doi:10.20944/preprints201911.0301.v1

The genetic code, algebraic codes and double numbers

Sergey V. Petoukhov[1]

[1]-Mechanical Engineering Research Institute of Russian Academy of Sciences. Russia, 101990,
Moscow, M. Kharitonievskiy pereulok, 4,
http://eng.imash.ru/, info@imash.ru

Comment: Some materials of this article were presented by the author in his keynote speech at the Third international conference "Artificial Intelligence, Medical Engineering, Education" (Moscow, Russia, 01-03 October 2019, http://www.ruscnconf.org/aimee2019/index.html) and in his lecture at the Sixth International Conference in Code Biology (Friedrichsdorf, Germany, 3-7 June 2019, http://www.codebiology.org/conferences/Friedrichsdorf2019/). They were also presented by the author in his keynote speech at the international Belgrade Bioinformatics Conference 2018 (Belgrade, Serbia, 18-22 June, 2018, http://belbi.bg.ac.rs/).

Abstract. The article shows materials to the question on algebraic features of the genetic code. Presented results testify in favor that the genetic code is an algebraic code related with a wide class of algebraic codes, which are a basis of noise-immune coding of information in communication technologies. Algebraic features of the genetic code are associated with hypercomplex double (or hyperbolic) numbers. The article also presents data on structural relations of some genetically inherited macrobiological phenomena with double numbers and with their algebraic extentions. The received results confirm that multidimensional numerical systems is effective for modeling and revealing the interconnections of structures of biological bodies at various levels of their organization. This allows one to think that living organisms are algebraically encoded entities.

Keywords: genetic code, DNA, alphabet, amino acids, hypercomplex numbers, double numbers, binary numbers, dyadic groups, dyadic shift, tensor product.

CONTENTS

1. Introduction.

The idea about special mathematical peculiarities of living matter exists long ago. For example V.I. Vernadsky [Vernadsky, 1965] put forward the hypothesis on a non-Euclidean geometry of living nature. Different branches of modern science use various kinds of multi-dimensional numbers – complex numbers, double numbers, dual numbers, quaternions and other hypercomplex numbers. These multi-dimensional numeric systems play the role of the magic tool for development of theories and calculations in problems of heat, light, sounds, fluctuations, elasticity, gravitation, magnetism, electricity, current of liquids, quantum-mechanical phenomena, special theory of relativity, nuclear physics, etc. It seems an important task to investigate what systems of multi-dimensional numbers are connected or can be connected with ensembles of parameters of the genetic code and inherited biological peculiarities. Some results of such investigation are presented in this article. They are connected with double hyperbolic numbers and their algebraic extensions, matrix forms of which give a new class of mathematical models in genetics and some other scientific fields.

The set of all two-dimensional double numbers (which are termed also as hyperbolic numbers, Lorentz numbers, split-complex numbers and perplex numbers) forms algebra over the field of real numbers [Harkin, Harkin, 2004; Kantor, Solodovnikov, 1989]. The algebra is not a division algebra or field since it contains zero divisors. Hyperbolic numbers aj_0+bj_1 (where j_0 is the real unit; j_1 is the imaginary unit; *a* and *b* are real numbers) are well known in mathematics and theoretical physics and they have matrix form of their representations by the following bisymmetric matrices: $G_2 = [a, b; b, a]$, where *a* and *b* are real numbers (Fig. 1). Such matrix represetations of double numbers we will be termed simply and briefly as matrix double numbers. In such bisymmetric matrices, components *a* and *b* are located along two diagonals in the cruciform shape, which is met below in this article many times. Any bisymmetric matrix of any order with real entries *a* and *b* has an orthogonal set of eigenvectors with real eigenvalues.

$$\begin{vmatrix} a, b \\ b, a \end{vmatrix} = a* \begin{vmatrix} 1, 0 \\ 0, 1 \end{vmatrix} + b* \begin{vmatrix} 0, 1 \\ 1, 0 \end{vmatrix} = a*j_0 + b*j_1;$$

*	1	j_1
1	1	j_1
j_1	j_1	1

Fig. 1. The decomposition of the bisymmetric matrix [a, b; b, a] into two sparse matrices, where the sparse matrices j_0 and j_1 are correspondingly matrix representations of the real unit and the imaginary unit of algebra of 2-dimensional double numbers. The multiplication table of these units are shown at right.

An important special case of double numbers and their matrix representations [*a, b; b, a*] are hyperbolic rotations, which satisfied the condition $a^2 - b^2 = 1$. Hyperbolic rotations are represented in the special theory of relativity, in Minkowski geometry and in some other physical and mathematical fields. The algebra of double numbers can be extended to algebras of 2^n-dimensional double numbers having also representations by bisymmetric (2^n*2^n)-matrices.

The article shows connections of genetic code stuctures with such bisymmetric (2*2)-matrices and their unions into square matrices of higher orders. Described author's results testify in favor of the statement that the genetic code is an algebraic code and is connected with a wide class of algebraic and algebraic-geometric codes used in modern technologies of noise-immune communication [Ahmed, Rao, 1975; Seberry, Wysocki, Wysocki, 2005; and many others). These new results add previous author's results of matrix analysis of structures of genetic systems and also his publications on united-hypercomplex numbers [Petoukhov, 2008, 2011, 2016b, 2017; 2018; Petoukhov, He, 2010; Petoukhov, Petukhova, Svirin, 2019].

2. The genetic code, DNA alphabets and genetic matrices

In DNA molecules genetic information is written in sequences of 4 kinds of nucleobases: adenine A, cytosine C, guanine G and thymine T. They form a DNA alphabet of 4 monoplets. In addition, DNA alphabets of 16 doublets and 64 triplets also exist. As known, the set of these 4 nucleobases A, C, G and T is endowed with binary-oppositional indicators:

- 1) in the double helix of DNA there are two complementary pairs of letters: the letters C and G are connected by three hydrogen bonds, and the letters A and T by two hydrogen bonds. Given these oppositional indicators, one can represent C = G = 1 and A = T = 0;
- 2) the two letters are keto molecules (G and T), and the other two are amino molecules (A and C). Given these oppositional indicators, one can represent A = C = 1, G = T = 0.

Taking this into account, it is convenient to present DNA alphabets of 4 letters, 16 doublets and 64 triplets in the form of square tables, the columns of which are numbered in accordance with oppositional indicators “3 or 2 hydrogen bonds” (C = G = 1, A = T = 0), and the rows in accordance with oppositional indicators “amino or keto” (C = A = 1, G = T = 0). In such tables, all letters, doublets and triplets automatically occupy their strictly individual places (Fig. 2).

	1	0
1	G	T
0	C	A

	11	10	01	00
11	GG	GT	TG	TT
10	GC	GA	TC	TA
01	CG	CT	AG	AT
00	CC	CA	AC	AA

	111	110	101	100	011	010	001	000
111	GGG	GGT	GTG	GTT	TGG	TGT	TTG	TTT
110	GGC	GGA	GTC	GTA	TGC	TGA	TTC	TTA
101	GCG	GCT	GAG	GAT	TCG	TCT	TAG	TAT
100	GCC	GCA	GAC	GAA	TCC	TCA	TAC	TAA
011	CGG	CGT	CTG	CTT	AGG	AGT	ATG	ATT
010	CGC	CGA	CTC	CTA	AGC	AGA	ATC	ATA
001	CCG	CCT	CAG	CAT	ACG	ACT	AAG	AAT
000	CCC	CCA	CAC	CAA	ACC	ACA	AAC	AAA

Fig. 2. The square tables of DNA-alphabets of 4 nucleotides, 16 doublets and 64 triplets with a strict arrangement of all components. Each of tables is constructed in line with the principle of binary numeration of its column and rows on the basis of binary-oppositional indicators of nucleobases A, C, G and T.

These three tables (Fig. 2) are not only simple tables but they are members of the tensor family of matrices: the second and the third tensor (Kronecker) powers of the matrix [C, A; G, T] generate similar arrangements of 16 doublets and 64 triplets in matrices $[C, A; G, T]^{(2)}$ and $[C, A; G, T]^{(3)}$ as shown in Fig. 2.

The genetic code is called a "degenerate code" because 64 triplets encode 20 amino acids and stop-codons so that several triplets can encode each amino acid at once and each triplet necessarily encodes only a single amino acid or a stop-codon. The (8x8)-matrix of 64 triplets (Fig. 2) was built formally without any mention of amino acids and stop-codons. How can these 20 amino acids and stop-codons be located in this matrix of 64 triplets? There are a huge number of possible options for the location and repetition of separate amino acids and stop-codons in 64 cells of this matrix. More precisely, the number of these options is much more than 10^{100} (for comparison, the entire time of the Universe existance is estimated in modern physics at 10^{17} seconds). But Nature uses - from this huge number of options - only a very specific repetition and arrangement of separate amino acids and stop-codons, the analysis of which is important for revealing the structural organization of the informational foundations of living matter.

Fig. 3 shows the real repetition and location of amino acids and stop-codons in the Vertebrate Mitochondrial Code, which is the most symmetrical among known dialects on the genetic code. This genetic code is called the most ancient and "ideal" in genetics [Frank-Kamenetskii, 1988] (other dialects of the genetic code have small differences from this basic one).

	111	110	101	100	011	010	001	000
111	**GLY** GGG	**GLY** GGT	**VAL** GTG	**VAL** GTT	**TRP** TGG	**CYS** TGT	**LEU** TTG	**PHE** TTT
110	**GLY** GGC	**GLY** GGA	**VAL** GTC	**VAL** GTA	**CYS** TGC	**TRP** TGA	**PHE** TTC	**LEU** TTA
101	**ALA** GCG	**ALA** GCT	**GLU** GAG	**ASP** GAT	**SER** TCG	**SER** TCT	**STOP** TAG	**TYR** TAT
100	**ALA** GCC	**ALA** GCA	**ASP** GAC	**GLU** GAA	**SER** TCC	**SER** TCA	**TYR** TAC	**STOP** TAA
011	**ARG** CGG	**ARG** CGT	**LEU** CTG	**LEU** CTT	**STOP** AGG	**SER** AGT	**MET** ATG	**ILE** ATT
010	**ARG** CGC	**ARG** CGA	**LEU** CTC	**LEU** CTA	**SER** AGC	**STOP** AGA	**ILE** ATC	**MET** ATA
001	**PRO** CCG	**PRO** CCT	**GLN** CAG	**HIS** CAT	**THR** ACG	**THR** ACT	**LYS** AAG	**ASN** AAT
000	**PRO** CCC	**PRO** CCA	**HIS** CAC	**GLN** CAA	**THR** ACC	**THR** ACA	**ASN** AAC	**LYS** AAA

Fig. 3. The location and repetition of 20 amino acids and 4 stop-codons (denoted by bold) in the matrix of 64 triplets $[C, A; G, T]^{(3)}$ (Fig. 2) for the Vertebrate Mitochondrial Code. The symbol “Stop” refers to stop-codons.

The location and repetition of all amino acids and stop-codons in the matrix of 64 triplets have the following feature (Fig. 3):

- Each of sixthteen (2*2)-subqudrants, forming this genetic matrix and denoted by bold frames, is bisymmerical: each of its both diagonals contains an identical kind of amino acids or stop-codon.

If each amino acid and stop-codon is represented by some characteristic parameter (for example, the number of carbon atoms in these organic formations or numbers of protons in its molecular structure, etc.), then a numerical (8*8)-matrix arises (Fig. 4) with bisymmetric (2*2)-subquadrants representing double numbers $a\mathrm{j}_0+b\mathrm{j}_1$ described above in the Section 1 (Fig. 1). In other words, this phenomenologic arrangement of amino acids and stop-codons in the matrix of 64 triplets is associated to the multiblock union of matrix presentations of 16 two-dimensional double numbers.

2	2	5	5	11	3	6	9
2	2	5	5	3	11	9	6
3	3	5	4	6	6	0	9
3	3	4	5	6	6	9	0
6	6	6	6	0	6	5	6
6	6	6	6	6	0	6	5
5	5	5	6	4	4	6	4
5	5	6	5	4	4	4	6

Fig. 4. The numeric analogue of the symbolic (8*8)-matrix of amino acids and stop-codons from Fig. 3 for the case of representing each of amino acids by numbers of its carbon atoms (stop-codons are conditionally represented by zero).

Demonstrated by the matrices in Fig. 3 and 4, the connection of the genetic code with double numbers supplements the following statement of the author, presented in a number of his publications [Petoukhov, 2008, 2011, 2016b, 2017, 2018; 2018; Petoukhov, He, 2010; etc.]. The genetic code is not just a mapping of one set of elements to other sets of elements by type, for example, of a phone book in which phone numbers encode names of people. But the genetic code is inherently an algebraic code, akin to those algebraic codes that are used in modern communication theory for noise-immune transmission of information. Algebraic features of the genetic code participate in noise-immune properties of this code and of the whole genetic system.

One can explain the meaning and possibilities of algebraic codes by the example of transmitting a photograph of the Marsian surface from Mars to Earth using electromagnetic signals. On the way to the Earth, these signals travel millions of kilometers of interference and arrive at the Earth in a very weakened and distorted form. But, in a magical way, based on these mutilated signals on Earth, a high-quality photograph of the surface of Mars is recreated. The secret of this magic lies in the fact that from Mars not the information signals about this photo are sent, but algebraically encoded versions of these signals that is quite other signals. At receivers on Earth, these algebraically encoded signals are algebraically decoded into signals, which recreate the original photographic image of the surface of Mars. It should be emphasized that algebraic coding of information in the theory of noise-immune communication actively uses the mathematical apparatus of matrices, which is also used in quantum informatics and quantum mechanics as matrix operators.

By analogy with this example from the theory of noise-immune communications, the author’s statement, that the genetic code of amino acids is algebraic one, entails the following author’s hypothesis: the molecular-genetic system is a system of certain algebraic codes, which serves to provide noise-immune transmission of genetic and - in addition - some important pra-genetic information along the chain of generations. The author’s works are aimed at studying algebraic properties of the genetic coding system for revealing hidden biological information algebraically encoded in the molecular genetic system [Petoukhov, 2008, 2011, 2016b, 2017, 2018; 2018; Petoukhov, He, 2010].

What possible reasons of such character of the coding of amino acids and stop-codons, which is built in accordance with a matrix having 16 bisymmetric sub-quadrants? The author seeks an answer to this question in the relations of the genetic code with foundations of algebraic codes in the theory of noise-immune coding of information. The next Section describes some of the search results connected with notions of dyadic groups, Hamming distances and matrices of dyadic shifts.

3. The genetic code, dyadic groups and the matrix of dyadic shifts

Many structural features of genetic coding systems indicate the important role of dyadic groups of binary numbers [Petoukhov, 2008, 2016c; Hu Z.B., Petoukhov S.V., Petukhova E.S., 2017].
Binary numbers and their dyadic groups occupy a very important place in modern science and technology including computers, digital noise-immune communication, systems of artificial intelligence, etc. DNA alphabets, having 4 monoplets, 16 doublets and 64 triplets, are connected namely with dyadic groups of binary n-bit numbers (n = 2,3,4, …), each of which contains 2^n members (Harmuth, 1989). For example, the dyadic group of 3-bit numbers contains 8 members:

000, 001, 010, 011, 100, 101, 110, 111 (1)

The known operation of the bitwise modulo-2 addition serves as the group operation in dyadic groups. It is denoted by the symbol ⊕ and has the following rules: $0 \oplus 0 = 0$; $0 \oplus 1 = 1$; $1 \oplus 0 = 1$; $1 \oplus 1 = 0$. Modulo-2 addition is utilized broadly in the theory of discrete signal processing and algebraic coding as a fundamental operation for binary variables [Ahmed and Rao, 1975] .

The modulo-2 addition of any two binary numbers from a dyadic group always results in a new number from the same group. For example, modulo-2 addition of two binary numbers 110 and 101 from (1), which are equal to 6 and 5 respectively in decimal notation, gives the result $110 \oplus 101 = 011$, which is equal to 3 in decimal notation. The number 000 serves as the unit element of this group: for example, $010 \oplus 000 = 010$. The reverse element for any number in this group is the number itself: for example, $010 \oplus 010 = 000$. Series (1) is transformed by modulo-2 addition of all its members with the binary number 001 into a new series of the same numbers: 001, 000, 011, 010, 101, 100, 111, 110. Such changes in the initial binary sequence, produced by modulo-2 addition of its members with any of binary numbers from (1), are termed dyadic shifts [Ahmed and Rao, 1975; Harmuth, 1989]. Fig. 5 shows an example of bisymmetric matrices of dyadic shifts where each of entries is received by modulo-2 addition of binary numerations of its column and row [Ahmed and Rao, 1975]. Such bisymmetric matrices are used in the theory of algebraic coding of noise-immune information transfering. To emphasize a close relation of the matrix of dyadic shifts with the genetic matrix of triplets in Figs. 2 and 4, appropriate triplets from Fig. 2 can be shown in Fig. 5 in all cells of the dyadic shift matrix.

	111	110	101	100	011	010	001	000
111	000 (0)	001 (1)	010 (2)	011 (3)	100 (4)	101 (5)	110 (6)	111 (7)
110	001 (1)	000 (0)	011 (3)	010 (2)	101 (5)	100 (4)	111 (7)	110 (6)
101	010 (2)	011 (3)	000 (0)	001 (1)	110 (6)	111 (7)	100 (4)	101 (5)
100	011 (3)	010 (2)	001 (1)	000 (0)	111 (7)	110 (6)	101 (5)	100 (4)
011	100 (4)	101 (5)	110 (6)	111 (7)	000 (0)	001 (1)	010 (2)	011 (3)
010	101 (5)	100 (4)	111 (7)	110 (6)	001 (1)	000 (0)	011 (3)	010 (2)
001	110 (6)	111 (7)	100 (4)	101 (5)	010 (2)	011 (3)	000 (0)	001 (1)
000	111 (7)	110 (6)	101 (5)	100 (4)	011 (3)	010 (2)	001 (1)	000 (0)

Fig. 5. The bisymmetric (8*8)-matrix of dyadic shifts. In each matrix cell, there is shown a binary number and its decimal value (in brackets).

One can see from Fig. 5 that this matrix of dyadic shifts consists of 16 bisymmetrical (2*2)-subquadrants in some analogy with the genetic matrices in Fig. 3 and 4. Each of these subquadrants is a matrix representation of 2-dimensional double number. It is obvious that this matrix has analogies with the phenomenological distribution of amino acids and stop-codons in a matrix of 64 triplets, which also consists of 16 bisymmetrical (2*2)-subquadrants.

If any system of elements demonstrates its connection with dyadic shifts, it indicates that the structural organization of the system is connected with the logic modulo-2 addition. The works of [Petoukhov, 2008, Petoukhov, 2011, Petoukhov and He, 2010] show additionally that the structural organization of the molecular-genetic system is connected with dyadic shifts and correspondingly with modulo-2 addition. Dyadic shifts are also involved in the patterns of molecular-genetic alphabets. The author pays special attention to non-trivial structures of interrelated and structured alphabets of DNA and RNA since these alphabets are key elements in the noise-immune transmission of genetic information.

4. The genetic code and the matrix of Hamming distances

In the theory of algebraic coding of information in modern communication technologies, the concept of code distance plays an extremely important role, and code distance most often means the so-called Hamming distance [Sagalovich, 2011]. The Hamming distance between two symbol strings of equal length is the number of positions at which the corresponding symbols are different. In other words, it measures the minimum number of substitutions required to change one string into the other, or the minimum number of errors that could have transformed one string into the other. For example, let us consider the triplet AAC, which is represented in Fig. 2 by the binary sequence 001 (in relation to the binary indicators “3 or 2 hydrogen bonds”) and by the binary sequence 111 (in relation to the binary indicators “amino or keto”). It is obvious that the Hamming distance between these two representations of the triplet AAC is equal to 2. By analogy, calculations of Hamming distances between such two binary representations of each of triplets in the matrix in Fig. 2 lead to the bisymmetric matrix of Hamming distances for triplets in Fig. 6.

	111	110	101	100	011	010	001	000
111	0	1	1	2	1	2	2	3
110	1	0	2	1	2	1	3	2
101	1	2	0	1	2	3	1	2
100	2	1	1	0	3	2	2	1
011	1	2	2	3	0	1	1	2
010	2	1	3	2	1	0	2	1
001	2	3	1	2	1	2	0	1
000	3	2	2	1	2	1	1	0

Fig. 6. The bisymmetric matrix of Hamming distances for two kinds of binary representations of 64 triplets in the genetic matrix in Fig. 2.

From Fig. 6 one can show that the bisymmetric (8*8)-matrix of Hamming distances consists of 16 bisymmetrical (2*2)-subquadrants, each of which is a matrix representation of 2-dimensional double number. It is obvious that this matrix has analogies with the phenomenological distribution of amino acids and stop-codons in a matrix of 64 triplets, which also consists of 16 bisymmetrical (2*2)-subquadrants.

5. Hypercomplex double numbers and inherited macrobiological phenomena

The organism is a single inherited whole. All its inherited physiological subsystems must be structurally coupled with genetic coding, otherwise they cannot be encoded and inherited (doomed to extinction). For this reason, it makes sense to study relationship of structures of inherited macrobiological phenomena with double numbers represented in the structures of the genetic coding system. This Section shows some data on such relationships.

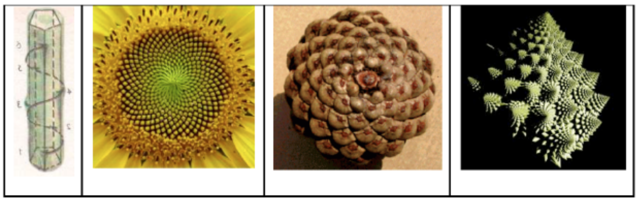


Fig. 7. Examples of phyllotaxis configurations in biological bodies.

For 150 years, in biology, inherited helical bio-lattices, associated with Fibonacci numbers, are studied under the title "phyllotaxis laws" [Jean, 2006]. (Fibonacci series: $F_n = F_{n-2}+F_{n-1}$: 0, 1, 1, 2, 3, 5, 8, 13, 21, …). For example, the numbers of left and right spirals in the heads of the sunflower are equal to the neighboring members of the Fibonacci series. Such phyllotaxis phenomena exist in plant and animal bodies at various levels and branches of biological evolution. The ratios F_{n+1}/F_n denote the order of symmetry of phyllotaxis lattices. In the process of growth of some organisms, their phyllotaxis lattices are transformed with the transition to other Fibonacci relations F_{k+1}/F_k.

Ukrainian Prof. O. Bodnar paid his attention that such growth transformations of phyllotaxis lattices correspond to hyperbolic rotations known in the special theory of relativity as Lorentz transformations [Bodnar, 1992, 1994]. On this basis, he declared that living matter is structurally related to Minkowski geometry.

Another example of the biological realization of structures associated with double numbers is given by the heritable organization of locomotion in animal organisms. As known, living bodies have innate abilities for locomotion. For example, newborn turtles and crocodiles, when they hatched from eggs, crawl by quite coordinated movements to water; millipedes manage the coordinated movement of dozens of their legs, using inherited algorithms, etc. One of the most respectable Russian journal “Uspekhi Fizicheskih nauk” published a large article by Prof. V. Smolyaninov “Spatio-temporal problems of locomotion control” with results of his 20 years of research on locomotion of a wide variety of animals and humans [Smolyaninov, 2000]. According to his results, spatio-temporal organization of locomotion control is related – by a special manner - with hyperbolic rotations and with Minkovsky geometry. On this basis, Smolyaninov put forward his “Locomotor theory of relativity” and wrote about a relativistic brain and relativistic biomechanics.

One more example of the structural connection of inherited biological phenomena with hyperbolic rotations (a special case of double numbers) is the basic psychophysical law of Weber-Fechner. Different types of inherited sensory perception are subordinated to this law: sight, hearing, smell, touch, taste, etc. The law states that the intensity of the perception is proportional to the logarithm of stimulus intensity; it is expressed by the equation:

$$p = k*\ln(x/x_0) = k*\{\ln(x) - \ln(x_0)\} \tag{2}$$

where p - the intensity of perception, x – stimulus intensity, x_0 - threshold stimulus, ln – natural logarithm, k – a weight factor. Because of this law, for example, the power of sound in engineering technologies is measured on a logarithmic scale in decibels.

One can suppose that the innate Weber–Fechner law is the law especially for nervous system. But it is not so since its meaning is much wider because it holds true in many kinds of lower organisms without a nervous system in them: “*this law is applicable to chemo-tropical, helio-tropical and geo-tropical movements of bacteria, fungi and antherozoids of ferns, … . The Weber-Fechner law, therefore, is not the law of the nervous system and its centers, but the law of protoplasm in general and its ability to respond to stimuli*" [Shults, 1916].

Let us explain a connection of hyperbolic rotations with the Veber-Fechner law (2). Hyperbolic rotations transform points of hyperbolas into points of the same hyperbolas (hyperbolas glide along themselves). It is known [Klein, 2004; Shervatov, 1954] that for any real number a > 1 the natural logarithm is defined as the area under the hyperbola y = 1/x from 1 to a (Fig. 8, left). Accordingly, two points (x, 1/x) and (x_0, $1/x_0$) of this hyperbola specify the value $\ln(x)-\ln(x_0)$ expressed the value of the perception intensity p in the Weber-Fechner law (Fig. 8, right). A change in the stimulus intensity x_1 to a new value x_2 corresponds to a hyperbolic rotation, which in this hyperbola transfers its point (x_1, $1/x_1$) to its point (x_2, $1/x_2$) and characterizes the magnitude of the change of perception intensity in this law: $\Delta p = k * \ln(x_2/x_1)$.

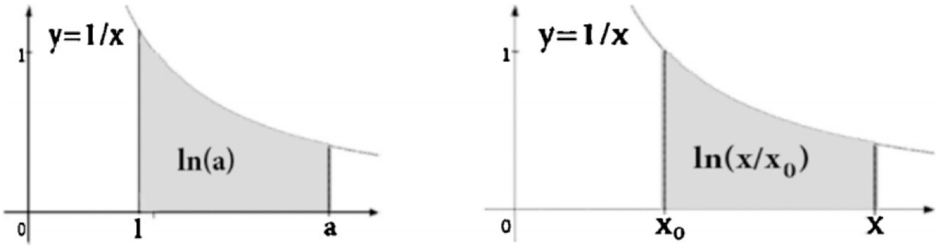


Fig. 8. Illustration of the connection of hyperbolic turns with the psychophysical law of Weber-Fechner (its explanation in the text).

It can be reminded here that when photons arrive at a single eye receptor from some luminous point of the observed image, then already coded signals in the form of sequences of nerve impulses run from the receptor along the nerve into the central nervous system. The author believes that all biological sensorics is based on the algebraic coding of information signals from the outside world. But the coding of information in sensory channels is only part of the overall picture of building the whole organism with all its genetically inherited subsystems as an algebraically encoded entity. From this point of view, the term "code biology" [Barbieri, 2015] can be interpreted as "algebraic coded biology".

One should note also on using double numbers in effective modeling of percentages (or frequencies) in contents of long genetic and literary texts. In DNA double helixes, nitrogenous bases C-G and A-T form complementary pairs by means of 3 and 2 hydrogen bonds (it can be represented as C=G=3 and A=T=2). Correspondingly, any DNA sequence contains a long chain of numbers 2 and 3 of hydrogen bonds, for example, 33223223233… . Studying such binary “hydrogen texts” 33223223233… of a wide number of various genomes, the author discovered that in them percentages (or frequencies) of hydrogen monoplets (3, 2), doublets (33, 32, 23, 22), triplets (333, 332, 323, 322, 233, 232, 223, 222), tetraplets and pentaplets are subordinated to hidden rules: percentages of monoplets (values %3 and %2) are strongly interrelated with percentages of other hydrogen *n*-plets ($n = 2, 3, 4, 5$). These interrelations are effectively described by a tensor family $[\%3, \%2; \%2, \%3]^{(n)}$ representing 2^n-dimensional double numbers:

- $\%3 + \%2*j$ (when n=1);
- $\%3*\%3 + \%3*\%2*e_1 + \%2*\%3*e_2 + \%2*\%2*e_3$ (n=2); etc.

As it turned out, coefficients of these double numbers effectively model percentages of corresponding hydrogen n-plets in long DNA sequences: for example, the value %3*%2 models the percentage of doublets 32, and the value %2*%3*%3 models the percentage of triplets 233. Knowing only percentages of monoplets %3 and %2, you can predict percentages of dozens of hydrogen *n*-plets in long DNA [Petoukhov, 2018b, 2019b].

Leading experts on structural linguistics believe for a long time that human languages are a continuation of the genetic language using the principle of binary oppositions (see for example fundamental works by Roman Jakobson [Jakobson, 1985, 1987, 1999; Ivanov, 1985] who organized jointly with Niels Bohr a united seminar at the Massachusetts Institute of Technology to discuss connections among biology, linguistics and physics).

Many researchers perceive a linguistic language as a living organism. The book “Linguistic genetics” [Makovsky, 1992] says: "*The opinion about language as about a living organism, which is submitted to the laws of a nature, ascends to a deep antiquity … Research of a nature, of disposition and of reasons of isomorphism between genetic and linguistic regularities is one of the most important fundamental problems for linguistics of our time*”.

The author’s studies of works by L.N. Tolstoy, F.M. Dostoevsky, A.S. Pushkin and others revealed new structural connections between long Russian literary texts and DNA texts [Petoukhov, 2018b, 2019b]. Let us explain this.

The DNA alphabet has a binary-oppositional structure: it contains two sub-alphabets of purines (A, G) and pyrimidines (T, C). Each sub-alphabet dichotomously divides into two subsub-alphabets according to indicators of 2 or 3 hydrogen bonds in its letters (Fig. 9, left).

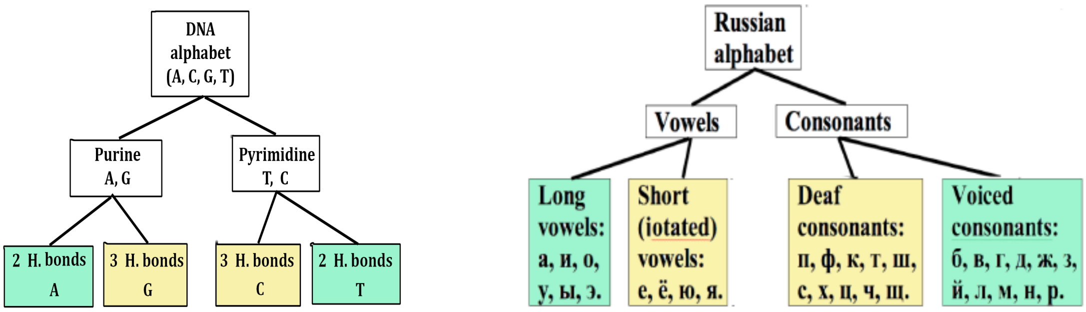


Fig. 9. Binary-oppositional structures of the DNA alphabet and of the Russian alphabet

The Russian alphabet, like the DNA alphabet, is phonetically based on binary oppositions, since it is divided into vowels and consonants. In turn, the set of vowels dichotomously divides into long and iotated vowels, and the set of consonants - into voiced and deaf consonants (Fig. 9, right).

To analyze long literary texts, the author introduced two equivalence classes:

- the first class combines all the iotated vowels and the unvoiced consonants (yellow boxes in Fig. 9) represented by the common symbol 0;
- the second class combines all the long vowels and voiced consonants (green boxes in Fig. 9) represented by the common symbol 1.

Leaving in an analysed literary text only these letters, and replacing each letter with the symbol of its equivalence class 0 or 1, we get the text representation as a binary sequence of the type 100101100 .... Denote by symbols %0 and %1 the percentages (frequencies) of characters 0 and 1 in this binary representation of the literary text.

The author studied the percentages of binary monoplets (0 and 1), doublets (00, 01, 10, 11), triplets (000, 001, 010, ..., 111) and tetraplets in the novels of L.N. Tolstoy, F.M. Dostoevsky, A.S. Pushkin, etc. It turned out that - by analogy with the case of long DNA texts - the percentages of these polyplets are effectively modeled by the tensor family of percent matrices $[\%0, \%1; \%1, \%0]^{(n)}$ representing 2^n-dimensional double numbers:

- $\%0 + \%1*e_1$ (for n = 1; e_1 is the imaginary unit of 2-dimensional double numbers);
- $\%0*\%0 + \%0*\%1*e_1 + \%1*\%0*e_2 + \%1*\%1*e_3$ (for n = 2; e_1, e_2 and e_3 are imaginary units of 4-dimensional double numbers);
- etc …

The coordinates of these 2^n-dimensional double numbers effectively model the percentages of the corresponding types of polyplets in these texts. For example, the coordinate %1*%0 models the percentage of the doublet 10. In any studied long literary text, knowing only the percentages of monoplets %0 and %1, one can predict the percentages of many types of polyplets in it with good accuracy [Petoukhov, 2018b, 2019b].

Now let us pay our attention to the bisymmetric (or cruciform) character, which is typical not only for matrix representations of 2-dimensional double numbers (and of 2^n-dimensional double numbers) but also for genetic matrices of dyadic shifts (Fig. 5) and for genetic matrices of Hamming distances (Fig. 6). It is interesting that many genetic inherited constructions of physiological macrosystems including sensory-motion systems have a similar cruciform character. For example, the connection between the hemispheres of human brain and the halves of human body possesses the similar cruciform character: the left hemisphere serves the right half of the body and the right hemisphere (Fig. 10) (Annett, 1985, 1992; Gazzaniga, 1995; Hellige, 1993). The system of optic cranial nerves from two eyes possesses the cruciform structures as well: the optic nerves transfer information about the right half of field of vision into the left hemisphere of brain, and information about the left half of field of vision into the right hemisphere. The same is held true for the hearing system [Penrose, 1989, Chapter 9]. It is naturally to think that these inherited physiological phenomena have relations with mentioned cruciform algebraic structures in the genetic code system.

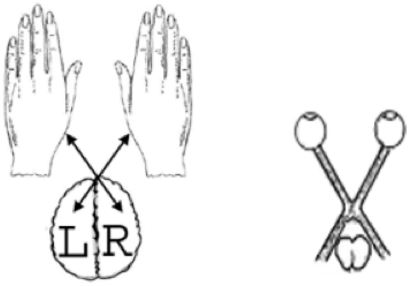
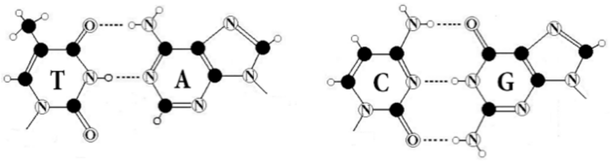


Fig. 10. The cruciform organisation of some morpho-functional structures in a human body. On the left side: cruciform connections of brain hemispheres with the left and the right halves of a human body. On the right side: the cruciform structure of optic nerves from eyes in brain.

6. Matrices of DNA alphabets, double numbers and the golden section

Let us return to Fig. 2 with matrices of DNA alphabets of 4 nucleobases [G, T; C, A], 16 doublets $[G, T; C, A]^{(2)}$ and 64 triplets $[G, T; C, A]^{(3)}$. Nucleobases A and G are purine nucleobases having two rings in their molecular configurations with 9 atoms in rings; nucleobases C and T are pyrimidine nucleobases having one ring in their molecular configurations with 6 atoms in the ring (11, top). Representing each of nucleobases by these numbers of atoms in rings, numeric representations of the matrices [G, T; C, A], $[G, T; C, A]^{(2)}$ and $[G, T; C, A]^{(3)}$ arise shown in Fig. 11, bottom. These numeric matrices consist of bisymmetric (2*2)-subquadrants representing appropriate 2-dimensional double numbers.



9	6
6	9

;

81	54	54	36
54	81	36	54
54	36	81	54
36	54	54	81

;

729	486	486	324	486	324	324	216
486	729	324	486	324	486	216	324
486	324	729	486	324	216	486	324
324	486	486	729	216	324	324	486
486	324	324	216	729	486	486	324
324	486	216	324	486	729	324	486
324	216	486	324	486	324	729	486
216	324	324	486	324	486	486	729

Fig. 11. At the upper row: molecular configurations of purine nucleobases A and G (having 9 atoms in their two rings) and pyrimidine nucleobases C and T (having 6 atoms in their ring). At the bottom row: numeric represntations [9 6; 6 9], $[9\ 6;\ 6\ 9]^{(2)}$ and $[9\ 6;\ 6\ 9]^{(3)}$ of the symbolic matrices of 4 nucleobases [G, T; C, A], 16 doublets $[G, T; C, A]^{(2)}$ and 64 triplets $[G, T; C, A]^{(3)}$ from Fig. 2.

The numeric matrices in Fig. 11 consist of bisymmetric (2*2)-subquadrants representing appropriate 2-dimensional double numbers. Moreover, the matrix [9 6; 6 9] represents 2-dimensional double number 9+6j; the matrix $[9\ 6;\ 6\ 9]^{(2)}$ represents 4-dimensional double number $81+54j_1+54j_2+36j_3$; the matrix $[9\ 6;\ 6\ 9]^{(3)}$ represents 8-dimensional double number $729+486j_1+486j_2+324j_3+486j_4+32j_5++324j_6+216j_7$ (here j_k are imaginary units with the property $j_k^2 = +1$).

Extracting the square root of these matrices [9 6; 6 9], $[9\ 6;\ 6\ 9]^{(2)}$ and $[9\ 6;\ 6\ 9]^{(3)}$ gives irrational matrices, all entries of which unexpectedly related with the famous golden section f (in integer powers) and which can be termed conditionally as golden matrices (Fig. 12):

$$([9\ 6;\ 6\ 9])^{1/2} = 3^{1/2}\,[f,\ f^{-1};\ f^{-1},\ f];\ ([9\ 6;\ 6\ 9]^{(2)})^{1/2} = 3[f,\ f^{-1};\ f^{-1},\ f]^{(2)};\ ([9\ 6;\ 6\ 9]^{(3)})^{1/2} = 3^{3/2}[f,\ f^{-1};\ f^{-1},\ f]^{(3)} \qquad (3)$$

The golden section $f = (1+5^{0.5})/2 = 1, 618\ldots$ is known long ago in aesthetics of proportions, in morphogenetic phyllotaxis laws and in some physiological processes as noted by many authors.

$$3^{1/2}\begin{array}{|c|c|}\hline f & f^{-1} \\ \hline f^{-1} & f \\ \hline\end{array}\;;\quad 3\begin{array}{|cc|cc|}\hline f^{2} & f^{0} & f^{0} & f^{-2} \\ f^{0} & f^{2} & f^{-2} & f^{0} \\ \hline f^{0} & f^{-2} & f^{2} & f^{0} \\ f^{-2} & f^{0} & f^{0} & f^{2} \\ \hline\end{array}\;;\quad 3^{3/2}\begin{array}{|cc|cc|cc|cc|}\hline f^{3} & f^{1} & f^{1} & f^{-1} & f^{1} & f^{-1} & f^{-1} & f^{-3} \\ f^{1} & f^{3} & f^{-1} & f^{1} & f^{-1} & f^{1} & f^{-3} & f^{-1} \\ \hline f^{1} & f^{-1} & f^{3} & f^{1} & f^{-1} & f^{-3} & f^{1} & f^{-1} \\ f^{-1} & f^{1} & f^{1} & f^{3} & f^{-3} & f^{-1} & f^{-1} & f^{1} \\ \hline f^{1} & f^{-1} & f^{-1} & f^{-3} & f^{3} & f^{1} & f^{1} & f^{-1} \\ f^{-1} & f^{1} & f^{-3} & f^{-1} & f^{1} & f^{3} & f^{-1} & f^{1} \\ \hline f^{-1} & f^{-3} & f^{1} & f^{-1} & f^{1} & f^{-1} & f^{3} & f^{1} \\ f^{-3} & f^{-1} & f^{-1} & f^{1} & f^{-1} & f^{1} & f^{1} & f^{3} \\ \hline\end{array}$$

Fig. 12. Bisymmetric enetic matrices $([9\ 6;\ 6\ 9])^{1/2}$, $([9\ 6;\ 6\ 9]^{(2)})^{1/2}$ and $([9\ 6;\ 6\ 9]^{(3)})^{1/2}$ are related with the golden section $f = (1+5^{1/2})/2$.

Golden matrices (Fig. 12) represent double numbers: the matrix $[f,\ f^{-1};\ f^{-1},\ f]$ represents 2-dimensional double number $f+f^{-1}j$; the matrix $[f,\ f^{-1};\ f^{-1},\ f]^{(2)}$ represents 4-dimensional double number $f^2+j_1+j_2+f^{-2}j_3$; the matrix $[f,\ f^{-1};\ f^{-1},\ f]^{(3)}$ represents 8-dimensional double number $f^3+fj_1+fj_2+f^{-1}j_3+fj_4+f^{-1}j_5+f^{-1}j_6+f^{-3}j_7$. Denoted quadrants and subquadrants of these golden matrices also represent double numbers.

Data of matrix genetics on the hidden connection of the genetic code system with the golden section allow thinking that various realizations of the golden section in inherited bio-phenomena are based on them.

7. Some mathematical features of algebras of multiblock united-double numbers

For possible understanding reasons of the construction of the genetic code in accordance with the genetic (8*8)-matrix in the form of the collection of bisymmetric (2*2)-matrices in Fig. 3, the author studies mathematical features of different unions of bisymmetric (2*2)-matrices into united square matrices of higher orders. This Section describes some initial results of such study. In particular, it turned out that the case of combining bisymmetric (2*2)-matrices with complex coefficients into a single square matrix turned out to be especially interesting. This case of the union leads to algebras of non-hypercomplex numeric systems over the field of complex numbers.

Let us construct for example a united (4*4)-matrix, whose (2*2)-quadrants are bisymmetric matrix representations of four different 2-dimensional double numbers aj_0+bj_1, cj_0+dj_1, pj_0+qj_1 and sj_0+rj_1, where coefficients a, b, c, d, p, q, s, r are complex numbers (Fig. 11): $a=a_0+a_1i$, $b=b_0+b_1i$, $c=c_0+c_1i$, $d=d_0+d_1i$, $p=p_0+p_1i$, $q=q_0+q_1i$, $s=s_0+s_1i$, $r=r_0+r_1i$ where $i^2 = -1$ (the imagine unit of complex numbers).

$$\begin{array}{|cc|cc|}\hline a & b & c & d \\ b & a & d & c \\ \hline p & q & s & r \\ q & p & r & s \\ \hline\end{array}$$

Fig. 11. The matrix representation of 4-blocked united-double numbers, where entries are complex numbers.

With such (4*4)-matrices, one can perform the same usual algebraic operations of their addition, multiplication, etc. as in algebra of 2-dimensional double numbers; in results of such operations, matrices of the same structure arise (if the determinant of the matrix is zero, then it is impossible to divide by it). In the general case, united matrices of this type are not bisymmetric. By a similar uniting sets of matrix representations of considered double numbers (having their complex numeric enries) into one united matrix (or one matrix colony), matrices with sizes (6*6), (8*8), ..., (2n*2n) can be constructed, which refer to appropriate algebras over the field of complex numbers.

One more remark regarding the (4*4)-matrix with complex entries in Fig. 11. Taking into account that complex numbers $a=a_0+a_1i$ have their matrix representation by (2*2)-matrices $[a_0, a_1; -a_1, a_0]$, the (4*4)-matrix in Fig. 10 can be rewriting into the (8*8)-matrix in Fig. 12 where all entries are real numbers. This matrix represents a special algebra over the field of real numbers.

a_0	a_1	b_0	b_1	c_0	c_1	d_0	d_1
$-a_1$	a_0	$-b_1$	b_0	$-c_1$	c_0	$-d_1$	d_0
b_0	b_1	a_0	a_1	d_0	d_1	c_0	c_1
$-b_1$	b_0	$-a_1$	a_0	$-d_1$	d_0	$-c_1$	c_0
p_0	p_1	q_0	q_1	s_0	s_1	r_0	r_1
$-p_1$	p_0	$-q_1$	q_0	$-s_1$	s_0	$-r_1$	r_0
q_0	q_1	p_0	p_1	r_0	r_1	s_0	s_1
$-q_1$	q_0	$-p_1$	p_0	$-r_1$	r_0	$-s_1$	s_0

Fig. 12. The matrix representation of 8-dimensional numbers of a special algebra (see explanation in the text).

In Fig. 12, the (8*8)-matrix consists of 16 (2*2)-subquadrants, each of which represents a complex numbers. In other words, this matrix is a colony of 16 matrix representations of complex numbers and it refers to the algebra of non-hyperbolic numbers. Similar types of numeric systems were termed as “united-hypercomplex numbers” (or briefly "U-numbers" by the first letter in the word "united") [Petoukhov, 2017].

7. Some concluding remarks

In the course of his structural researches of the genetic system, the author is increasingly convinced in the following:

- The genetic code is an algebraic code associated with the wide class of algebraic codes from theory of noise-immunity coding of information;
- The use of algebras of multidimensional numerical systems is effective both for revealing the interconnections of structures of biological bodies at various levels of their organization, and for understanding the noise-immune properties of genetic informatics. This allows one to think that living organisms are algebraically encoded entities (or, briefly, algebraic entities).

The notion of “number” is the main notion of mathematical natural sciences. Pythagoras has formulated the idea: “*Numbers rule the world*” since he noted that numbers can dictate different geometric shapes. In view of this idea, natural phenomena should be explained by means of systems of numbers. As W. Heisenberg noted, modern physics is moving along the same Pythagorean path [Heisenberg, 1958]. B. Russell stated that he did not know any other person who could exert such influence on the thinking of people as Pythagoras [Russell, 1945]; correspondingly there is no more fundamental scientific idea in the world than this idea about a basic meaning of numbers. Our proposed approach using algebras of multidimensional numeric systems can be considered as a further development of this fundamental idea of Pythagoras in connection with the genetic system and inherited biological structures.

The matrix approach to structural ensembles of the genetic system, proposed and developed by the author (under the unifying name "matrix genetics"), provides the possibility of mathematical analysis of this system for revealing hidden interrelationships in it and for deeper understanding living matter.

The basic alphabet of DNA (and RNA) is closely related with binary numbers since it is represented by the set of 4 specific polyatomic molecular constructions, which bears the symmetric system of pairs of binary-oppositional attributes and forms three binary sub-alphabets (Fig. 2 and 3). This peculiarity of the alphabet is associated with thoughts about biological computers on the base of binary-oppositional resonances of genetic molecules [Petoukhov, 2015, 2016; Petoukhov, Petukhova, 2017].

Acknowledgments: Some results of this paper have been possible due to a long-term cooperation between Russian and Hungarian Academies of Sciences on the topic "Non-linear models and symmetrologic analysis in biomechanics, bioinformatics, and the theory of self-organizing systems", where S.V. Petoukhov was a scientific chief from the Russian Academy of Sciences. The author is grateful to G. Darvas, E. Fimmel, M. He, Z.B. Hu, I. Stepanyan, V. Svirin, G. Tolokonnikov for their collaboration.

References

Ahmed N.U., Rao K.R. *Orthogonal transforms for digital signal processing*. Springer-Verlag New York, Inc. (1975).

Annett M. *Left, right, hand and brain: the right shift theory*. New Jersey: Lawrence Erlbaum (1985).

Annett M. Spatial ability in subgroupt of left- and right-handers. *British Journal of Psychology,* v.83, pp. 493-962 (1992).

Barbieri M. Code Biology: A New Science of Life. Springer (2015), 246 pages.

Bodnar O.Ya. Geometry of phyllotaxis. *Reports of the Academy of Sciences of Ukraine*, №9, pp. 9-15 (1992).

Bodnar O.Ya. *Golden Ratio and Non-Euclidean Geometry in Nature and Art*. Lviv: Publishing House "Sweet" (1994).

Frank-Kamenetskii M.D. The most important molecule. Moscow, Nauka, 1988 (in Russian).

Gazzaniga M. S. Principles of human brain organization derived from split brain studies. *Neuron, 14*, 217-228. (1995).

Harkin A.A., Harkin J.B. Geometry of Generalized Complex Numbers. *Mathematics Magazine*, v. 77(2), p. 118-29 (2004).

Harmuth, H. F. *Information theory applied to space-time physics*. Washington: The Catholic University of America, DC (1989)

Heisenberg W. *Physics and philosophy*. New York: Harper & Row (1958).

Hellige J.B. *Hemispheric Asymmetry: What's Right and What's Left. Cambridge*. Massachusetts: Harvard University Press. (1993).

Hu Z.B., Petoukhov S.V., Petukhova E.S. I-Ching, dyadic groups of binary numbers and the geno-logic coding in living bodies. - *Progress in Biophysics and Molecular Biology,* v. 131, pp. 354-368 (2017). (https://doi.org/10.1016/j.pbiomolbio.2017.08.018).

Ivanov Viach.Vs. Linguistic way of Roman Jakobson. – In: Jakobson R.O. *Selected works*. M., Progress (1985, in Russian).

Jakobson R.O. Selected works. M., Progress (1985, in Russian).

Jakobson R. *Language in Literature.* Cambridge: MIT Press (1987).

Jakobson R.O. *Texts, Documents, Studies*. Moscow: RGGU (1999, in Russian).

Jean R. *Phyllotaxis. A systemic study in plant morphogenesis*. Cambridge Univ. Press (2006).

Kantor I.L., Solodovnikov A.S. *Hypercomplex numbers*. Berlin, New York: Springer-Verlag (1989). ISBN 978-0-387-96980-0.

Klein F. Elementary Mathematics from an Advanced Standpoint: Arithmetic, Algebra, Analysis. London: Dover Publications (2004).

Makovsky M.M. Linguistic genetics. M., Nauka (1992, in Russian).

Penrose R. *The Emperor's New Mind*. Oxford University Press, USA (1989).

Petoukhov S.V. *Matrix genetics, algebrases of genetic code, noise immunity*. Moscow, RCD, 316 p. (2008, in Russian).

Petoukhov S.V. Matrix genetics and algebraic properties of the multi-level system of genetic alphabets. *Neuroquantology*, v. 9, №4, p. 60-81 (2011).

Petoukhov S.V. The concept of resonances in genetics ("resonant bioinformatics"). Selected proceedings of the VII International Congress "Weak and Super-Weak Fields and Radiations in Biology and Medicine", 7. 09.2015, St. Petersburg, pp.1-41 (2015) (in Russian). http://www.biophys.ru/lib/sci/resonance/460-resonance-00001.

Petoukhov S.V. The system-resonance approach in modeling genetic structures. *Biosystems*, v. 139, p. 1-11 (January 2016).

Petoukhov S.V. Symmetries of the genetic code, Walsh functions and the theory of genetic logical holography. - *Symmetry: Culture and Science*, v.27, №2, p. 95-98 (2016b).

Petoukhov S.V. The genetic code, 8-dimensional hypercomplex numbers and dyadic shifts. (2016c), https://arxiv.org/pdf/1102.3596v11.pdf

Petoukhov S.V. Genetic coding and united-hypercomplex systems in the models of algebraic biology. *Biosystems*, v. 158, August 2017, pp. 31–46 (2017).

Petoukhov S.V. The Genetic Coding System and Unitary Matrices. Preprints 2018, 2018040131 (doi: 10.20944/preprints201804.0131.v2), submitted 27.09.2018. http://www.preprints.org/manuscript/201804.0131/v2 (2018a).

Petoukhov S.V. Structural Connections between Long Genetic and Literary Texts. - *Preprints* 2018, 2018120142, online 15 02 2019. (2018b). DOI: 10.20944/preprints201812.0142.v2, https://www.preprints.org/manuscript/201812.0142/v2

Petoukhov S.V. Nucleotide Epi-Chains and New Nucleotide Probability Rules in Long DNA Sequences. *Preprints* 2019, 2019040011 (doi: 10.20944/preprints201904.0011.v2) (2019a). https://www.preprints.org/manuscript/201904.0011/v2.

Petoukhov S.V. Connections Between Long Genetic and Literary Texts. The Quantum-Algorithmic Modeling. - In: Hu Z., Petoukhov S., Dychka I., He M. (eds) *Advances in Computer Science for Engineering and Education II*. pp 534-543, ICCSEEA 2019. *Advances in Intelligent Systems and Computing*, vol 938. Springer, Cham. Online publication on 29 March 2019b, https://link.springer.com/chapter/10.1007/978-3-030-16621-2_50#citeas, DOI https://doi.org/10.1007/978-3-030-16621-2_50

Petoukhov S.V., He M. *Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications*. IGI Global, USA (2010). http://petoukhov.com/Petoukhov,%20He%20-%202010%20-%20Symmetrical%20Analysis%20Techniques%20for%20Genetic%20Systems%20and%20Bioinformatics.pdf.

Petoukhov S.V., **Petukhova E.S**. The concept of systemic-resonance bioinformatics. Resonances and the quest for transdisciplinarity.- In the book: Information Studies and the Quest for Transdisciplinarity. World Scientific Series in Information Studies, volume 9, Chapter 17. Editors – M. Burgin, W.Hofkirchner, World Scientific, 2017, p. 467-487. http://petoukhov.com/PETOUKHOV_worldScientific2017.pdf

Petoukhov S.V., Petukhova E.S., Svirin V.I. Symmetries of DNA alphabets and quantum informational formalisms. *Symmetry: Culture and Science*, Vol. 30, No. 2, 161-179 (2019), https://doi.org/10.26830/symmetry_2019_2_161

Russell B. A *history of western philosophy*. New York: Touchstone (1945).

Sagalovich Yu.L. Introduction to Algebraic Codes, Moscow: Moscow Physical-Technical Institute (2011, in Russian).

Seberry J., Wysocki D.J., Wysocki T.A. Some applications of Hadamard matrices. *Metrika,* 62, p. 221-239 (2005). https://www.uow.edu.au/~jennie/WEBPDF/2005_12.pdf

Shervatov V.G. *Hyperbolic functions*. Moscow, GITTL (1954, in Russian).

Shults E. The organism as a creativity. In the book "*Questions of theory and psychology of creativity" ("Voprosy teorii i psikhologii tvorchestva")*, Russia, Kharkov, vol.7, pp. 108-190 (1916) (in Russian).

Smolyaninov V.V. Spatio-temporal problems of locomotion control. Uspekhi Fizicheskikh Nauk, v.170, N 10, pp. 1063–1128 (2000), DOI: https://doi.org/10.3367/UFNr.0170.200010b.1063.

Vernadsky V.I. *The chemical structure of the biosphere and its environment*. Moscow, Nauka (1965, in Russian).