left table above)

CC	CT	TC	TT		1	1	1	-1
CA	CG	TA	TG	$\rightarrow 2^{-1}*$	-1	1	-1	-1
AC	AT	GC	GT		1	-1	1	1
AA	AG	GA	GG		-1	-1	-1	1

$[C\ T;\ A\ G]^{(2)}=$ (left table above)

Figure 8. Some examples of matrix projector operators (the numeric matrices on the right side) that correspond to mosaic matrices of duplets.

8 Unitary symmetries in matrix presentations of the genetic code

Now we will pay our attention again to the fact that the genetic code is the bearer of the three pairs of binary-oppositional attributes which are showed on Figure 2. One can see that for a determination of any of genetic letters inside the genetic alphabet it is enough to indicate two from thesethree kinds of the mentioned binary-oppositional attributes. For example let us take the first two kinds of the binary-oppositional attributes from Figure 2. Let us mark each genetic letter with the amino-mutating property by the symbol "+1" (such genetic letter is amino from the viewpoint of its radical content), and each genetic letter without this property by the symbol "-1" (such genetic letter is keto from the viewpoint of its radical content). Let us mark else each pyrimidine by the symbol "+i" and each purine by the symbol "-i".Figure 9 shows what kind of pairs of these symbols (and of these attributes) determines each genetic letter.

	+i	-i
+1	C	A
-1	T	G

Figure 9. The individual determination of each genetic letter by means of the individual pair of the attributes (explanation in text)

So, each genetic letter can be considered as a 2-parametric object inside the genetic alphabet. In view of this we put forward the following working hypothesis: one can reveal useful knowledge in mathematical bioinformatics (or in mathematical modeling of genetic systems) if each of the genetic letters is interpreted in the field of matrix genetics as a relevant 2-dimensional complex number:

$$C = 1+i,\ A = 1-i,\ T = -1+i,\ G = -1-i. \tag{3}$$

The author has received some interesting results in matrix genetics on the base of this hypothesis (or of this numeric approach). One of them is a natural presentation of some families of genetic matrices as families of unitary matrices. This result seems to be interesting from the viewpoint of importance of unitary symmetries in theoretical physics [Lichtenberg, 1978; Louck, 2008; Rumer, Fet, 1970].

How many (2x2)-matrices can be constructed under the condition that each row and each column of each matrix contains only those genetic letters that belong to one of the mentioned binary-oppositional attributes (amino-keto and pyrimidine-purine)? In other words, each row and each column of such matrices should consist of the pairs C-A, C-T, G-A, G-T only. This

condition is identical with the condition that such matrices should contain complementary pairs of the letters C-G and A-T along their diagonals (this condition exists already in the previous paragraph 7 about genetic projectors). One can check that only 8 symbolic matrices $P^{[CATG]}$, $P^{[CTAG]}$, $P^{[GATC]}$, $P^{[GTAC]}$, $P^{[ACGT]}$, $P^{[TCGA]}$, $P^{[AGCT]}$, $P^{[TGCA]}$ on Figure 10 satisfy this condition.

$$P^{[CATG]} = \begin{vmatrix} C & A \\ T & G \end{vmatrix} \rightarrow W_1 = (1+i)*8^{-0.5}* \begin{vmatrix} (1+i) & (1-i) \\ (-1+i) & (-1-i) \end{vmatrix}, \det(W_1) = 1$$

$$P^{[CTAG]} = \begin{vmatrix} C & T \\ A & G \end{vmatrix} \rightarrow W_2 = (1+i)*8^{-0.5}* \begin{vmatrix} (1+i) & (-1+i) \\ (1-i) & (-1-i) \end{vmatrix}, \det(W_2) = 1$$

$$P^{[GATC]} = \begin{vmatrix} G & A \\ T & C \end{vmatrix} \rightarrow W_3 = (1+i)*8^{-0.5}* \begin{vmatrix} (-1-i) & (1-i) \\ (-1+i) & (1+i) \end{vmatrix}, \det(W_3) = 1$$

$$P^{[GTAC]} = \begin{vmatrix} G & T \\ A & C \end{vmatrix} \rightarrow W_4 = (1+i)*8^{-0.5}* \begin{vmatrix} (-1-i) & (-1+i) \\ (1-i) & (1+i) \end{vmatrix}, \det(W_4) = 1$$

$$P^{[ACGT]} = \begin{vmatrix} A & C \\ G & T \end{vmatrix} \rightarrow W_5 = (1+i)*8^{-0.5}* \begin{vmatrix} (1-i) & (1+i) \\ (-1-i) & (-1+i) \end{vmatrix}, \det(W_5) = -1$$

$$P^{[TCGA]} = \begin{vmatrix} T & C \\ G & A \end{vmatrix} \rightarrow W_6 = (1+i)*8^{-0.5}* \begin{vmatrix} (-1+i) & (1+i) \\ (-1-i) & (1-i) \end{vmatrix}, \det(W_6) = -1$$

$$P^{[AGCT]} = \begin{vmatrix} A & G \\ C & T \end{vmatrix} \rightarrow W_7 = (1+i)*8^{-0.5}* \begin{vmatrix} (1-i) & (-1-i) \\ (1+i) & (-1+i) \end{vmatrix}, \det(W_7) = -1$$

$$P^{[TGCA]} = \begin{vmatrix} T & G \\ C & A \end{vmatrix} \rightarrow W_8 = (1+i)*8^{-0.5}* \begin{vmatrix} (-1+i) & (-1-i) \\ (1+i) & (1-i) \end{vmatrix}, \det(W_8) = -1$$

Figure 10. The algorithmic presentation of the eight symbolic genomatrices $P^{[CATG]}$, $P^{[CTAG]}$, $P^{[GATC]}$, $P^{[GTAC]}$, $P^{[ACGT]}$, $P^{[TCGA]}$, $P^{[AGCT]}$, $P^{[TGCA]}$ in the form of numeric matrices W_k (k=1, 2, ..., 8), which are unitary matrices.

Let us replace symbols C, A, T, G in these 8 matrices by means of their complex presentations from expressions (3). Additionally each numeric matrix is normalized by means of its multiplication with the factor $(1+i)*8^{-0.5}$ to provide the value ± 1 for the matrix determinant. Figure 10 shows the result of this action in a form of numeric matrices.

By definition a unitary matrix is a complex (n*n)-matrix W satisfying the condition

$$W*\hat{W} = \hat{W}*W = E_n \qquad (4)$$

Where E_n is the identity matrix in n dimensions and $\hat{W}$ is the conjugate transpose of W (also called the Hermitian adjoint). One can check that all eight matrices W_k (k = 1, 2, ..., 8) on Figure 10 satisfy the condition (4). So they are unitary matrices.

Determinants of the first four matrices W_1, W_2, W_3, W_4 are equal to "+1". Determinants of the last four matrices W_5, W_6, W_7, W_8 are equal to "-1". Each of the first four matrices W_1, W_2, W_3, W_4 is the basis of the cyclic group of unitary transformations $(W_m)^s$ where m = 1, 2, 3, 4 and "s" is integer number. The period of these cyclic groups is equal to 4: $(W_m)^s = (W_m)^{s+4}$. Each of the last four matrices W_5, W_6, W_7, W_7 is the basis of the cyclic group of unitary transformations $(W_n)^s$ where n = 5, 6, 7, 8 and "s" is integer number. The period of these cyclic groups is equal to 2: $(W_n)^s = (W_n)^{s+2}$.

It is known that Kronecker product of unitary matrices is creating a new unitary matrix. Different Kronecker products of all these 8 unitary matrices W_k (k = 1, 2, …., 8) on Figure 10 create new unitary matrices. For example each matrix $W_k^{(3)}$ is the unitary (8*8)-matrix. Each family of $(W_k^{(3)})^s$, where s is integer number, gives a cyclic group of unitary transformations also.

Some variants of permutations of genetic elements in genetic matrices lead to new unitary genetic matrices by analogical algorithm. These new unitary genomatrices are generating their new cyclic groups of unitary transformations.

It should be noted that the idea of presentation of the genetic letters in a form of complex numbers is not the new idea. For example, a presentation of genetic letters by means of complex numbers was made in the work (Cristea, 2005). But our approach has one very important aspect: we use such presentation for matrix analysis of ensemble of genetic multiplets. In the result the connection of the genetic code with unitary symmetries was discovered. Such matrix approach was not done by other authors as we know.

In the beginning of this section we have taken the pair of binary-oppositional attributes "amino-keto" and "pyrimidine-purine" to construct Figure 9 with the expression (3). But one can take another pair of the binary-oppositional attributes from Figure 2, for example the attribute "amino-keto" and the attribute "two hydrogen bonds – three hydrogen bonds". By analogy in this case one can make another presentation of the genetic letters in a form of complex numbers to consider another genetic (2*2)-matrices [C A; G T], [A C; T G], etc. where the pyrimidine C-T belong to one matrix diagonal and the purine A-G belong to another matrix diagonal. It is obvious that analogical unitary matrices are generated in this case. We do not consider such cases separately because they are identical to the previous case in general from the formal viewpoint.

9. About complementary palindromes, reproductions and the Rademacher genomatrices

One of important problems in molecular genetics is the problem of "complementary palindromes" in nucleotide sequences. In linguistics the notion "palindrome" means a rowthat is read identically in both directions (the words *civic, radar, level* are examples of linguistic palindromes). In genetics the notion "complementary palindrome" is important. By definition, a complementary palindrome is a row of DNA or RNA that becomes a simple palindrome if each symbol in one of halves of this row is replaced by its complementary symbol (in DNA the complementary pairs are A-T and C-G, and in RNA complementary pairs are A-U and C-G). For example CTCGCGAG is a complementary palindrome in DNA. Many complementary palindromes exist in DNA sequences. For example the fourth chromosome of the genome Arabidopsis th. contains the complementary palindrome TGTCGATCGACA which is repeated 194 times there [Gusev et al, 2009]. The problem of complementary palindromes in genetics is considered in many works (see for example [Gusev et al., 2009; Gusfield, 1999]).

This phenomenological problem has some unexpected relations with mathematical properties of the genomatrices [C T; A G]$^{(2)}$ and [C T; A G]$^{(3)}$ (Figure 1). On the base of these relations, mathematical models can be developed for a description of realizations of 2^n-dimensional vectors of the complementary-palindromic type together with a description of 2^n-reproductions of such 2^n-dimensional vectors. Let us consider these relations more attentively.

Figure 11 shows the genomatrix [C T; A G]$^{(3)}$ of 64 triplets where all the triplets with strong roots CC, CT, CG, AC, TC, GC, GT, GG are marked by black color. Figure 11 shows also the genomatrix [C A; T G]$^{(2)}$ of 16 duplets where all of these "strong" duplets CC, CT, CG, AC, TC, GC, GT, GG are marked by black color as well. From the viewpoint of the black-and-white mosaics, each row of these genomatrices corresponds to one of Rademacher functions which contains only elements "+1" and "-1". Figures 11 shows the Rademacher representations R_4 and R_8 of these genomatrices also.

$$[C\ T;\ A\ G]^{(2)}=$$

CC	CT	TC	TT
CA	CG	TA	TG
AC	AT	GC	GT
AA	AG	GA	GG

;

$$R_4 =$$

1	1	1	-1
-1	1	-1	-1
1	-1	1	1
-1	-1	-1	1

CCC	CCT	CTC	CTT	TCC	TCT	TTC	TTT
CCA	CCG	CTA	CTG	TCA	TCG	TTA	TTG
CAC	CAT	CGC	CGT	TAC	TAT	TGC	TGT
CAA	CAG	CGA	CGG	TAA	TAG	TGA	TGG
ACC	ACT	ATC	ATT	GCC	GCT	GTC	GTT
ACA	ACG	ATA	ATG	GCA	GCG	GTA	GTG
AAC	AAT	AGC	AGT	GAC	GAT	GGC	GGT
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG

$$R_8=$$

1	1	1	1	1	1	-1	-1
1	1	1	1	1	1	-1	-1
-1	-1	1	1	-1	-1	-1	-1
-1	-1	1	1	-1	-1	-1	-1
1	1	-1	-1	1	1	1	1
1	1	-1	-1	1	1	1	1
-1	-1	-1	-1	-1	-1	1	1
-1	-1	-1	-1	-1	-1	1	1

Figure 11 The genomatrices $[C\ T;\ A\ G]^{(2)}$ (in the upper row) and $[C\ T;\ A\ G]^{(3)}$ and their Rademacher representations R_4 and R_8 are shown. Black cells contain strong duplets CC, CT, CG, AC, TC, GC, GT, GG and triplets with these strong roots. Each column in R_4 and R_8 corresponds to one of Rademacher functions.

These Rademacher genomatrices R_4 and R_8 possess interesting properties. Firstly, their actions on the arbitrary 4-dimensional and 8-dimensional vectors $V_4 = [a_0\ \ a_1\ \ a_2\ \ a_3]$ and $V_8 = [a_0\ a_1\ a_2\ a_3\ a_4\ a_5\ a_6\ a_7]$ correspondingly are leading to new vectors in a form of complementary palindromes (Figure 12). Each of these new vectors becomes a simple palindrome by means of inversion of signs of all components in one of two its halves. In the case of 8-dimensional vectors on Figure 12, new palindromic vectors possess an additional peculiarity: each pair of adjacent members in such 8-dimensional palindromic vectors contains identical components.

4-dimensional vectors	Numeric example	$R_4*[3, -8, 5, 7]^T = [-7, -23, 23, 7]^T$
	General case	$R_4*[a_0, a_1, a_2, a_3]^T =$ $[a_0+a_1+a_2-a_3, -a_0+a_1-a_2-a_3, a_0-a_1+a_2+a_3, -a_0-a_1-a_2+a_3]^T$
8-dimensional vectors	Numeric example	$R_8*[3\ \ -8\ \ 5\ \ 7\ 6\ 9\ 1\ -4]^T =$ $= [25\ 25\ 55\ -5\ -5\ -25\ -25]^T$
	General case	$R_8*[a_0\ a_1\ a_2\ a_3\ a_4\ a_5\ a_6a_7]^T = [a_0+a_1+a_2+a_3+a_4+a_5-a_6-a_7,$ $a_0+a_1+a_2+a_3+a_4+a_5-a_6-a_7, -a_0-a_1+a_2+a_3-a_4-a_5-a_6-a_7,$ $-a_0-a_1+a_2+a_3-a_4-a_5-a_6-a_7, a_0+a_1-a_2-a_3+a_4+a_5+a_6+a_7, a_0+a_1-a_2-a_3+a_4+a_5+a_6+a_7, -a_0-a_1-a_2-a_3-a_4-a_5+a_6+a_7,$ $-a_0-a_1-a_2-a_3-a_4-a_5+a_6+a_7]^T$

Figure12. Transformations of arbitrary 4-dimensional and 8-dimensional vectors into vectors of the complementary-palindrome type. Complementary pairs of components in both halves of the vectors of the complementary-palindrome type are marked by identical colors. The symbol T over vectors means transpose of these vectors.

The second heuristic property of such Rademacher genomatrices R_4 and R_8 is the following. A repeating action of the genomatrix R_4 on any complementary-palindrome vector $[a_0,\ a_1,\ -a_1,\ -a_0]^T$ generates a dichotomous reproduction of this vector:

$$R_4*[a_0,\ a_1,\ -a_1,\ -a_0]^T = \mathbf{2}*[a_0,\ a_1,\ -a_1,\ -a_0] \qquad (5)$$

It can be used as a model of inherited dichotomous reproductions of biological cells in a course of mitosis when genetic materials are reproduced in dichotomous manner. One can mention else that each column of the Rademacher genomatrix R_4 is a complementary-palindrome vector itself. By this reason the exponentiation of this genomatrix generates its dichotomic reproduction also: $R_4{}^2 = \mathbf{2}*R_4$.

A similar situation exists for the Rademacher genomatrix R_8:

$$R_8*(R_8*[a_0\ a_1\ a_2\ a_3\ a_4\ a_5\ a_6 a_7]^T) = \mathbf{4}*R_8*[a_0\ a_1\ a_2\ a_3\ a_4\ a_5\ a_6\ a_7]^T \qquad (6)$$

It can be used as a model of inherited tetra-reproductions of germ cells in a course of meiosis when genetic materials are reproduced in tetra-reproduction manner (four germ cells arise from one germ cell in a course of meiosis). Each column of the Rademacher genomatrix R_8 is a complementary-palindrome vector itself. By this reason the exponentiation of this genomatrix generates its tetra-reproduction also: $R_8{}^2 = \mathbf{4}*R_8$.

The author's works [Petoukhov, 2011, 2012a] describes other interesting properties of these Rademacher genomatrices R_4 and R_8 which are close connected with special types of 4-dimensional and 8-dimensional hypercomplex numbers well-known in physics: split-quaternions and bi-split-quaternions by J.Cockle.

10 Transformations of the genomatrix [C T; A G]$^{(3)}$ by removing separate positions in the triplets

The mosaic genomatrix [C T; A G]$^{(3)}$ (Figure 11) possesses interesting properties relative to removing separate positions in its triplets (this method provides a positional convolution of each triplet into a corresponding duplet). This operation leads to new mosaic genomatrices (Figures 13-15) where the strong roots (the duplets CC, CT, CG, AC, TC, GC, GT, GG) are again marked by black color and the weak roots (CA, AA, AT, AG, TA, TT, TG, GA) are marked by white color. Removing the first positions of triplets in [C T; A G]$^{(3)}$ leads to the (8*8)-genomatrix of duplets (Figure 13, left) where each column corresponds to one of Rademacher functions relative to its black-and-white mosaic. Removing the second positions of triplets in [C T; A G]$^{(3)}$ leads to the (8*8)-genomatrix of duplets (Figure 14, left) where each column corresponds again to one of Rademacher functions relative to its black-and-white mosaic. Removing the third positions of triplets in [C T; A G]$^{(3)}$ leads to the (8*8)-genomatrix of duplets (Figure 15, left) where each column corresponds again to one of Rademacher functions relative to its black-and-white mosaic.

The Rademacher representations R1, R2 and R3 (Figure 13-15, right sides) of these new genomatrices and the Rademacher representation R_8 of the initial genomatrix [C T; A G]$^{(3)}$ possess some similar properties. For example, the exponentiation of these genomatrices R_8, R1, R2 and R3 generates their tetra-reproduction: $R_8{}^2=\mathbf{4}*R_8$, $R1^2=\mathbf{4}*R1$, $R2^2=\mathbf{4}*R2$ and $R3^2=\mathbf{4}*R3$. The dyadic-shift decomposition of each of these Rademacher genomatrices R1, R2 and R3 generates an individual set of 8 sparse matrices; each of these sets is closed relative to multiplication and its multiplication table is identical to the multiplication table of 8-dimensional hypercomplex numbers which are well-known in mathematics and physics under the name bi-split-quaternions by J.Cockle (see details in our works [Petoukhov, 2011, 2012a]).

CC	CT	TC	TT	CC	CT	TC	TT
CA	CG	TA	TG	CA	CG	TA	TG
AC	AT	GC	GT	AC	AT	GC	GT
AA	AG	GA	GG	AA	AG	GA	GG
CC	CT	TC	TT	CC	CT	TC	TT
CA	CG	TA	TG	CA	CG	TA	TG
AC	AT	GC	GT	AC	AT	GC	GT
AA	AG	GA	GG	AA	AG	GA	GG

1	1	1	-1	1	1	1	-1
-1	1	-1	-1	-1	1	-1	-1
1	-1	1	1	1	-1	1	1
-1	-1	-1	1	-1	-1	-1	1
1	1	1	-1	1	1	1	-1
-1	1	-1	-1	-1	1	-1	-1
1	-1	1	1	1	-1	1	1
-1	-1	-1	1	-1	-1	-1	1

Figure 13. Left: the transformation of the genomatrix [C T; A G]$^{(3)}$ (Figure 11) by means of removing the first position in each triplets. Right: the Rademacher form R1 of this new genomatrix (black and white cells contain elements +1 and -1 correspondingly). Explanations in the text.

CC	CT	CC	CT	TC	TT	TC	TT
CA	CG	CA	CG	TA	TG	TA	TG
CC	CT	CC	CT	TC	TT	TC	TT
CA	CG	CA	CG	TA	TG	TA	TG
AC	AT	AC	AT	GC	GT	GC	GT
AA	AG	AA	AG	GA	GG	GA	GG
AC	AT	AC	AT	GC	GT	GC	GT
AA	AG	AA	AG	GA	GG	GA	GG

1	1	1	1	1	-1	1	-1
-1	1	-1	1	-1	-1	-1	-1
1	1	1	1	1	-1	1	-1
-1	1	-1	1	-1	-1	-1	-1
1	-1	1	-1	1	1	1	1
-1	-1	-1	-1	-1	1	-1	1
1	-1	1	-1	1	1	1	1
-1	-1	-1	-1	-1	1	-1	1

Figure 14. Left: the transformation of the genomatrix [C T; A G]$^{(3)}$ (Figure 11) by means of removing the second position in each triplets. Right: the Rademacher form R2 of this new genomatrix (black and white cells contain elements +1 and -1 correspondingly). Explanations in the text.

CC	CC	CT	CT	TC	TC	TT	TT
CC	CC	CT	CT	TC	TC	TT	TT
CA	CA	CG	CG	TA	TA	TG	TG
CA	CA	CG	CG	TA	TA	TG	TG
AC	AC	AT	AT	GC	GC	GT	GT
AC	AC	AT	AT	GC	GC	GT	GT
AA	AA	AG	AG	GA	GA	GG	GG
AA	AA	AG	AG	GA	GA	GG	GG

1	1	1	1	1	1	-1	-1
1	1	1	1	1	1	-1	-1
-1	-1	1	1	-1	-1	-1	-1
-1	-1	1	1	-1	-1	-1	-1
1	1	-1	-1	1	1	1	1
1	1	-1	-1	1	1	1	1
-1	-1	-1	-1	-1	-1	1	1
-1	-1	-1	-1	-1	-1	1	1

Figure 15. Left: the transformation of the genomatrix [C T; A G]$^{(3)}$ (Figure 11) by means of removing the third position in each triplets. Right: the Rademacher form R3 of this new genomatrix (black and white cells contain elements +1 and -1 correspondingly). Explanations in the text.

The stability of algebraic properties of these genomatrices adds materials to the author's idea about importance of "positional languages" for molecular genetics or, in other words, to the idea of positioning of the binary languages in genetic sequences (we are talking about reading each of the three positions inside triplets based on one of the three pairs of binary sub-alphabets from Figure 2) [Petoukhov S.V., 2003, p. 14; 2008; 2012a; 2012b; Petoukhov, He, 2010].

This method of a positional convolution of triplets and other n-plets (or oligonucleotides) will be used in the next section to construct fractal genetic nets (FGN) as a new tool to reveal hidden rules of long nucleotide sequences.

11 Fractal genetic nets and the Symmetry Principles of long nucleotide sequences

On the base of his results in the field of matrix genetics, the author proposes a new notion "fractal genetic nets" (FGN) which is a useful tool to study long genetic sequences, first of all, to study symmetrical properties of long nucleotide sequences. In general case each variant of FGN is constructed by means of the author's "method of a positional convolution of long genetic sequences" to get a bunch of long sequences, each of which, respectively, shorter than the original sequence. In the particular case, this method lies in the positional convolution of long sequences of triplets through the removal or retention of individual positions (items) in each triplet by an analogy to the steps in the previous section (Figures 13-15).

In literature sources, long genetic sequences are termed those that contain no less that 50.000 nucleotides (see for example [Yamagishi, Herai, 2011]). In results of our preliminary researches of long nucleotide sequences of organisms of various taxonomic types, we reveal evidences of the author's hypothesis: hidden regularities of long genetic sequences are connected with fractal genetic nets (FGN); studying of long genetic sequences by means of using FGN allows discovering new hidden rules of living nature.

Let us explain a construction of FGN of various types on an example of FGN for sequences of triplets (Figure 16). Three positions in each triplet are numerated by numbers 0, 1 and 2 correspondingly. At the first level of a convolution, an initial long sequence S_0 of triplets is transformed by means of a positional convolution into three new sequences of nucleotides $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, each of which is shorter in 3 times in comparison with the initial sequence (numerator of the index in this notation of sequences shows the level of the convolution, and the denominator - the position of the triplets, which is used for the convolution): the sequence $S_{1/0}$ includes one by one all the nucleotides that are in the initial position "0" of triplets of the original sequence S_0; the sequence $S_{1/1}$ includes one by one all the nucleotides that are in the middle position "1" of triplets of the original sequence S_0; the sequence $S_{1/2}$ includes one by one all the nucleotides that are in the last position "2" of triplets of the original sequence S_0. At the final stage of the first level of the positional convolution, each of the sequences of nucleotides $S_{1/0}$, $S_{1/1}$, $S_{1/2}$ is represented as a sequence of triplets where three positions inside each triplets are numerated again by numbers 0, 1 and 2. To construct the second level of the convolution, each of the sequences $S_{1/0}$, $S_{1/1}$, $S_{1/2}$ is transformed by means of the same positional convolution in three new sequences: $S_{1/0}$ is convolved in $S_{2/00}$, $S_{2/01}$, $S_{2/02}$; $S_{1/1}$ − in $S_{2/10}$, $S_{2/11}$, $S_{2/12}$; $S_{1/2}$ − in $S_{2/20}$, $S_{2/21}$, $S_{2/22}$. The third level and subsequent levels of the convolution are constructed by analogy to form a multi-level net of sequences of nucleotides, which is termed "the fractal genetic net for the triplet convolution" or briefly "FGN-3" (Figure 16).
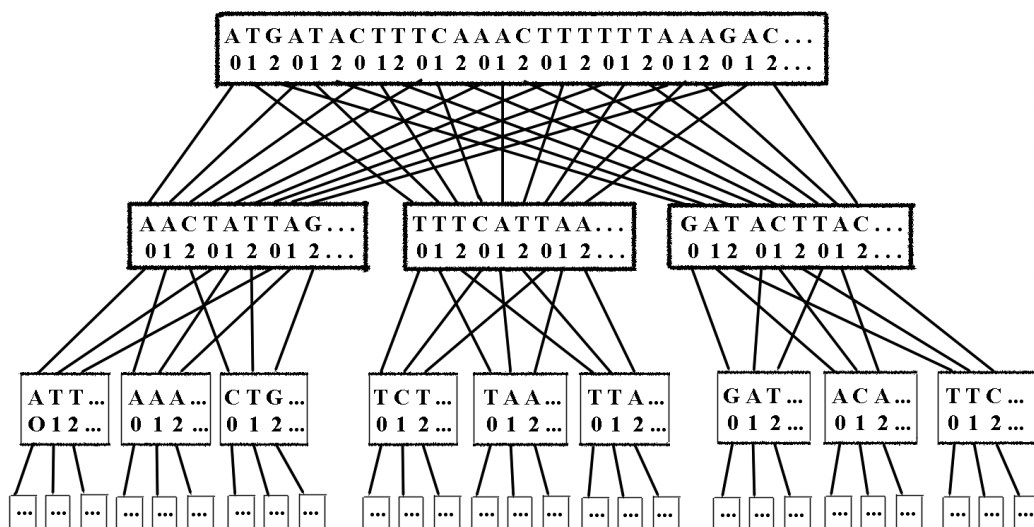

Figure 16. The scheme of the fractal genetic net (FGN-3) for a sequence of triplets

This FGN possesses a fractal-like character if the numeration of positions is only taken into account: each of long sequences of this FGN can be taken as an initial sequence to form a similar genetic net on its basis (Figure 17). In general case, the FGN can be built not only for triplets, but also for other n-plets (n = 2, 4, 5, ...) or oligonucleotides by means of a repeated positional convolution of each of sequences from the previous level into "n" sequences of the next level of the convolution. In this way one can built FGN-2, FGN-4, FGN-5, etc. for n=2, 3, 4, 5,… correspondingly. (Each of these FGN-2, FGN-3, FGN-4, FGN-5, etc. is a tree, but all of them form a net of separate trees; in a wide sense, FGN is the complete set of such separate trees). But this article describes some our results only for the FGN-3.
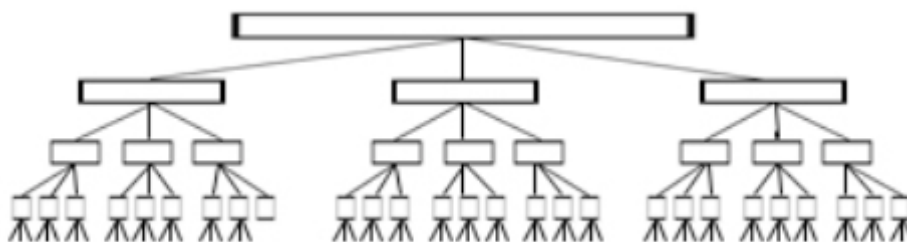

Figure 17. The fractal scheme of the triple branching in the case of the FGN-3

To test the author's hypothesis that structures of long nucleotide sequences of different organisms are connected with fractal genetic nets (first of all with FGN-3), we analyze an implementation of the known «Symmetry Principle» [Yamagishi, Herai, 2011, p.2] for long nucleotide sequences of different levels of a positional convolution in the fractal genetic net for the triplet convolution (FGN-3). Let us remind briefly about this Symmetry Principle which was studied or described in many publications [Bell, Forsdyke, 1999; Chargaff, 1971, 1975; Dong, Cuticchia, 2001; Forsdyke, 2002; Forsdyke, Bell, 2004; Kong, et al. 2009; Mitchell, Bridge, 2006; Prabhu, 1993; Sueoka, 1999; Yamagishi, Herai, 2011].

The Chargaff's first parity rule speaks that in any double-stranded DNA segment, the quantities (or frequencies) of adenine and thymine are equal, and so are the frequencies of cytosine and guanine [Chargaff, 1950]. This rule was used by Watson and Crick to support their famous DNA double-helix structure model [Watson & Crick, 1953]. Chargaff also perceived that the parity rule approximately holds in the single-stranded DNA segment. This last rule is known as Chargaff's second parity rule (CSPR), and it has been confirmed in several organisms [Mitchell & Bride, 2006]. Originally, CSPR is meant to be valid only to mononucleotide frequencies (that is quantities of monoplets) in the single-stranded DNA. “*But, it occurs that oligonucleotide frequencies follow a generalized Chargaff's second parity rule (GCSPR) where the frequency of an oligonucleotide is approximately equal to its complement reverse oligonucleotide frequency [Prahbu, 1993]. This is known in the literature as the Symmetry Principle*” [Yamagishi, Herai, 2011, p. 2]. The work [Prahbu, 1993] shows the implementation of the Symmetry Principle in long DNA-sequences for cases of complementary reverse n-plets with n = 2, 3, 4, 5 at least.

In our article we use two different notions of complementary oligonucleotides (or n-plets): 1) complementary oligonucleotides in a traditional sense (for example ACGTG and TGCAC are the pair of complementary oligonucleotides in a traditional sense); 2) complementary reverse oligonucleotides or briefly CR-oligonucleotides or reverse complements (for example ACGTG and CACGT are the pair of CR-oligonucleotides). The mentioned Symmetry Principle has been revealed for pairs of CR-oligonucleotides. Taking this into account we began testing the author's hypothesis by means of analyzing frequencies (or quantities) of all variants of pairs of CR-oligonucleotides in long DNA-sequences of different organisms at different levels of their FGN. We test frequencies of n-plets in the FGN-3 with n =

1, 2, 3, 4, 5 only because of our computer limitations, but we suppose that our described results for FGN-3 hold true also for n > 5. Initial nucleotide sequences for testing are taken from http://www.ncbi.nlm.nih.gov/. To test the author's hypothesis we use a special software written by V.I.Svirin on the basis of the computer language Python under the technical project by the author.

In the result of our preliminary studies we have revealed the following: 1) the Symmetry Principle for pairs of CR-oligonucleotides is realized in each of long nucleotide sequences at different levels of the convolution in FGN-3 (the length of oligonucleotides or n-plets under consideration is equal to n = 1, 2, 3, 4, 5 at least); 2) a series of new Symmetry Principles exists in those initial long nucleotide sequences where the famous Symmetry Principle for pairs of CR-oligonucleotides is performed; 3) each of these new Symmetry Principles is performed for n-plets in each of long nucleotide sequences at different levels of the convolution in FGN-3 (n = 1, 2, 3, 4, 5 at least).

Let us take for example the long nucleotide sequence of Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1 http://www.ncbi.nlm.nih.gov/nuccore/294155300). This sequence contains 934379 nucleotides. Figure 18 shows realisations of the known Symmetry Principle (we'll name it as the Symmetry Principle №1) in the 13 sequences of the first three levels of convolution in the FGN-3 of this genome. It displays the number of occurences of 32 triplets (AAA, AAC, AAG, AAT, ACA, ACC, ACG, ACT, AGA, AGC, AGG, ATA, ATC, ATG, CAA, CAC, CAG, CCA, CCC, CCG, CGA, CGC, CTA, CTC, GAA, GAC, GCA, GCC, GGA, GTA, TAA, TCA) and their 32 CR-triplets (TTT, GTT, CTT, ATT, TGT, GGT, CGT, AGT, TCT, GCT, CCT, TAT, GAT, CAT, TTG, GTG, CTG, TGG, GGG, CGG, TCG, GCG, TAG, GAG, TTC, GTC, TGC, GGC, TCC, TAC, TTA, TGA) in the long sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, $S_{2/01}$, $S_{2/02}$, $S_{2/10}$, $S_{2/11}$, $S_{2/12}$, $S_{2/20}$, $S_{2/21}$, $S_{2/22}$ at the first three levels of the FGN-3 (a limited volume of the article doesn't allow showing other levels of this FGN).

The straight line in each frame is of slope 1 (it is a bisector of the coordinate angle). Each dot in a frame represents one pair "triplet and CR-triplet"; its coordinate X shows number of occurences (or the frequence) of the triplet, and its coordinate Y shows number the frequence of its CR-triplet on the same strand of the sequence. Each frame contains all 32 pairs «triplet and its CR-triplet». The dots agglutinate at the line of slope 1, demonstrating that amounts of occurrences (or frequences) of two members of each of 32 pairs «triplet and its CR-triplet» are aproximately equal in each of the sequences at each of the levels of convolution in the FGN-3. It means that the Symmetry Principle №1 is performed for each of these sequences.
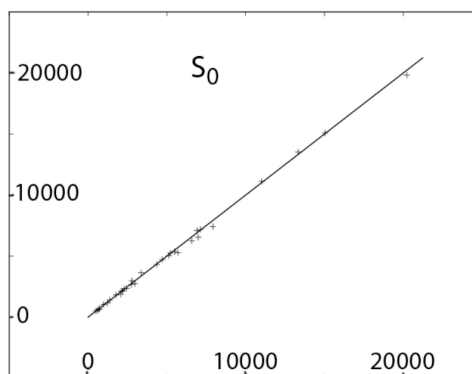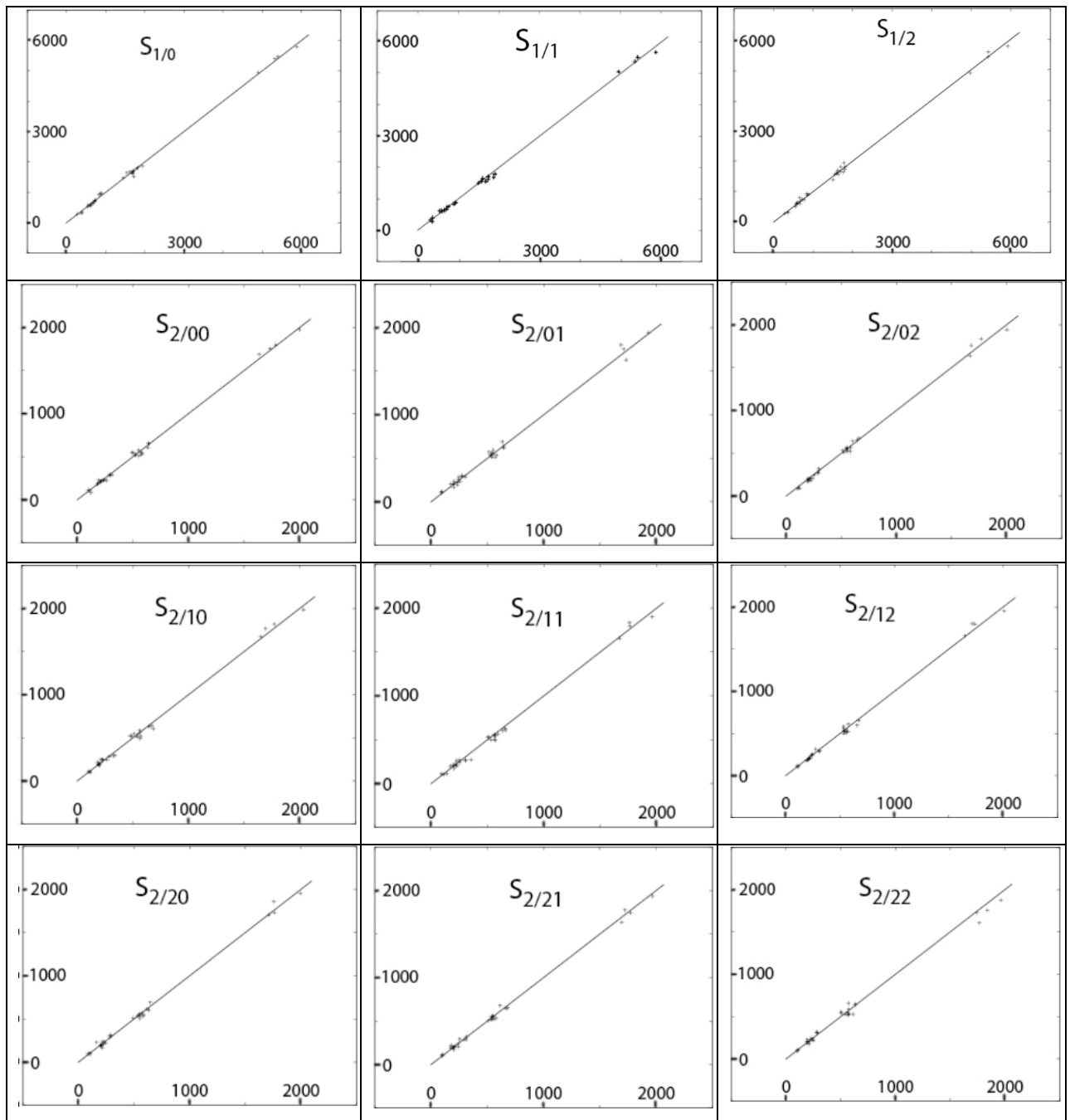
Figure 18. Realizations of the Symmetry Principle №1 in the long sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, $S_{2/01}$, $S_{2/02}$, $S_{2/10}$, $S_{2/11}$, $S_{2/12}$, $S_{2/20}$, $S_{2/21}$, $S_{2/22}$ at the first three levels of the FGN-3 for Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1   http://www.ncbi.nlm.nih.gov/nuccore/294155300). The initial sequence S_0 contains 934379 nucleotides.

On this basis the author notes existence of
the generalized Symmetry Principle № 1:
- in long nucleotide sequences at different levels of convolution in FGN-3, oligonucleotide frequencies follow a generalized Chargaff's second parity rule where the frequency of each oligonucleotide is approximately equal to its complement reverse oligonucleotide frequency.

Now let us describe new Symmetry Principles discovered by us for long nucleotide sequences in a connection with obtained results of matrix genetics.

The Symmetry Principle № 2 (concerning to FGN): the frequency of each oligonucleotide is approximately the same in all the long nucleotide sequences of each of levels of FGN-3.

Figure 19 shows an example of frequencies of the triplet ACG in 40 long nucleotide sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, $S_{2/01}$, $S_{2/02}$, $S_{2/10}$, $S_{2/11}$, $S_{2/12}$, $S_{2/20}$, $S_{2/21}$, $S_{2/22}$, ….., $S_{3/221}$, $S_{3/222}$ at the first four levels of the FGN-3 of the same initial sequences as on Figure 18.
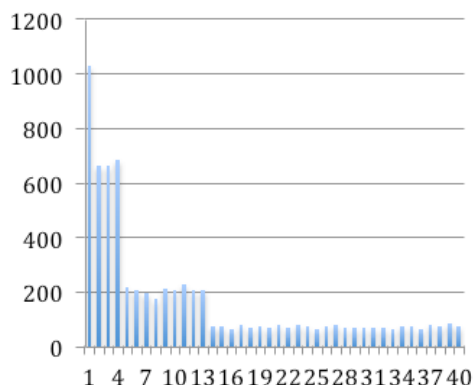

Figure 19. Frequencies of the triplet ACG in 40 long nucleotide sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, $S_{2/01}$, $S_{2/02}$, $S_{2/10}$, $S_{2/11}$, $S_{2/12}$, $S_{2/20}$, $S_{2/21}$, $S_{2/22}$, ….., $S_{3/221}$, $S_{3/222}$ at the first four levels of the FGN-3 of Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1 http://www.ncbi.nlm.nih.gov/nuccore/294155300). Coordinates X show the 40 sequences and coordinate Y show appropriate frequencies of the triplet ACG in them.

Figure 20 shows examples of frequencies of all 64 triplets in 13 long nucleotide sequences at the first three levels of FGN-3 of the same genome.

	S_0	$S_{1/0}$	$S_{1/1}$	$S_{1/2}$	$S_{2/00}$	$S_{2/01}$	$S_{2/02}$	$S_{2/10}$	$S_{2/11}$	$S_{2/12}$	$S_{2/20}$	$S_{2/21}$	$S_{2/22}$
AAA	19832	5786	5679	5768	1975	1944	1944	1986	1899	1952	1954	1935	1876
AAC	6246	1709	1707	1643	550	560	567	587	543	557	504	531	534
AAG	7087	1859	1783	1940	607	619	651	607	630	611	615	679	649
AAT	15037	5320	5352	5428	1784	1685	1769	1770	1758	1743	1757	1775	1742
ACA	5049	1527	1564	1635	542	513	546	492	566	521	537	517	519
ACC	2363	747	755	747	233	253	266	241	273	253	231	203	236
ACG	1029	660	663	684	214	205	197	175	210	208	228	203	203
ACT	4714	1713	1745	1702	526	548	553	536	568	544	552	537	506
AGA	5272	1784	1688	1737	657	635	640	631	600	598	691	644	638
AGC	2754	590	623	586	226	216	200	220	199	181	198	223	204
AGG	2150	973	880	912	293	294	322	292	259	287	314	288	307
AGT	4713	1700	1704	1820	530	595	543	513	492	523	562	549	543
ATA	11126	4952	5051	4886	1688	1629	1637	1671	1655	1659	1706	1635	1606
ATC	5250	1619	1570	1568	507	537	511	518	527	583	531	522	549
ATG	5499	1450	1488	1505	494	547	582	510	529	538	551	514	539
ATT	15079	5397	5390	5419	1797	1802	1835	1816	1832	1799	1857	1745	1726

CAA	7427	1620	1615	1661	526	538	568	565	502	508	540	561	529
CAC	1872	700	746	733	225	236	201	255	262	243	222	238	224
CAG	2105	553	653	605	212	206	211	205	203	221	197	203	249
CAT	5375	1473	1497	1388	547	546	519	548	497	539	543	507	528
CCA	2750	727	712	664	235	248	252	267	252	246	218	255	238
CCC	569	522	622	513	181	166	170	188	198	183	164	196	174
CCG	681	336	390	326	81	113	84	105	109	118	94	109	108
CCT	2181	887	945	885	292	277	293	323	302	307	281	292	286
CGA	1171	635	607	600	189	208	178	196	207	194	204	208	200
CGC	508	321	341	319	106	113	89	104	101	107	109	116	94
CGG	693	402	365	366	124	93	102	121	137	105	85	97	109
CGT	989	671	663	684	214	175	194	199	189	215	164	204	190
CTA	4326	1664	1659	1562	545	515	520	526	532	542	543	524	523
CTC	1786	832	893	841	310	306	295	289	306	316	283	312	279
CTG	2115	577	647	636	215	236	206	207	172	211	196	173	222
CTT	6917	1950	1913	1785	635	646	641	684	653	577	617	614	632
GAA	7190	1823	1801	1812	651	689	675	640	610	655	602	654	660
GAC	1404	585	598	611	208	204	178	195	223	208	189	201	185
GAG	1820	932	833	930	289	289	274	284	275	295	291	291	315
GAT	5225	1664	1563	1555	555	530	523	488	507	534	577	557	564
GCA	2974	572	580	631	228	195	197	241	210	196	196	198	227
GCC	710	276	353	288	97	91	110	102	92	118	106	99	106
GCG	497	377	321	361	113	97	121	109	108	109	103	104	102
GCT	2973	622	582	585	227	233	218	181	227	192	207	178	198
GGA	2330	958	875	888	283	302	296	297	272	316	308	318	317
GGC	676	286	275	283	115	110	100	112	112	108	93	104	97
GGG	616	551	546	555	185	200	193	187	170	200	215	174	209
GGT	2446	733	755	728	246	240	281	232	249	246	229	243	227
GTA	3636	1680	1606	1709	516	537	532	518	544	501	513	546	555
GTC	1374	601	577	578	199	198	218	194	217	226	202	203	190
GTG	2083	711	720	777	265	257	238	219	226	237	244	239	243
GTT	6587	1694	1736	1770	575	541	553	560	559	530	551	577	574
TAA	13334	5401	5418	5430	1732	1708	1678	1693	1760	1717	1762	1723	1839
TAC	3369	1625	1685	1624	520	528	509	571	571	535	492	554	501
TAG	4368	1685	1596	1641	498	538	556	475	505	561	587	544	572
TAT	11019	4895	4950	4973	1635	1730	1667	1648	1672	1649	1711	1695	1767
TCA	6993	1542	1679	1586	549	514	546	542	559	575	573	542	570

TCC	2302	872	904	854	291	276	293	340	353	277	295	316	283
TCG	1240	681	662	669	183	201	204	193	204	206	220	212	214
TCT	5710	1794	1866	1798	639	645	600	646	634	658	647	669	632
TGA	6550	1642	1533	1602	577	570	560	530	557	525	568	556	590
TGC	2790	616	610	611	190	233	201	219	219	213	205	191	194
TGG	2658	720	689	796	222	285	245	246	241	240	239	293	242
TGT	5123	1727	1583	1619	585	568	547	565	592	546	531	536	566
TTA	13519	5470	5525	5585	1755	1753	1760	1765	1793	1802	1733	1777	1758
TTC	7131	1839	1864	1809	644	631	659	669	660	672	632	680	571
TTG	7918	1700	1745	1689	576	579	583	563	562	559	541	553	612
TTT	20219	5886	5876	5921	1997	1929	2004	2034	1960	2010	1995	1969	1963

Figure 20. The table of frequencies of 64 triplets in long nucleotide sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, $S_{2/01}$, $S_{2/02}$, $S_{2/10}$, $S_{2/11}$, $S_{2/12}$, $S_{2/20}$, $S_{2/21}$, $S_{2/22}$ at the first three levels of FGN-3 of Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1 http://www.ncbi.nlm.nih.gov/nuccore/294155300).

The Symmetry Principle № 3: for each of long nucleotide sequences at each level of FGN-3 the following rules hold true: sum of the frequencies of all the oligonucleotides, that begin with the letter A, approximately equal to the sum of the frequencies of all the oligonucleotides that begin with the letter T; sum of the frequencies of all the oligonucleotides, that begin with the letter C, approximately equal to the sum of the frequencies of all the oligonucleotides that begin with the letter T.

In particularly, these rules hold true not only for long sequences at lower levels of FGN-3 but also for an initial long sequence S_0. Figure 21 illustrates the Symmetry Principle № 3 by examples of n-plets (n=2, 3, 4, 5) in sequences S_0, $S_{1/0}$,…, $S_{2/22}$ of the first levels in FGN-3 of the same genome as on Figures 18-20.

The total frequencies of the sets of duplets in sequences of FGN-3:

	S_0	$S_{1/0}$	$S_{1/1}$	$S_{1/2}$	$S_{2/00}$	$S_{2/01}$	$S_{2/02}$	$S_{2/10}$	$S_{2/11}$	$S_{2/12}$	$S_{2/20}$	$S_{2/21}$	$S_{2/22}$
F(A)	169757	56674	56197	56747	19065	18857	18836	18764	18756	18713	18949	18815	18871
F(T)	171420	57022	57247	57179	18870	18937	19067	19102	19155	19040	19161	19105	19083
F(C)	62531	20763	21486	20600	6929	6903	6882	7113	7148	7178	6772	6900	6800
F(G)	63471	21265	20794	21198	7044	7211	7123	6929	6849	6977	7026	7088	7154

The total frequencies of the sets of triplets in sequences of FGN-3:

	S_0	$S_{1/0}$	$S_{1/1}$	$S_{1/2}$	$S_{2/00}$	$S_{2/01}$	$S_{2/02}$	$S_{2/10}$	$S_{2/11}$	$S_{2/12}$	$S_{2/20}$	$S_{2/21}$	$S_{2/22}$
F(A)	113200	37786	37642	37980	12623	12582	12763	12565	12540	12557	12788	12500	12377
F(T)	114243	38095	38185	38207	12593	12688	12612	12699	12842	12745	12731	12810	12874
F(C)	41465	13870	14268	13568	4637	4622	4523	4782	4622	4632	4460	4609	4585
F(G)	42541	14065	13721	14061	4752	4713	4707	4559	4601	4671	4626	4686	4769

The total frequencies of the sets of 4-plets in sequences of FGN-3:

	S_0	$S_{1/0}$	$S_{1/1}$	$S_{1/2}$	$S_{2/00}$	$S_{2/01}$	$S_{2/02}$	$S_{2/10}$	$S_{2/11}$	$S_{2/12}$	$S_{2/20}$	$S_{2/21}$	$S_{2/22}$
F(A)	84955	28475	27999	28493	9522	9391	9274	9342	9417	9434	9453	9379	9371
F(T)	85573	28439	28601	28639	9531	9532	9624	9552	9570	9538	9663	9573	9555
F(C)	31189	10286	10758	10270	3409	3438	3499	3573	3578	3594	3331	3423	3356
F(G)	31867	10662	10504	10460	3492	3593	3557	3487	3389	3388	3507	3579	3672

The total frequencies of the sets of 5-plets in sequences of FGN-3:

	S_0	$S_{1/0}$	$S_{1/1}$	$S_{1/2}$	$S_{2/00}$	$S_{2/01}$	$S_{2/02}$	$S_{2/10}$	$S_{2/11}$	$S_{2/12}$	$S_{2/20}$	$S_{2/21}$	$S_{2/22}$
F(A)	67729	22626	22512	22788	7551	7506	7542	7491	7417	7431	7587	7445	7539
F(T)	68688	22951	22918	22764	7620	7613	7684	7626	7668	7677	7619	7700	7534

F(C)	25144	8242	8503	8217	2780	2762	2701	2851	2907	2849	2704	2785	2736
F(G)	25304	8470	8356	8520	2812	2882	2836	2795	2771	2806	2853	2833	2954

Figure 21. The illustration of the Symmetry Principle № 3 in the case of Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1 http://www.ncbi.nlm.nih.gov/nuccore/294155300). Here F(A), F(T), F(C) and F(G) mean sum of the frequencies of oligonucleotides (or n-plets) that begin with the letters A, T, C or G correspondingly. The tables show the $F(A) \approx F(T)$ and $F(C) \approx F(G)$ for sets of n-plets (n=2, 3, 4, 5) in each of long nucleotide sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, $S_{2/01}$, $S_{2/02}$, $S_{2/10}$, $S_{2/11}$, $S_{2/12}$, $S_{2/20}$, $S_{2/21}$, $S_{2/22}$ at the first three levels of FGN-3 of this genome.

One can note that each of 4 quadrants of the genomatrices $[C\ T;\ A\ G]^{(n)}$ (Figure 1) contain all oligonucleotides that begin with one of these 4 letters C, T, A or G. In these genomatrices each oligonucleotide and its complementary oligonucleotide are disposed inverse-symmetrical relative to the centre of the appropriate matrix. In accordance with the Symmetry Principle № 3, the total frequencies of oligonucleotides in both quadrants along the main diagonal of these gemomatrices are approximately equal each other ($F(C) \approx F(G)$); the total frequencies of oligonucleotides in both quadrants along the second diagonal of these gemomatrices are also approximately equal each other ($F(A) \approx F(T)$).

An additional illustration of the Symmetry Principle № 3 is obtained from data about the whole human genome from the work [Perez, 2010]. This genome contains 2.843.411.612 triplets. Figure 22 shows the total frequencies of sets of triplets that begin with one of the four letters A, C, G or T.

The total frequencies of the sets of triplets that begin with A	The total frequencies of the sets of triplets that begin with T
f(ACC+ACT+ACA+ACG+ ATC+ATT+ATA+ATG+ AAC+AAT+AAA+AAG+ AGC+AGT+AGA+AGG)= **839.827.642**	f(TGG+TGA+TGT+TGC+ TAG+TAA+TAT+TAC+ TTG+TTA+TTT+TTC+ TCG+TCA+TCT+TCC)= **841.214.589**

The total frequencies of the sets of triplets that begin with C:	The total frequencies of the sets of triplets that begin with G:
f(CCC+CCT+CCA+CCG+ CTC+CTT+CTA+CTG+ CAC+CAT+CAA+CAG+ CGC+CGT+CGA+CGG) = **581.026.275**	f(GGG+GGA+GGT+GGC+ GAG+GAA+GAT+GAC+ GCG+GTA+GTT+GTC+ GTG+GCA+GCT+GCC)= **581.343.106**

Figure 22. The approximate equality of the total frequencies of sets of triplets that begin with letters A and T (upper table) and with letters C and G (bottom table) in the case of the whole human genome. Initial data about frequencies of separate triplets are taken from the work [Perez, 2010].

The Symmetry Principle № 3 speaks about pairs of complete sets of complementary olygonucleotides that begin with complementary letters (A=T and C=G). If one consider sub-sets of complementary oligonucleotides from these complete sets, the equality of their total frequences is violated, and this violation is the more the less scale of sub-sets is under consideration. For example, in the case of FGN-3 of long nucleotide sequences, the equality of the total frequencies of two sets of 4 pentaplets, which are disposed in two complementary (2*2)-sub-sub-quadrants of the matrix $[C\ T;\ A\ G]^{(5)}$, is performed less accurately than the

equality of the total frequencies of two sets of 16 pentaplets in two complementary (4*4)-sub-quadrants in this matrix.

The author would like to mention about the additional Symmetry Principles № 4, which can be interpreted as simple consequences of the generalized Symmetry Principle № 1 and the Symmetry Principle № 2, though today it is difficult to say what of these Principles are more fundamental. Our article [Petoukhov, 2012a, http://arxiv.org/abs/1102.3596] describes the method of dyadic-shift numeration of triplets inside genomatrices [C A; G T]$^{(3)}$ and [C T; G A]$^{(3)}$ on the base of the binary-oppositional attributes of nucleotides A, C, G, T. In the result, the sets of 8 triplets with identical dyadic-shift numerations 000, 001,…., 111 arise, and they obey the following rule in long nucleotide sequences: the frequency of triplets with a dyadic shift numeration (for example "010") is approximately equal to the frequency of the triplet with inverse dyadic shift numeration ("101" in this example) (other oligonucleotides can be dyadic-shift numerated by analogy). Inverse numeration is produced by replacement of numbers 0➔1 and 1➔0. Such sets of oligonucleotides are main participants in the **Symmetry Principle № 4**:
- for each of long nucleotide sequences at each level of FGN-3, the total frequency of each set of oligonucleotides, which have the same dyadic-shift numeration on the base of the method of such numeration from the work [Petoukhov, 2012a], is equal approximately to the total frequency of the set of oligonucleotides, which have inverse dyadic-shift numeration.

Now let us represent the Symmetry Principle № 5 which speaks about reading frame shifts, deletion mutations and also positional permutations in oligonucleotides. Concerning those DNA-sequences (including the mentioned genome on Figures 18-21), which have been tested till today in the author's laboratory, we have revealed the following phenomenological facts (this study is continued now for a wide list of DNA-sequences of different organisms and organelles):
- a transformation of long nucleotide sequences by means of a reading frame shift in them preserves implementations of all described Symmetry Principles inside new long nucleotide sequences (in our tests, a reading frame shift means that the reading of sequence does not begin with its first position, but with one of subsequent positions; the missing fragment of the sequence can be moved into the end of the sequence, and in this case a reading frame shift leads to a simple change of order of all sequences at each of lower levels of FGN);
- a transformation of long nucleotide sequences by means of a deletion mutation (when their short parts are missing) preserves implementations of all described Symmetry Principles in new long nucleotide sequences.

One should consider separately the question about positional permutations in oligonucleotides. The theory of noise-immunity coding pays a special attention to permutations of elements of transmitted signals. It is obvious that for different n-plets different quantities of variants of permutation of their positions exist:
- for duplets two variants of positional permutations exist (1-2 and 2-1);
- for triplets six variants of positional permutations exist (1-2-3, 2-3-1, 3-1-2, 3-2-1, 2-1-3, 1-3-2);
- for 4-plets 24 variants of positional permutations exist (1-2-3-4, 2-3-4-1, …..);
- for 5-plets 120 variants of positional permutations exist (1-2-3-4-5, 2-3-4-5-1, …..).

It is also obvious that if a long nucleotide sequence is interpreted as a sequence of a certain type of oligonucleotides (duplets, or triplets, or 4-plets, or 5-plets, …), and one of possible positional permutations is done simultaneously inside all of its oligonucleotides, then a quite new long nucleotide sequence appears. For example if we have initially a sequence of triplets CGA-TAA-AGC-GTC-TAG-CGC-ATC -…, then after changing of the positional order from the initial order 1-2-3 to new order 2-3-1 inside each of triplets, we obtain the quite different sequence GAC-AAT-GCA-TCG-AGT-GCC-TCA -… . But FGN-3 for this new long

nucleotide sequence is obeyed the same Symmetry Principles №№ 1-3 which are described above. We name simultaneous positional permutations inside all oligonucleotides of a certain type as "collective positional permutations" inside these oligonucleotides. The author proposes a brief formulation of these phenomenological facts by the following way.

The Symmetry Principle № 5:
- reading frame shifts and deletion mutations in long nucleotide sequences and also collective positional permutations inside their oligonucleotides don't essentially violate implementations of all the Symmetry Principles described in this article for long nucleotide sequences and their fractal genetic net (FGN-3).

It appears that the described FGN-3 and fractal-like properties of long genetic sequences, which are related to the invariance of these Symmetry Principles, have a biological value (a biological sense) associated with mutational changes of such sequences and with evolutionary producing new types of DNA-sequences. The author supposes that mechanisms of biological evolution use these permutational and other described properties of long nucleotide sequences in producing new biological organisms and organelles. For instance new DNA-sequences can be constructed in the course of biological evolution of organisms by means of combinatorics of nucleotide sequences from different levels of FGN (including genetic crossing among long nucleotide sequences from different levels of FGN by analogy with well-known examples of genetic crossing). One should note here that the question about permutational properties of DNA-sequences is very important because some biological organisms differ each from other only by permutations in their DNA-sequences (see for example the book [Pevzner, 2000]). The proposed method of FGN is the new effective and useful method in the field of bioinformatics, molecular genetics and evolutionary biology.

The author supposes that for long nucleotide sequences the following Symmetry Principle № 6 exists also, which compares a total frequency F_{even} of all n-plets (oligonucleotides) in columns with even numerations in matrices $[C\ T;\ A\ G]^{(n)}$ (n=1, 2, 3, …) with a total frequency F_{odd} of all n-plets in columns with odd numerations in the same matrices. Let us numerate columns from left to right in these matrices by numbers 0, 1, 2, 3, … and then let us pay our attention separately to the first set of n-plets in columns with even numeration (0, 2, 4, …) and to the second set of n-plets in columns with odd numeration. We name conditionally the first set as the set of the even type (or briefly, the even-set) and the second set as the set of the odd type (or the odd-set). For example, the genomatrix $[C\ T;\ A\ G]^{(2)}$ contains two sets of duplets (Figure 11): 1) the even-set, which represents the columns with even numerations 0 and 2, contains the 8 duplets (CC, CA, AC, AA, TC, TA, GC, GA); 2) the odd-set, which represents the columns with odd numerations 1 and 3, contains the 8 duplets (CT, CG, AT, AG, TT, TG, GT, GG). Or in the genomatrix $[C\ T;\ A\ G]^{(3)}$ we have two sets of triplets (Figure 11): 1) the even-set, which represents the columns with even numerations 0, 2, 4, 6, contains the 32 triplets (CCC, CCA, CAC, CAA, ACC, ACA, AAC, AAA, CTC, CTA, CGC, CGA, ATC, ATA, AGC, AGA, TCC, TCA, TAC, TAA, GCC, GCA, GAC, GAA, TTC, TTA, TGC, TGA, GTC, GTA, GGC, GGA); 2) the odd-set, which represents the columns with odd numerations 1, 3, 5, 7, contains the 32 triplets (CCT, CCG, CAT, CAG, ACT, ACG, AAT, AAG, CTT, CTG, CGT, CGG, ATT, ATG, AGT, AGG, TCT, TCG, TAT, TAG, GCT, GCG, GAT, GAG, TTT, TTG, TGT, TGG, GTT, GTG, GGT, GGG).

We are studying of long nucleotide sequences to compare the total frequencies F_{even} and F_{odd} of n-plets from the even-sets and from the odd-sets at different levels of FGN-3. Our initial research results confirm that these frequencies are approximately equal. Figure 23 confirms this fact for the case of duplets from the even-set and the odd-set of sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, …, $S_{3/222}$ at the first four levels of the FGN-3 of the above-considered Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1 http://www.ncbi.nlm.nih.gov/nuccore/294155300). More precisely, Figure 23 shows percentage

differences between the total frequencies F_{even} and F_{odd} of duplets from the even-set and the odd-set of the Mycoplasma crocodyli MP145 chromosome. Here F_{odd} is taken as 100%, and its percentage difference Δ in relation to F_{even} is calculated in each case by means of the formula $\Delta = 100*(1 - F_{evev}/F_{odd})$. For example, in the initial nucleotide sequence S_0, duplets from the even-set are met 232415 times (F_{even}=232415) and duplets from the odd-set are met 234764 times (F_{odd}=234764). In accordance with the formula we have $\Delta S_0 = 100*(1 - 232415/234764) = 1,001\%$ (see ΔS_0 in Figure 23).

ΔS_0	$\Delta S_{1/0}$	$\Delta S_{1/1}$	$\Delta S_{1/2}$	$\Delta S_{2/0}$	$\Delta S_{2/01}$	$\Delta S_{2/02}$	$\Delta S_{2/10}$
1,001%	1,618%	0,259%	1,598%	2,225%	1,749%	1,142%	-0,611%

$\Delta S_{2/11}$	$\Delta S_{2/12}$	$\Delta S_{2/20}$	$\Delta S_{2/21}$	$\Delta S_{2/22}$	$\Delta S_{3/000}$	$\Delta S_{3/001}$	$\Delta S_{3/002}$
0,300%	0,997%	0,974%	-0,008%	1,991%	0,737%	0,438%	2,781%

$\Delta S_{3/010}$	$\Delta S_{3/011}$	$\Delta S_{3/012}$	$\Delta S_{3/020}$	$\Delta S_{3/021}$	$\Delta S_{3/022}$	$\Delta S_{3/100}$	$\Delta S_{3/101}$
1,446%	1,605%	1,332%	0,553%	1,309%	0,461%	-3,362%	0,415%

$\Delta S_{3/102}$	$\Delta S_{3/110}$	$\Delta S_{3/111}$	$\Delta S_{3/112}$	$\Delta S_{3/120}$	$\Delta S_{3/121}$	$\Delta S_{3/122}$	$\Delta S_{3/200}$
-0,510%	0,783%	0,392%	0,046%	1,423%	0,966%	1,058%	1,241%

$\Delta S_{3/201}$	$\Delta S_{3/202}$	$\Delta S_{3/210}$	$\Delta S_{3/211}$	$\Delta S_{3/212}$	$\Delta S_{3/220}$	$\Delta S_{3/221}$	$\Delta S_{3/222}$
3,3640%	2,601%	0,507%	1,149%	0,069%	4,7188%	0,966%	2,894%

Figure 23. Percentage differences Δ between the total frequencies F_{even} and F_{odd} of duplets from the even-set of duplets (CC, CA, AC, AA, TC, TA, GC, GA) and from the odd-set of duplets (CT, CG, AT, AG, TT, TG, GT, GG) in sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, …, $S_{3/222}$ at the first four levels of the FGN-3 of the Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1 http://www.ncbi.nlm.nih.gov/nuccore/294155300). The initial sequence S_0 contains 934379 nucleotides. Percentages are shown with a precision up to three decimal places.

Data of Figure 24 confirms the approximate equality of F_{even} and F_{odd} of triplets in the same sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, …, $S_{3/222}$ at the first four levels of the FGN-3 of the Mycoplasma crocodyli MP145 chromosome.

ΔS_0	$\Delta S_{1/0}$	$\Delta S_{1/1}$	$\Delta S_{1/2}$	$\Delta S_{2/0}$	$\Delta S_{2/01}$	$\Delta S_{2/02}$	$\Delta S_{2/10}$
1,455%	1,472%	0,741%	2,074%	0,605%	1,679%	2,359%	-0,713%

$\Delta S_{2/11}$	$\Delta S_{2/12}$	$\Delta S_{2/20}$	$\Delta S_{2/21}$	$\Delta S_{2/22}$	$\Delta S_{3/000}$	$\Delta S_{3/001}$	$\Delta S_{3/002}$
-0,830%	0,179%	2,268%	0,237%	2,697%	-1,837%	-0,644%	-3,296%

$\Delta S_{3/010}$	$\Delta S_{3/011}$	$\Delta S_{3/012}$	$\Delta S_{3/020}$	$\Delta S_{3/021}$	$\Delta S_{3/022}$	$\Delta S_{3/100}$	$\Delta S_{3/101}$
-0,713%	0,260%	3,459%	1,804%	1,224%	3,459%	-3,260%	-1,555%

$\Delta S_{3/102}$	$\Delta S_{3/110}$	$\Delta S_{3/111}$	$\Delta S_{3/112}$	$\Delta S_{3/120}$	$\Delta S_{3/121}$	$\Delta S_{3/122}$	$\Delta S_{3/200}$
-3,475%	3,358%	-2,156%	-1,485%	-0,017%	0,536%	-1,379%	0,017%

$\Delta S_{3/201}$	$\Delta S_{3/202}$	$\Delta S_{3/210}$	$\Delta S_{3/211}$	$\Delta S_{3/212}$	$\Delta S_{3/220}$	$\Delta S_{3/221}$	$\Delta S_{3/222}$
1,018%	0,812%	4,492%	-1,239%	1,052%	2,686%	-1,168%	2,212%

Figure 24. Percentage differences Δ between the total frequencies F_{even} and F_{odd} of triplets from the even-set of triplets (CCC, CCA, CAC, CAA, ACC, ACA, AAC, AAA, CTC, CTA, CGC, CGA, ATC, ATA, AGC, AGA, TCC, TCA, TAC, TAA, GCC, GCA, GAC, GAA, TTC, TTA, TGC, TGA, GTC, GTA, GGC, GGA) and from the odd-set of triplets (CCT, CCG, CAT, CAG, ACT, ACG, AAT, AAG, CTT, CTG, CGT, CGG, ATT, ATG, AGT, AGG, TCT, TCG, TAT, TAG, GCT, GCG, GAT, GAG, TTT, TTG, TGT, TGG, GTT, GTG, GGT, GGG) in sequences S_0, $S_{1/0}$, $S_{1/1}$, $S_{1/2}$, $S_{2/00}$, …, $S_{3/222}$ at the first four levels of the FGN-3 of the Mycoplasma crocodyli MP145 chromosome, complete genome (NCBI Reference Sequence: NC_014014.1 http://www.ncbi.nlm.nih.gov/nuccore/294155300). The initial sequence S_0 contains 934379 nucleotides. Percentages are shown with a precision up to three decimal places.

In a favor of existence of the Symmetry Principle № 6, the additional evidence is the following. Let us compare the total frequencies F_{even} and F_{odd} of triplets from the whole human genome, which contains the huge number 2.843.411.612 (about three billion) triplets.

Figure 25 shows frequencies of each of 64 triplets in the whole human genome from the article [Perez, 2010]. One can see from this Figure that frequencies of different triplets can differ in many times. For example, the frequency of the triplet CGA is equal to 6.251.611 and the frequency of the triplet TTT is equal to 109.591.342. These two frequencies differ in 18 times approximately. But values of the total frequencies F_{even} and F_{odd} of triplets are equal to within 0.12%.

triplet	triplet frequency	triplet	triplet frequency	triplet	triplet frequency	triplet	triplet frequency
AAA	109143641	CAA	53776608	GAA	56018645	TAA	59167883
AAC	41380831	CAC	42634617	GAC	26820898	TAC	32272009
AAG	56701727	CAG	57544367	GAG	47821818	TAG	36718434
AAT	70880610	CAT	52236743	GAT	37990593	TAT	58718182
ACA	57234565	CCA	52352507	GCA	40907730	TCA	55697529
ACC	33024323	CCC	37290873	GCC	33788267	TCC	43850042
ACG	7117535	CCG	7815619	GCG	6744112	TCG	6265386
ACT	45731927	CCT	50494519	GCT	39746348	TCT	62964984
AGA	62837294	CGA	6251611	GGA	43853584	TGA	55709222
AGC	39724813	CGC	6737724	GGC	33774033	TGC	40949883
AGG	50430220	CGG	7815677	GGG	37333942	TGG	52453369
AGT	45794017	CGT	7137644	GGT	33071650	TGT	57468177
ATA	58649060	CTA	36671812	GTA	32292235	TTA	59263408
ATC	37952376	CTC	47838959	GTC	26866216	TTC	56120623
ATG	52222957	CTG	57598215	GTG	42755364	TTG	54004116
ATT	71001746	CTT	56828780	GTT	41557671	TTT	109591342

Figure 25. Quantities of repetitions of each triplet in the whole human genome (data are taken from the work [Perez, 2010])

Really from Figure 25, one can calculate the total frequencies F_{even} and F_{odd} of triplets from the whole human genome and receive the confirmation of their approximate equality:
- F_{even} = **1.420.853.821** for the even-set of 32 triplets (CCC, CCA, CAC, CAA, ACC, ACA, AAC, AAA, CTC, CTA, CGC, CGA, ATC, ATA, AGC, AGA, TCC, TCA, TAC, TAA, GCC, GCA, GAC, GAA, TTC, TTA, TGC, TGA, GTC, GTA, GGC, GGA);
- F_{odd} = **1.422.557.791** for the odd-set of 32 triplets (CCT, CCG, CAT, CAG, ACT, ACG, AAT, AAG, CTT, CTG, CGT, CGG, ATT, ATG, AGT, AGG, TCT, TCG, TAT, TAG, GCT, GCG, GAT, GAG, TTT, TTG, TGT, TGG, GTT, GTG, GGT, GGG);
- The percentage difference between these F_{even} and F_{odd} is equal to 0,12%.

The appropriate **Symmetry Principle № 6**, which should be studied in additional researches of long nucleotide sequences, can be formulated in the following manner:

- for each of long nucleotide sequences at each level of FGN-3 the following rules hold true: the total frequency F_{even} of all n-plets from the columns with even numerations inside the genomatrix [C T; A G]$^{(n)}$ (here n =1, 2, 3, at least) is approximately equal to the total frequency F_{odd} of all n-plets from the columns with odd numerations inside the same genomatrix.

Our approaches concern to one of important questions of modern science also: the existence of fractal images in genetic systems. A number of publications are devoted to fractal features of genetic texts [Jeffry, 1990; Pellionisz et al, 2011; Petoukhov, 2008b; Petoukhov, He, 2009; Skaletsky et al., 2003; Yam, 1995, etc]. Interesting data about fractal approaches in genetics, including materials about an important connection of fractal defects with cancer, are presented at the WEB site by A.Pellionisz [http://www.junkdna.com/the_genome_is_fractal.html]). Researches in this direction proceed all over the world. In this article the author proposes Fractal Genetics Nets (FGN) as a new tool to study fractal-like properties of long DNA-sequences and also describes new fractal-like properties of such nucleotide sequences. The author supposes that these FGN and fractal-like properties of long nucleotide sequences can lead to new principles and systems in the field of signal processing, recognition of images and artificial intellect. They are used now in the author's laboratory to create new genetic algorithms for different mathematical and technological applications.

We plan to publish in the future other our results on study of FGN and the Symmetry Principles concerning to a wide list of long DNA-sequences of different organells and organisms from different taxonomical classes.

12 Conclusion remarks

Many general bioinformation properties exist which should be studied in the field of bioinformatics:
- noise-immunity of genetic coding;
- management and synchronization in a huge hierarchy of cyclic bioprocesses;
- compression of inherited information data;
- primary structures of proteins, etc.

The list of these scientific problems can be added by a list of mathematical and technological problems from the field of genetic algorithms which is developed intensively in world science

during last decades (for example see [Goldberg, Korb, Deb, 1989; Forrest, Mitchell,1991]). One can think that results of matrix genetics will be useful in many directions of such studies.

Described results demonstrate that the matrix approach to hierarchical systems of the genetic code can discover hidden interrelations among these systems. The matrix representation of the genetic systems is the effective cognitive form to reveal their algebraic properties, etc. Matrix genetics gives new knowledge about deep analogies between the structure of the genetic code and methods of the theory of digital signal processing. Matrix genetics proposes new mathematical models of biological self-reproduction systems. In our opinion, the condition of noise immunity is the basis of many structural peculiarities of the genetic code systems. The utilization of this condition in matrix analysis of the genetic code systems can lead to discovers of new biological rules and of new mathematical models. It can lead also to new effective decisions in the fields of DNA-computers, quantum computers, nanotechnologies, spectral analysis and theoretical biology. The algebraic essence of the code degeneracy, reflected in mosaics of the described genomatrices, are represented in the publications [Petoukhov, arXiv:0803.3330, arXiv:0805.4692, arXiv:0809.2714; Petoukhov, 2008b; Petoukhov, He, 2009].

The revealed connection of genetic code structures with projector operators is one of new promising ways to introduce powerful algebraic methods into bioinformatics and genetic algorithms. Special attention should be paid to mentioned Boolean algebras of genoprojectors because Boolean algebras are explores in many scientific fields from psychology to computers. How Boolean algebras of genoprojectors are connected with physiological computers of biological organisms? It is one of many thematic questions which should be studied in future.

The described data about natural possibilities of representations of ensembles of molecular-genetic elements in a form of families of unitary matrices testify that the nature has chosen such scheme of the genetic code which is related with unitary symmetries and with a special set of cyclic groups of unitary transformations. Why the nature has constructed the genetic alphabet which consists of the four nitrogenous bases with their binary-oppositional attributes? The possible reason of this is that the simplest unitary matrix consists of four complex numbers. This thesis is supported by the fact that the genetic molecules belong to the world of quantum mechanics, where unitary transformations play an important role since the evolution of a closed quantum system is unitary.

This version of the article contains new materials about the method of fractal genetic nets (FGN) and about new Symmetry Principles in long nucleotide sequences. These materials represent new tools to study hidden regularities of molecular-genetic systems. The described Symmetry Principles are leading to new understanding and new models of genetic information. In our opinion, materials of this article are important to develop algebraic biology.

REFERENCES

Ahmed N., Rao K. (1975) *Orthogonal transforms for digital signal processing.* N-Y, Springer-Verlag Inc.
Albrecht-Buehler, G. (2012) The "functional anarchy" of genomes. – http://www.basic.northwestern.edu/g-buehler/genomes/g_contents.htm
Bell S. J., Forsdyke, D. R. (1999) Deviations from Chargaff's Second Parity Rule Correlate with Direction of

Transcription, J. Theo. Bio., 197, 63-76

Blattner,F.R., Plunkett,G. 3rd, Bloch,C.A., Perna,N.T., Burland,V., Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J., Mau,B. and Shao,Y. (1997) The complete genome sequence of Escherichia coli K-12. - *Science*, 277, 1453–1462.

Capra F. (2000) *The Tao of Physics: An Exploration of the Parallels between Modern Physics and Eastern Mysticism (25th Anniversary Edition).* Shambhala Publications, Inc, http://worldbook.ariom.ru/book/-Fritjof+Capra

Chargaff, E. (1950) Chemical specificity of nucleic acids and mechanism of their enzymatic degradation, Experimentia, 6, 201

Chargaff, E. (1971) Preface to a Grammar of Biology: A hundred years of nucleic acid research, Science, 172, pp. 637-642

Chargaff, E. (1975) A fever of reason, Annu. Rev. Biochem, 44: pp. 1-20

Cristea P.D. (2005). "Representation and analysis of DNA sequences. *Genomic Signal Processing and Statistics*, Chapter 1, E. Daugherty *et al.* Eds., Hindawi Publishing Corp., pp. 15–65.

Dong, Q., Cuticchia, A.J. (2001) Compositional symmetries in complete genomes. - *Bioinformatics*, 17, 557-559.

Forrest S., Mitchell M. (1991) The performance of genetic algorithms on Walsh polynomials: Some anomalous results and their explanation. – In R.K.Belew and L.B.Booker, editors, *Proceedings of the Fourth International Conference on Genetic Algorithms*, p.182-189. Morgan Kaufmann, San Mateo, CA.

Forsdyke, D.R. (1981) Are introns in-series error-detecting sequences? - *J. Theor. Biol.*, 93, 861–866.

Forsdyke, D.R. (1996) Different biological species 'broadcast' their DNAs at different (G + C)% 'wavelengths'. - *J. Theor. Biol.*, 178, 405–417.

Forsdyke, D. R. (2002) Symmetry observations in long nucleotide sequences: a commentary on the Discovery Note of Qi and Citicchia. – *Bioinformatics letter*, v. 18, # 1, 215-217.

Forsdyke, D. R., Bell, S. J. (2004) A discussion of the application of elementary principles to early chemical observations. - *Applied Bioinformatics*, 3, pp. 3-8.

Frank-Kamenetskiy M.D. (1988) *The most principal molecule.* Moscow, Nauka (in Russian).

Gierer A., Mundry K.W. (1958) Production of mutants of tobacco mosaic virus by chemical alteration of its ribonucleic acid in vitro. - *Nature* (London),**182**, pp.1457-1458.

Goldberg D.E., Korb B., Deb K. (1989) Messy genetic algorithms: Motivation, analysis, and first results. – *Complex systems*, 1989, 3(5), p. 493-530.

Gusev V., Miroshnichenko L., Chuzhanova N. (2009). Detection of fractal structures in the DNA sequences. - International Book Series "Information Science and Omputing", Book 8, Classification, Forecasting, Data Mining, p.117-124, in Russian (*Supplement to International Journal "Information Technologies and Knowledge*", v. 3) http://www.foibg.com/ibs_isc/ibs-08/ibs-08-p17.pdf

GusfieldD. (1997). *Algorithms on strings, trees and sequences. Computer science and computational biology.*– University of California, Davis, Cambridge University Press

Halmos P.R. (1974) *Finite-dimensional vector spaces*. London: Springer, 212 p.

He M., Petoukhov S.V., Ricci P. (2004) Genetic code, Hamming distance and stochastic matrices. - *Bulletin for Mathematical Biology*, **66**, p.1405-1421.

He M., Petoukhov S.V. (2007) Harmony of living nature, symmetries of genetic systems and matrix genetics. - *International journal of integrative medicine*, **1**, 1, 41-43.

Jacob F. (1974) Le modele linguistique en biologie.- *Critique, Mars*, tome XXX, № 322, p. 197-205.

Jacob F. (1977) The linguistic model in biology.- In: D. Armstrong & C.H. van Schooneveld (eds.). *Roman Jakobson: Echoes of his scholarship*. Lisse: Peter de Ridder, 1977, p. 185-192

Jeffrey H.J. (1990) Chaos game representation of gene structure. *Nucleic Acids Research*, v.18, No.8, p. 2163-2170

Kong S-G, Fan W-L, Chen H-D, Hsu Z-T, Zhou N, et al. (2009) Inverse Symmetry in Complete Genomes and Whole-Genome Inverse Duplication, PLoS ONE 4(11): e7553. doi:10.1371/journal.pone.0007553

Lichtenberg D.B. (1978). *Unitary symmetry and elementary particles*. Academic Press, 290 p.

Louck J.D. (2008). *Unitary symmetry and combinatorics*. World Scientific Publishing Company, 644 p.

Messiah A. (1999) *Quantum mechanics*. New York: Dover Publications, 1152 p.

Mitchell D., Bridge R. (2006) A test of Chargaff's second rule. – *Biochem Biophys Res Commun*, 340(1): 90-94, http://www.ncbi.nlm.nih.gov/pubmed/16364245 .

Pellionisz, A.J., Graham, R., Pellionisz, P.A., Perez J.C. (2011) Recursive genome function of the cerebellum: geometric unification of neuroscience and genomics. - Chapter in: *Handbook "The Cerebellum and Cerebellar Disorders"*. Ed. Manto M., Springer Verlag. Submitted Oct. 20, Accepted Nov. 1, 2011 (in print).

Perez J.-C. (2010). Codon populations in single-stranded whole human genome DNA are fractal and fine-tuned by the golden ratio 1.618. - *Interdiscip Sci Comput Life Sci* (2010) 2: 1–13.

Petoukhov S.V. (2001a) Genetic codes I: binary sub-alphabets, bi-symmetric matrices and the golden section; Genetic codes II: numeric rules of degeneracy and the chronocyclic theory. *Symmetry: Culture and Science*, **12**, #3-4, p. 255-306.

Petoukhov S.V. (2001b) *The bi-periodic table of the genetic code and number of protons*. M, MKC, 2001, 258 p. (in Russian),http://members.tripod.com/vismath/sg/petoukhov.htm

Petoukhov S.V. (2003) Fractal matrices, Fibonacci genetic matrices and a positioning in biological code. Elements

of the matrix mechanics of development. – The deposited article in VINITI RAN, 14.08.2003, №1593-B2003 (VINITI Index of publications "Deposited scientific work», № 10, 2003) (in Russian)

Petoukhov S.V. (2003-2004) Attributive conception of genetic code, its bi-periodic tables and problem of unification bases of biological languages. *Symmetry: Culture and Science*, **14-15**, part 1, 281-307.

Petoukhov S.V. (2005) The rules of degeneracy and segregations in genetic codes. The chronocyclic conception and parallels with Mendel's laws. - In: *Advances in Bioinformatics and its Applications, Series in Mathematical Biology and Medicine*, **8**, p. 512-532, World Scientific.

Petoukhov S.V. (2006a) Bioinformatics: matrix genetics, algebras of the genetic code and biological harmony. *Symmetry: Culture and Science*, **17**, #1-4, p. 251-290.

Petoukhov S.V. (2006b) The genetic code, Hadamard genomatrices and quantum computers. *United scientific journal*, # 24(184), p. 51-53 (in Russian).

Petoukhov S.V. (2008a) The degeneracy of the genetic code and Hadamard matrices. arXiv:0802.3366 [q-bio.QM].

Petoukhov S.V. (2008b) *Matrix genetics, algebras of the genetic code, noise immunity*. M., RCD, 316 p. (in Russian).

Petoukhov S.V. (2008c) Matrix genetics, part 2: the degeneracy of the genetic code and the octave algebra with two quasi-real units (the "Yin-Yang octave algebra"),arXiv:0803.3330[q-bio.QM].

Petoukhov S.V. (2008d) Matrix genetics, part 3: the evolution of the genetic code from the viewpoint of the genetic octave Yin-Yang-algebra. arXiv:0805.4692[q-bio.QM].

Petoukhov S.V. (2011) Hypercomplex numbers and the algebraic system of genetic alphabets. Elements of algebraic biology. – *Hypercomplex numbers in geometry and physics*, v.8, 2(16), p. 118-139 (*Gipercompleksnyie chisla v geometrii i fizike*, in Russian)

Petoukhov S.V. (2012a) The genetic code, 8-dimensional hypercomplex numbers and dyadic shifts. (7th version from January, 30, 2012), http://arxiv.org/abs/1102.3596

Petoukhov S.V. (2012b) On fractal structure of long nucleotide sequences. – *Joint scientific journal (Ob'edinennyi nauchnyi journal)*, # 6-7, p. 50 (in Russian)

Petoukhov S.V., **He M.** (2009) *Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications*. Hershey, USA: IGI Global. 271 p.

Petoukhov S.V., Svirin V.I. (2012) Fractal genetic nets and the rules of long genetic sequences. - *Joint scientific journal (Ob'edinennyi nauchnyi journal)*, # 8-9, p. 50-52 (in Russian)

Pevzner P.A. (2000) *Computational molecular biology. An algorithmic approach*. – Cambridge, Massachusetts: MIT Press.

Prabhu, V. V. (1993) Symmetry observation in long nucleotide sequences. - *Nucleic Acids Res.*, 21, 2797-2800.

Rumer Yu. B. (1968). Systematization of the codons of the genetic code. *Doklady Akademii Nauk SSSR,* **183**(1), p. 225-226 (in Russian).

Rumer Yu.B., Fet A.I. (1970). *The theory of unitary symmetry*. Moscow: Nauka, 400 p.

Schrodinger E. (1955) *What is life? The physical aspect of the living cell*. Cambridge, University Press

Schuster H., Schramm G. (1958) Bestimmung der biologisch wirksamen Einheit in der RNS des TMV auf chemischen Wege. - *Z. Naturforsch.,***13b**, S. 697-704.

SchutskiyYu.K.(1997) *The Chinese classical "The Book of Changes"*. Moscow, Vostochnaya literatura, 605 p. (in Russian).

Skaletsky H., Kuroda-KawaguchiT., Minx P.J., Cordum H.S., Hillier L., Brown L.G., Repping S., Pyntikova T., Ali J., BieriT., Chinwalla A., Delehaunty A., Delehaunty K., Du H., Fewell G., Fulton L., Fulton R., Graves T., Hou S.-F., Latrielle P., Shawn L., Mardis E., Maupin R., McPherson J., Miner T., Nash W., Nguyen C., Ozersky P., Pepin K., Rock S., Rohlfing T., Scott K., Schultz B., Strong C., Tin-Wollam A., Yang S.-P., Waterston R.H., Wilson R.K., RozenS., Page D. C. (2003). The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. – *Nature,* v.423, p. 825-837 (19 June 2003) http://www.nature.com/nature/journal/v423/n6942/full/nature01722.html

Stent G.S. (1969) *The Coming of the Golden Age*. N-Y, The Natural Histore Press.

Sueoka, N. (1999) Two aspects of DNA base composition: G + C content and translation-coupled deviation from intra-strand rule of A = T and G = C. - *J. Mol. Evol.*, **49**, 49–62

Waterman M.S., editor (1999) *Mathematical methods for DNA sequences*. Florida, CRC Press, Inc.

Yam, Ph. (1995). Talking trash (Linguistic patterns show up in junk DNA). – *Sci. Amer*., 272(3), p.12-15.

Yamagishi M.E.B., Herai R.H. (2011) Chargaff's "Grammar of Biology": New Fractal-like Rules. arXiv:1112.1528v1 from 07.12.2011

Watson, J. D., Crick, F. H. C. (1953) Molecular Structure of Nucleic Acids. - *Nature*, 4356, 737.