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

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Abstract. The article shows materials to the question about algebraic features of the genetic code and about the dictatorial influence of the DNA and RNA molecules on the whole organism. 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. Structural features of the genetic systems are associated with hypercomplex double (or hyperbolic) numbers and with bisymmetric doubly stochastic matrices. The received results confirm that represented matrix approaches are effective for modeling genetic phenomena 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 where structures of genetic molecules have the dictatorial influence on inherited structures of the whole organism. New described algebraic approaches and results are discussed.

Keywords: genetic code, DNA, alphabet, amino acids, hypercomplex numbers, doubly stochastic matrix, binary numbers, dyadic groups, tensor product, palindrome.

CONTENTS

1. Introduction.

What is the main difference between living cells and inanimate objects? One of the creators of quantum mechanics P. Jordan pointed out the following main difference [McFadden, Al-Khalili, 2018]. Inanimate objects are governed by the average random motion of millions of particles, such that the motion of a single molecule has no influence whatsoever on the whole object. By contrast, the few molecules control dynamics of living cells and have dictatorial influence through quantum-level events that govern their motion and are amplified to influence the entire organism. This insight is usually credited to Erwin Schrödinger, who later claimed that life was different from inorganic chemistry because of its dependence on the dynamics of a small number of molecules. P. Jordan, credited with the authoring the first work on quantum biology, postulated that the mechanisms of living organisms are associated with what he referred to as his 'amplifier theory', based on Bohr's notion of the '*irreversible act of amplification*', required to bring the fuzzy quantum reality into sharp focus by '*observing*' it [Jordan, 1932]. Jordan claimed that «*life's missing laws were the rules of chance and probability (the indeterminism) of the quantum world that were somehow scaled up inside living organisms*» [McFadden, Al-Khalili, 2018].

Living bodies are ensembles of a huge number of molecules interrelated by quantum-mechanical, resonant, stochastic and other principles. These ensembles have an amazing ability to inherit their biological traits to their descendants. G.Mendel in his experiments on the crossing of organisms discovered that the inheritance of these characters occurs according to algebraic rules, despite the colossal heterogeneity of the molecular structure of bodies. These algebraic rules of polyhybrid crossbreeding are presented in textbooks since 1906 in the form of Punnett squares, reminiscent of the structure of mathematical matrices. To explain the discovered statistical rules, Mendel proposed the remarkable idea of binary-opposition forms of existence of inheritance factors: dominant and recessive forms, combinations of which are shown in Punnett squares. In our days, many binary-oppositional features of the molecular-genetic systems and the dictatorial influence of genetic molecules on the whole organism are intensively studied [Petoukhov, 2008, 2011, 2016-2019; Petoukhov, He, 2010; Petoukhov, Petukhova, 2017a,b; Petoukhov, Petukhova, Svirin, 2019]. All inherited physiological systems, as parts of a whole organism, must be structurally coupled with a genetic code for transmission to descendants in encoded form. Therefore, inherited macrostructures can bear the imprint of structural features of the genetic code. Taking this into account, genetic biomechanics is developing as a new scientific direction in biomechanics, where symmetrologic approaches play an important role [Petoukhov, 2001, 2003-2006, 2008, 2012, 2015, 2016a,b, 2018a,b, 2019a,b; Petoukhov, He, 2010]. The presented article is devoted to some symmetrologic thematic researches related with DNA binary-opposition structures. The author notes that binary-oppositional structures in the genetic systems can be modeled by means of bisymmetric matrices representing 2-dimensional hypercomplex double (or hyperbolic) numbers and doubly stochastic matrices jointly with their tensor extensions.

The purpose of this and other works of the author is to cognize and demonstrate the dictatorial influence of DNA and RNA molecules on living organisms and the relationship of the parts in them. These works develop modern algebraic biology, where attention is focused on the named dictatorial influence of genetic molecules in contrast to works of many other

authors in the field of mathematical biology. For example, the fine book about the history of mathematical biology "The Mathematics of Life: Numbers in biology and ecology" [Rafael Lahoz-Beltra, 2014] doesn't mention molecules DNA and RNA at all though they have algebraic features of key meaning for biological informatics.

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 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. Double 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. 1.1). Such matrix represesetations 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. 1.1. 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, 2011a,b, 2016b, 2017, 2018; Petoukhov, He, 2010; Petoukhov, Petukhova, Svirin, 2019].

2. The genetic code 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. 2.1. 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 (see explanations in the text).

These three tables (Fig. 2.1) 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 inside matrices [C, A; G, T]$^{(2)}$ and [C, A; G, T]$^{(3)}$ as shown in Fig. 2.1.

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. 2.1) was built formally without any mention of amino acids and stop-codons. Nothing data preliminary exist on a possible correspondence between triplets and amino acids. 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. 2.2 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 one, which is considered in the theory of symmetries as the basic from the structural standpoint).

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

Fig. 2.2. 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. 2.2):

- Each of sixthteen (2*2)-subquadrants, 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. 2.3) with bisymmetric (2*2)-subquadrants representing double numbers aj_0+bj_1 described above in the Section 1

(Fig. 1.1). 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.

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

Fig. 2.3. The numeric analogue of the symbolic (8*8)-matrix of amino acids and stop-codons from Fig. 2.2 for the case of representing each of amino acids by numbers of its carbon atoms (stop-codons are conditionally represented by zero).

One should note an additional connection of genetic matrices in Fig. 2.1 with double numbers. Let us denote in these matrices purines A and G by the traditional symbol R, and pyrimidines C and T by the symbol Y. Then these matrices (Fig. 2.4) will represent 2-, 4- and 8-dimensional double numbers $R + Yj_1$, $RR + RYj_1 + YRj_2 + YYj_3$, $RRR+RRYj_1+RYRj_2+RYYj_3+YRRj_4+YRYj_5+YYRj_6+YYYj_7$ correspondingly.

R	Y
Y	R

RR	RY	YR	YY
RY	RR	YY	YR
YR	YY	RR	RY
YY	YR	RY	RR

RRR	RRY	RYR	RYY	YRR	YRY	YYR	YYY
RRY	RRR	RYY	RYR	YRY	YRR	YYY	YYR
RYR	RYY	RRR	RRY	YYR	YYY	YRR	YRY
RYY	RYR	RRY	RRR	YYY	YYR	YRY	YRR
YRR	YRY	YYR	YYY	RRR	RRY	RYR	RYY
YRY	YRR	YYY	YYR	RRY	RRR	RYY	RYR
YYR	YYY	YRR	YRY	RYR	RYY	RRR	RRY
YYY	YYR	YRY	YRR	RYY	RYR	RRY	RRR

Fig. 2.4. Transformations of the genetic matrices from Fig. 2.1 under denotations of their purines A and G by the symbol R, and pyrimidines C and T by the symbol Y.

The mentioned connection between the matrices in Fig. 2.4 correspondingly with 2-, 4- and 8-dimensional double numbers is revealed by the decompositions of these matrices on the basis of dyadic shifts described below. Fig. 2.5 shows an explanation example of the dyadic-shift dcomposition of the (4*4)-matrix of 16 doublets from Fig. 2.4 into the sum of 4 sparse matrices, which represent basis units j_0, j_1, j_2, and j_3 of 4-dimensional double numbers. This set of 4 sparse matrices is closed relative multiplication and it defines the multiplication table of the algebra of 4-dimensional double numbers.

$$
\begin{vmatrix} RR & RY & YR & YY \\ RY & RR & YY & YR \\ YR & YY & RR & RY \\ YY & YR & RY & RR \end{vmatrix} = RR \begin{vmatrix} 1&0&0&0 \\ 0&1&0&0 \\ 0&0&1&0 \\ 0&0&0&1 \end{vmatrix} + RY \begin{vmatrix} 0&1&0&0 \\ 1&0&0&0 \\ 0&0&0&1 \\ 0&0&1&0 \end{vmatrix} + YR \begin{vmatrix} 0&0&1&0 \\ 0&0&0&1 \\ 1&0&0&0 \\ 0&1&0&0 \end{vmatrix} + YY \begin{vmatrix} 0&0&0&1 \\ 0&0&1&0 \\ 0&1&0&0 \\ 1&0&0&0 \end{vmatrix}
$$

Fig. 2.5. The dyadic-shift decomposition of the genetic (4*4)-matrix from Fig. 2.4.

Demonstrated by the matrices in Figs. 2.2-2.5, 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, 2016a,b, 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.

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, 2016; 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:

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

The known operation of the bitwise modulo-2 addition serves as the group operation in dyadic groups. It is denoted by the symbol $\oplus$ 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. 2.1 and 4.1, appropriate triplets from Fig. 2.1 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. 3.1. 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. 3.1 that this matrix of dyadic shifts consists of 16 bisymmetrical (2*2)-subquadrants in some analogy with the genetic matrices in Fig. 2.2 and 2.3. 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, 2011a, 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. 2.1 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. 2.1 lead to the bisymmetric matrix of Hamming distances for triplets in Fig. 4.1.

	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. 4.1. The bisymmetric matrix of Hamming distances for two kinds of binary representations of 64 triplets in the genetic matrix in Fig. 2.1.

From Fig. 4.1 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. 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.
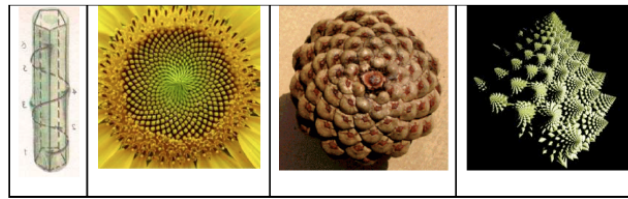
Fig. 5.1. Examples of phyllotaxis configurations in biological bodies.

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:

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

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 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. 5.2, 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. 5.2, 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: $\Delta p = k * \ln(x_2/x_1)$. Each of these points $(x_1, 1/x_1)$ and $(x_2, 1/x_2)$ of the hyperbola can be considered as double number.
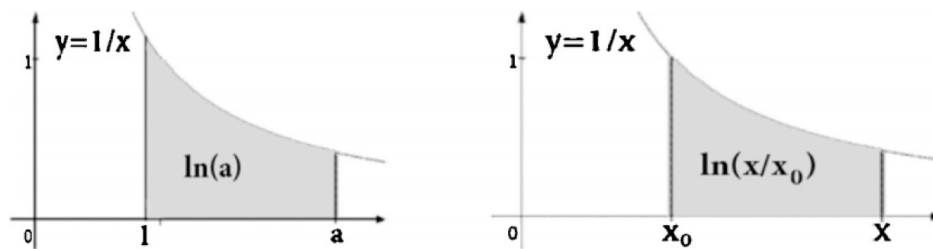
Fig. 5.2. Illustration of the connection of hyperbolic rotations with the psychophysical law of Weber-Fechner (its explanation in the text).

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, 2018, 2019a,b].

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] 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, 2018, 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. 5.3, left).
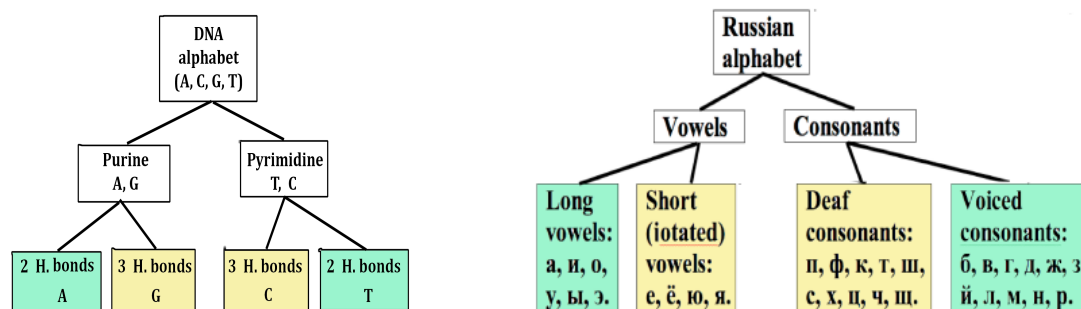

Fig. 5.3. Binary-oppositional structures of the DNA alphabet and of the Russian alphabet.

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. 5.3, 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. 5.3) represented by the common symbol 0;
- the second class combines all the long vowels and voiced consonants (green boxes in Fig. 5.3) 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, 2018, 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. 3.1) and for genetic matrices of Hamming distances (Fig. 4.1). 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 serves the left half of the body (Fig. 5.4) [Annett, 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.
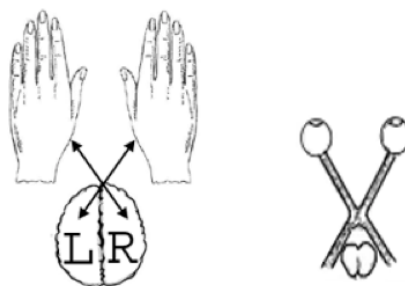

Fig. 5.4. The cruciform organisation of some morpho-functional structures in a human body. On the left side: cruciform connections of brain hemispheres with the left and the right halves of a human body. On the right side: the cruciform structure of optic nerves from eyes in brain.

6. Double numbers, bisymmetric doubly stochastic matrices and unitary matrices

Above we noted tensor families of bisymmetric $(2^n * 2^n)$-matrices of percentages $[q, p; p, q]^{(n)}$, where $q + p = 1$, which are matrix representations of particular cases of 2^n-dimensional double numbers and which model hidden rules of percentages in long genetic and literary Russian texts. Such matrices simultaneously belong to an important class of so called doubly

stochastic matrices. By definition, a square matrix is called *doubly stochastic* if all entries of the matrix are nonnegative and the sum of the elements in each row and each column is unity.

Such matrices have long been known and important for many problems of game theory and linear programming: optimizing access to resources, forming winning coalitions, logistics, growth models in oncology, etc. [Bapat, Raghavan, 1997; Prasolov, 1994]. This can allow you to transfer some already known mathematical results from game theory and from other fields into the field of models of algebraic biology. As far as the author knows, the first mention about a connection of some kinds of genetic matrices with doubly stochastic matrices was made by Prof. Matthew He in the book [Petoukhov, He, 2010].

The bisymmetric doubly stochastic matrices considered above are associated with unitary matrices that are important for quantum informatics, quantum mechanics, noise-immune coding of information, etc. and that are used in matrix genetics [Petoukhov, 2008, 2018; Petoukhov, He, 2010] The following known theorem states this connection [Prasolov, 1994]:

- if a square $(n*n)$-matrix M=$\|m_{ij}\|$ is unitary then a $(n*n)$-matrix B=$\|b_{ij}\|$, where $b_{ij} = |m_{ij}|^2$, is a doubly stochastic.

For example, the unitary matrix [0.6481, -0.7616; 0.7616, 0.6481] under squaring its components becomes the doubly stochastic matrix [0.6481^2, $(-0.7616)^2$; 0.7616^2, 0.6481^2] = [0.42, 0.58; 0.58, 0.42]. Transformations based on unitary matrices are transformations of the rotation and reflection of vectors, preserving their lengths and angles.

Representations of DNA alphabets by genetic matrices like as in Fig. 2.1 show connections of the genetic system with unitary matrices, first of all, with Hadamard matrices. One of the types of binary oppositions in the DNA alphabet is the opposition of the letter T to the other three letters A, C, G:

-1) when switching from DNA to RNA, only this letter T replaced by another (uracil U);

- 2) only this letter T has not the important amino group NH_2.

Representing this opposition as A = C = G = +1, T = -1, we get the representation of the symbolic matrix [G, T; C, A] in the form of one of famous Hadamard matrices H_2 (Fig. 6.1) satisfying the definition $H_nH_n^T = n*E$, where n refers the order of the matrix and E is the identity matrix. Under its normalization to the unit determinant by means of the factor $2^{-0.5}$, this Hadamard matrix H_2 becomes one of unitary matrices $M=2^{-0.5}*H_2$. In accordance with the mentioned theorem, the unitary matrix M = [$2^{-0.5}$, $2^{-0.5}$; $-2^{-0.5}$, $2^{-0.5}$] - under squaring its components - becomes the doubly stochastic matrix [$(2^{-0.5})^2$, $(2^{-0.5})^2$; $(-2^{-0.5})^2$, $(2^{-0.5})^2$] = [0.5, 0.5; 0.5, 0.5]. Tensor powers of any unitary matrix always generate new unitary matrices of increased orders; each of these new unitary matrices under squaring its components becomes an appropriate doubly stochastic matrix.

The alphabetic systems of DNA and RNA with their binary-oppositional features have links with many families of Hadamard matrices. For example, any interchange of positions of letters inside the matrix [G, T; C, A] gives a new symbolic matrix, which becomes a new Hadamard matrix under replacing its symbols by the same numeric opposition A = C = G = +1, T = -1. Fig. 6.2 shows one of examples of these operations.

$$\begin{array}{|c|c|} \hline C & A \\ \hline T & G \\ \hline \end{array} \quad \rightarrow H_2 = \begin{array}{|c|c|} \hline 1 & 1 \\ \hline -1 & 1 \\ \hline \end{array}$$

Fig. 6.2. One of examples of Hadamard matrices related with matrix representations of the DNA alphabet.

These relations DNA-alphabets with Hadamard matrices and with their normalized unitary versions are interesting because of the important role of Hadamard matrices in quantum mechanics (unitary Hadamard operators), quantum computers (Hadamard gates), spectral analysis, multichannel spectrometers, noise-immune coding of information, where a whole class of noise-immune codes are based on them, etc.

Unitary genetic matrices define transformations of rotation and reflection. When unitary matrices are raised to a power, they form cyclic groups with different periods for modeling cyclic biostructures. For example, when taking into account some binary-oppositional features of DNA-alphabets of 16 doublets and 64 triplets, Hadamard matrices H_4 and H_8 appear, which represent Hamilton quaternions and biquaternions with unit coordinates (Fig. 6.3).

Fig. 6.3. Hadamard matrices representing Hamilton quaternions and biquaternions with unit coordinates.

Under their normalisation to unit determinants, these matrices H_4 and H_8 are unitary matrices $0.5*H_4$ and $2^{-3/2}*H_8$. When these matrices are raised to a power, they form cyclic groups with periods 6 and 24 correspondingly: $(0.5*H_4)^{n+6} = (0.5*H_4)^n$ and $(2^{-3/2}*H_8)^{n+24} = (2^{-3/2}*H_8)^n$. Due to their internal structures, these groups are used for modeling some cyclic biophenomena as it was described, for example, in works [Petoukhov, 2011b, 2016].

All calculations in quantum computers are built on unitary matrices, and each unitary matrix can be used as a logical gate in quantum computers. Our data on the relationship of the alphabetic system of DNA with unitary matrices suggests that inherited control of physiological processes is also largely based on unitary operators that represent rotation and reflection transformations. In particular, we note that the entire kinematic scheme of movements of our body and its parts is built on rotations in its joints and mirror reflections. Additional relations of DNA-alphabets with unitary matrices are described in [Petoukhov, 2018a; Petoukhov, Petukhova, 2020].

In addition to the mentioned theorem, one can also note another connection between bi-symmetric doubly stochastic (2^n*2^n)-matrices and unitary matrices: the set of 2^n eigenvectors of these doubly stochastic matrices serve as columns of unitary (2^n*2^n)-matrices with real components. This relationship will be shown with a concrete example in the next paragraph.

7. Mendel's laws of heredity and their matrix modeling

This section is devoted to modeling the phenomenologic ratios based on the probabilities of individual gene combinations for the case of Mendel's laws of segregation and also an independent assortment of traits [Miko, 2008].

The law of segregation of genes applies when two individuals, both heterozygous for a certain trait are crossed, for example, hybrids of the first generation. The offspring

in the second generation differ in genotype and phenotype so that the characteristics of the grandparents regularly occur again. In a dominant-recessive inheritance, an average of 25 % are homozygous with the dominant trait, 50 % are heterozygous showing the dominant trait in the phenotype (genetic carriers), 25 % are homozygous with the recessive trait and therefore express the recessive trait in the phenotype. So, in this basic case, the phenotypic ratio is 3: 1 (or 3/4: 1/4).

Let us represent these phenomenologic data in the form of an appropriate bi-symmetric doubly stochastic (2*2)-matrix D, which is shown jointly with its set of 2 eigenvectors serving as columns of the matrix M_2 in Fig. 7.1 (eigenvalues of these eigenvectors are equal to 0.5 and 1.0 correspondingly). It is easy to check that the matrix of eigenvectors M_2 is unitary. Moreover, it is a normalized Hadamard matrix (the factor $2^{-0.5}$ normalized the Hadamard matrix [-1, 1; 1 1] to the unit determinant). This reveals one more connection of genetics with Hadamard matrices.

$$D = \begin{vmatrix} 3/4, & 1/4 \\ 1/4, & 3/4 \end{vmatrix}; \qquad M_2 = 2^{-0.5} \begin{vmatrix} -1, & 1 \\ 1, & 1 \end{vmatrix}$$

Fig. 7.1. The bi-symmetric doubly stochastic matrix D, representing the phenotypic ratio 3/4: 1/4 in the considered basic case of mendelian genetics, and the unitary matrix M_2 of its eigenvectors.

The matrix D from Fig. 7.1 is also a representation of 2-dimensional double number $3/4 + j_1*1/4$. The second tensor power of the matrix D gives a new bi-symmetric doubly stochastic matrix $D^{(2)}$ representing 4-dimensional double number $9/16 + j_1*3/16 + j_2*3/16 + j_3*1/16$. Ratios of coordinates of this double number 9:3:3:1 model well-known phenotypic ratios 9:3:3:1 in the case of dihybrid crosses in mendelian genetics. Fig. 7.2 shows the (4*4)-matrix $D^{(2)}$, whose 4 eigenvectors are columns of the unitary (4*4)-matrix M_4. Using higher tensor powers n for the doubly stochastic matrix D, you automatically get phenotypic ratios for the cases of mendelian n-hybrid crosses in the form of coordinates of an appropriate 2^n-dimensional double number $D^{(n)}$; the set of eigenvectors of the matrix $D^{(n)}$ will define a unitary (2^n*2^n)-matrix again.

$$D^{(2)} = \begin{vmatrix} 0.5625 & 0.1875 & 0.1875 & 0.0625 \\ 0.1875 & 0.5625 & 0.0625 & 0.1875 \\ 0.1875 & 0.0625 & 0.5625 & 0.1875 \\ 0.0625 & 0.1875 & 0.1875 & 0.5625 \end{vmatrix}; \quad M_4 = \begin{vmatrix} -0.5000 & -0.5973 & 0.3785 & 0.5000 \\ 0.5000 & -0.3785 & -0.5973 & 0.5000 \\ 0.5000 & 0.3785 & 0.5973 & 0.5000 \\ -0.5000 & 0.5973 & -0.3785 & 0.5000 \end{vmatrix}$$

Fig. 7.2. On the right side: the second tensor power of the matrix D from Fig. 7.1. On the left side: the unitary matrix M_4 formed by eigenvectors of the matrix $D^{(2)}$.

8. Tensor families of genetic matrices and the conception of tensor-matrix memory

Any Hadamard matrix H, raised to the tensor powers of $H^{(n)}$, generates new Hadamard matrices. In these new Hadamard matrices one can see fractal-like repetitions of the original mosaic of the matrix H at new levels (Fig. 8.1). This reflects the property of the tensor product of matrices to generate fractal-like patterns.
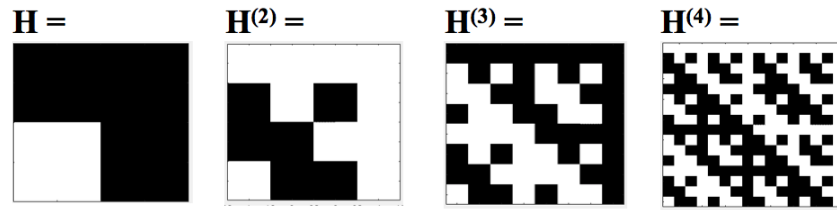
Fig. 8.1. An example of fractal-like mosaics in the tensor family of Hadamard matrices $H^{(n)} =$ $[1\ 1, -1\ 1]^{(n)}$. Here black cells mean entries +1 and white cells mean entries -1.

The fractal properties of tensor families of Hadamard matrices can be represented by graphs when in Hadamard matrices entries -1 are replaced by entries 0. Then the Hadamard matrices take the form of adjacency matrices known in graph theory. Tensor family of adjacency matrices $[1,\ 1;\ 0\ 1]^{(n)}$, which corresponds to the tensor family of Hadamard matrices $[1,\ 1;\ 0\ 1]^{(n)}$, has the same grafical representation shown in Fig. 8.1, only in this case white cells mean entries 0. Fig. 8.2 shows examples of graphs corresponding to adjacency matrices $[1,\ 1;\ 0\ 1]^{(n)}$.
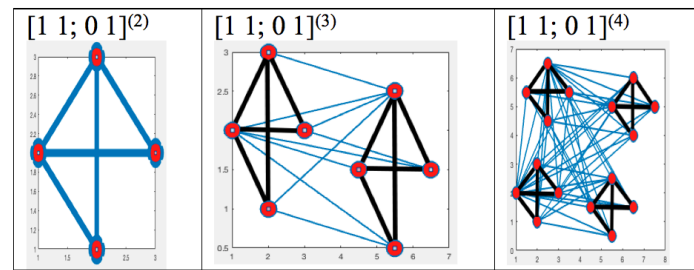

Fig. 8.2. Graphs corresponding to initial members of the tensor family of adjacency matrices $[1,\ 1;\ 0,\ 1]^{(n)}$, where $n = 2, 3, 4,$ related with the tensor family of Hadamard matrices $[1,\ 1;\ -1,\ 1]^{(n)}$.

In the graphs on the basis of these matrices, groups of cooperative links of the graph of the previous matrix can be inherited into the graphs of matrices of higher tensor degrees as one can see in Fig. 8.2. This inheritance of groups of cooperative links in a tensor family of graphs the author conventionally termes "tensor-matrix memory."

In the genetic system, much is associated with cyclic rearrangements. Taking a different matrix of the DNA-alphabet with cyclically shifted positions [A, G; C, T], you obtain a different tensor family of Hadamard matrices and appropriate tensor family of adjacency matrices $[1,\ 1;\ 1,\ 0]^{(n)}$, with a different tensor family of graphs and a different tensor-matrix memory (Fig. 8.3).
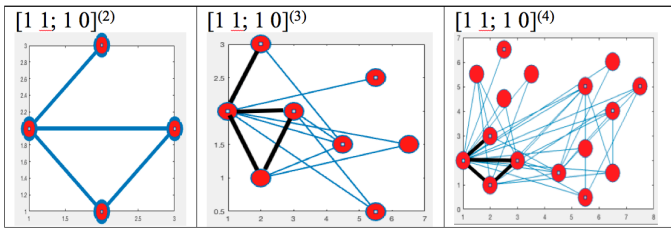
Fig. 8.3. Upper row: the graphical representation of the tensor family of Hadamard matrices $[1, 1; 1, -1]^{(n)}$, and corresponding tensor family of adjacency matrices $[1, 1; 1, 0]^{(n)}$, where $=$ 2, 3, 4. Bottom row: graphs corresponding to initial members of this tensor family of adjacency matrices $[1, 1; 0, 1]^{(n)}$.

Properties of different tensor families of graphs related cyclic shifts in matrices representing DNA-alphabets, allow thinking about networks of cyclic tensor-matrix memory in genetic systems and studying such networks. Here it should be noted a lot of research that is being conducted in cognitive neurobiology regarding networks of cooperative link groups of neurons. The author believes that it makes sense to compare the networks of cooperative linking groups in genetics and neurobiology for mutual enrichment of genetics and cognitive neurobiology. Here one should remark that the nervous system appeared in biological evolution relatively recently. Billions of organisms perfectly existed and exist without nerve fibers at all, but with successfully solving the problems of food search, rescue from predators, etc. The nervous system in evolution did not appear at an empty place, but as a superstructure over the corresponding networks of protein and nuclein structures in relation with them on the basis of similar genetic algorithms.

9. Genetic matrices of generating and replications of vectors of complementary palindromes

One of important types of binary-oppositional features in the genetic coding system was noted by Yu.Rumer [Rumer, 1968; Fimmel, Strüngmann, 2016]. He described that the set of 64 triplets, according to their features of coding 20 amino acids, is divided into two subsets of 32 triplets in each:
- 32 triplets with "strong roots" (that is, with 8 doublets CC, CT, CG, AC, TC, GC, GT, GG at the beginning of triplets), whose code meanings do not depend on the letter in their third position;
- 32 triplets with "weak roots" (that is, with the remaining 8 doublets CA, AA, AT, AG, TA, TT, TG, GA at the beginning of triplets), whose code meanings depend on the letter in their third position.

Fig. 9.1 shows the beginning of the tensor family of matrices $[C, A; T, G]^{(n)}$, which we used in many of our previous works [Petoukhov, 2008; Petoukhov, He, 2009, etc]. The mentioned strong doublets and also triplets with strong roots are marked by black color in symbolic matrices in Fig. 9.1 by contrast to other doublets and triplets.

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

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

Fig. 9.1. Symbolic matrices [C, A; T, G]$^{(2)}$ and [C, A; T, G]$^{(3)}$ for 16 doublets and 64 triplets. Black color denotes strong doublets and also triplets with strong roots.

Dispositions of "black" and "white" doublets and triplets in the matrices in Fig. 9.1 form the very symmetric black-and-white mosaics. For instance, left and right halves of each matrix are mirror-anti-symmetric to each other in its colors: any pair of cells, disposed by the mirror-symmetrical manner in these halves, has opposite colors (correspondingly a mosaic of each rows represents a complementary or inverse palindrom). Both quadrants along each of diagonals are identical in their mosaics and – by this reason – these mosaic matrices remind a figure of the cross (below special «cross-operators» are introduced on basis of such mosaic matrices with interesting algebraic properties). A sequence of black and white cells in each of rows has a meander character and corresponds to one of Rademacher functions. In the matrix [C, A; T, G]$^{(3)}$ rows 1-2, 3-4, 5-6, 7-8 are identical to each other from the viewpoint of the mosaic, etc.

These symbolic matrices from Fig. 8.1 can be represented by appropriate numeric matrices (Fig. 9.2) under using the following numeric denotations in this binary opposition: black 8 doublets and 32 triplets are denoted by +1 and white 8 doublets and 32 triplets are denoted by -1. The author termes such matrices conditionally as «cross-matrices» taking into account their cross-like mosaics.

$$\mathbf{B_{12}} = \begin{bmatrix} 1 & -1 & 1 & -1 \\ 1 & 1 & -1 & -1 \\ 1 & -1 & 1 & -1 \\ -1 & -1 & 1 & 1 \end{bmatrix} \qquad \mathbf{B_{123}} = \begin{bmatrix} 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ 1 & 1 & 1 & 1 & -1 & -1 & -1 & -1 \\ 1 & 1 & 1 & 1 & -1 & -1 & -1 & -1 \\ 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ -1 & -1 & -1 & -1 & 1 & 1 & 1 & 1 \\ -1 & -1 & -1 & -1 & 1 & 1 & 1 & 1 \end{bmatrix}$$

Fig. 9.2. Numeric representations of cross-matrices from Fig. 9.1 using denotations of all their black doublets and triplets by +1, and all other doublets and tripets – by -1.

Why is the genetic code structured in accordance with these matrices? Have they any interesting algebraic properties? Yes, they have! Let us first explain this on the cross-matrix B_{12} of doublets, which is a colony of 4 Hadamard matrices recorded in its quadrants (Fig. 9.2).

Consider the 4-dimensional state vector of some system $\overline{X}$ whose coordinates are arbitrary functions of time $\overline{X} = [a_0(t), a_1(t), a_2(t), a_3(t)]$. The action of the cross-matrix B_{12} on $\overline{X}$ gives a state vector, which consists of pairs of coordinates opposite in sign and has the form of a complementary palindrome. Its left and right halves differ each other only by oppositte signs; figuratively speaking, they form a Yin-Yang system, represented by the symbol ☯, which was the personal emblem of Niels Bohr:

$$\overline{X}*B_{12} = [a_0+a_1+a_2-a_3,\ a_1-a_0-a_2-a_3,\ -(a_1-a_0-a_2-a_3),\ -(a_0+a_1+a_2-a_3)] = [b_0, b_1, -b_1, -b_0] \qquad (9.1)$$

In the expression (9.1) identical coordinates, which differ each other only by opposite signs, are marked by identical color. Here the term "complementary palindrome" regarding a vector

refers that the sequence of its coordinates in the inverse direction (from its end to its beginnig) differs from the sequence of its direct direction only by opposite signs.

The second special feature of the cross-matrix operator B_{12} is the following: repeated action of the cross-matrix B_{12} to the initial vector $\overline{X}$ leads to the repeated dichotomous reproductions of the vector of the complementary palindrome $[b_0, b_1, -b_1, -b_0]$ obtained under its first action: $(\overline{X}*B_{12})*B_{12}{}^n = 2^n*[b_0, b_1, -b_1, -b_0]$. These dichotomous reproductions of such vectors resemble the dichotomous reproduction of somatic cells in mitosis with appropriate dichotomous reproduction of all genetic materials of each cell; it can be conditionally represented as repeated dichotomous reproduction of Yin-Yang systems (Fig. 9.3).

Fig. 9.3. The artistic image of repeated dichotomous reproductions of complementary palindromic vectors as Yin-Yang systems under repeated actions of the cross-matrix B_{12}.

One can note that it is possible to get a complementary palindromic vector from voluntary vector $[a_0(t), a_1(t), a_2(t), a_3(t)]$ by action of another kind of matrices: [1,1,-1,-1; 1,1,-1,-1; 1,1,-1,-1; 1,1,-1,-1]. But the second action of such matrix leads to vectors with zero coordinates without reproduction of the vector obtained under its first action.

It is not for nothing that the considered structures of the genetic coding system are coordinated precisely with cross-matrices, which provide both the generation of the indicated Yin-Yang systems and their reproduction according to the type observed during cell divisions.

One should remind here that in genetics, thousands of publications are devoted to the important topic of complementary palindromes since DNA sequences of different genomes contain an abundance of such palindromes. In the human genome, they represent about a third of the DNA texts. In evolutionary biology, the abundance of such palindromes in genomes is regarded as evidence of not randomness of DNA texts, and their not reducibility to a set of random mutations. We are talking about sequences of letters that are read in both directions in the same way, if when reading in the opposite direction, replace each letter with a complementary one (A↔T, C↔G). An example of a complementary palindrome in DNA: AGACTGAGTCT. The initial work about complementary palindromes in matrix genetics was [Petoukhov, 2012].

Let us add briefly that action of the cross-matrix B_{12} on the (4*4)-matrix with voluntary entries generates a matrix, whose rows are complementary palindroms. Such generated matrices have interesting properties in their eigenvalues and form special closed sets regarding some algebraic operations.

Returning to the cross-matrix [C, A; T, G][2] of 16 doublets in Fig. 9.1, one can consider its transformation by cyclic shifts of positions 1-2 → 2-1 in all doublets (for example the doublet CA becomes the doublet AC). Such transformation leads to a symbolic matrix with a new mosaic of strong and weak doublets. Fig. 9.4 shows the new symbolic matrix and its similar numeric representation B_{21} (here the matrix index 21 corresponds of the order of positions in doublets).
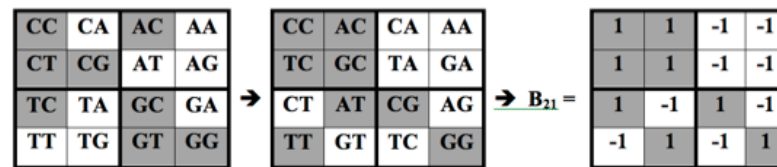
Fig. 9.4. Cyclic changes of positions 1-2→2-1 in all doublets transform the mosaic matrix $[C, A; T, G]^{(2)}$ of 16 doublets in Fig. 9.1 to the new symbolic matrix with its numeric representation B_{21}.

But this new genetic matrix B_{21} also turns out to be the operator of generating and dichotomous reproduction of a vector of complementary palindromes when acting on an arbitrary vector $\overline{X} = [a_0(t), a_1(t), a_2(t), a_3(t)]$:

$$\overline{X}*B_{21} = [a_0+a_1+a_2-a_3,\ a_0+a_1-a_2+a_3,\ -(a_0+a_1-a_2+a_3),\ -(a_0+a_1+a_2-a_3)] = [c_0, c_1, -c_1, -c_0] \qquad (9.2)$$

$$(\overline{X}*B_{21})*B_{21}{}^{n} = 2^{n}*[c_0, c_1, -c_1, -c_0] \qquad (9.3)$$

In genetics, the topic of cyclic shifts and cyclic changes is very important since all organism is a huge chorus of coordinated cyclic processes. Since ancient times, chronomedicine claims that all our diseases are the result of violations in their coordination. The proteins of our body are also included in continuous cycles "life-death" of assembly and their disassembly into amino acids. For example, the half-life of the hormone insulin is 6-9 minutes, proteins of the intestinal mucosa - 10 days, proteins of the liver and blood plasma - 10 days, and on average for human proteins - 80 days.

Let us turn now to the mosaic cross-matrix $[C, A; T, G]^{(3)}$ of 64 triplets and its numerical representation B_{123} (Figs. 9.1 and 9.2). The action of this cross-matrix B_{123} on an arbitrary 8-dimensional state vector of the system $\overline{Y} = [a_0(t), a_1(t), a_2(t), a_3(t), a_4(t), a_5(t), a_6(t), a_7(t)]$ also generates a vector with binary-oppositional sets of coordinates in a form of a complementary palindrome, whose left and right halves can be considered as a Yin-Yang pair:

$$\overline{Y}*B_{123} = [b_0, b_0, b_1, b_1, -b_1, -b_1, -b_0, -b_0] \qquad (9.4)$$

The repeated action of the cross-matrix B_{123} leads to tetratomically reproductions of the complementary-palindromic vector obtained under its first action:

$$(\overline{Y}*B_{123})*B_{123}{}^{n} = 4^{n}*[b_0, b_0, b_1, b_1, -b_1, -b_1, -b_0, -b_0] \qquad (9.5)$$

This tetratomous reproduction of such vectors resembles the tetratomous reproduction of germ cells with their complete genetic contents in meiosis; it can be conditionally represented as tetratomous reproduction of Yin-Yang systems (Fig. 9.5).
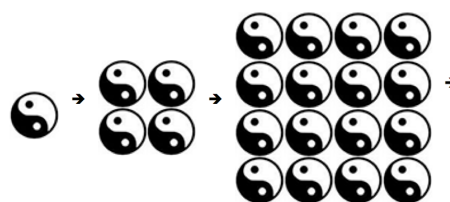
Fig. 9.5. The artistic image of repeated tetratomous reproductions of complementary-palindromic vectors as Yin-Yang systems under repeated actions of the cross-matrix B_{123}.

Cyclic shifts of positions ($1\text{-}2\text{-}3\to2\text{-}3\text{-}1\to3\text{-}1\text{-}2\to3\text{-}2\text{-}1\to2\text{-}1\text{-}3\to1\text{-}3\text{-}2$) in all triplets of the mosaic matrix $[C, A; T, G]^{(3)}$ (Fig. 9.1) transforms this matrix into 5 new mosaic matrices B_{231}, B_{312}, B_{321}, B_{213}, B_{132} whose indexes correspond to orders of transformed positions in triplets (Fig. 9.6).

$B_{123} =$

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

$B_{231} =$

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

$B_{312} =$

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

$B_{321} =$

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

$B_{213} =$

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

$B_{132} =$

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

Fig. 9.6. Transformations of the mosaic cross-matrix $[C, A; T, G]^{(3)}$ (Fig. 9.1) under cyclic shifts of positions $1\text{-}2\text{-}3\to2\text{-}3\text{-}1\to3\text{-}1\text{-}2\to3\text{-}2\text{-}1\to2\text{-}1\text{-}3\to1\text{-}3\text{-}2$ in all its triplets.

Denoting 32 black triplets by +1 and 32 white triplets by -1 in each of these symbolic matrices, you get additionally five mosaic numeric (8*8)-matrices B_{231}, B_{312}, B_{321}, B_{213}, B_{132}. Their actions regarding a voluntary 8-dimensional vector $\overline{Y} = [a_0(t), a_1(t), a_2(t), a_3(t), a_4(t), a_5(t), a_6(t), a_7(t)]$ give five new 8-dimensional complementary-palindromic vectors (8.6) and also tetratomic reproductions of these vectors under repeated actions of the matrices (by analogy with the above cases represented in expressions (9.4) and (9.5)):

$$\overline{Y}*B_{231} = [c_0\ c_1\ -c_1\ -c_0\ c_0\ c_1\ -c_1\ -c_0], \quad (\overline{Y}*B_{231})*B_{231}^{\,n} = 4^n*[c_0\ c_1\ -c_1\ -c_0\ c_0\ c_1\ -c_1\ -c_0],$$

$$\overline{Y}*B_{312} = [d_0\ d_1\ d_0\ d_1\ -d_1\ -d_0\ -d_1\ -d_0], \quad (\overline{Y}*B_{312})*B_{312}^{\,n} = 4^n*[d_0\ d_1\ d_0\ d_1\ -d_1\ -d_0\ -d_1\ -d_0],$$

$$\overline{Y}*B_{132} = [e_0\ e_1\ e_0\ e_1\ -e_1\ -e_0\ -e_1\ -e_0], \quad (\overline{Y}*B_{132})*B_{132}^{\,n} = 4^n*[e_0\ e_1\ e_0\ e_1\ -e_1\ -e_0\ -e_1\ -e_0],$$

$$\overline{Y}*B_{213} = [f_0\ f_0\ f_1\ f_1\ -f_1\ -f_1\ -f_0\ -f_0], \quad (\overline{Y}*B_{213})*B_{213}^{\,n} = 4^n*[f_0\ f_0\ f_1\ f_1\ -f_1\ -f_1\ -f_0\ -f_0],$$

$$\overline{Y}*B_{321} = [j_0\ j_1\ -j_1\ -j_0\ j_0\ j_1\ -j_1\ -j_0], \quad (\overline{Y}*B_{321})*B_{321}^{\,n} = 4^n*[j_0\ j_1\ -j_1\ -j_0\ j_0\ j_1\ -j_1\ -j_0] \quad (9.6)$$

All these results show that the genetic coding system is algebraically structured in accordance with tensor families of matrix operators for generating and reproducing binary-opposition vectors (replicating Yin-Yang systems) of complementary-palindromic types! The tensor families of these operators of complementary-binarization give many kinds of such

operators. The revealed relationship of the genetic coding system with binarization operators is consistent with many types of binary oppositions in it, as well as with the general physiological law "all or nothing" of binary responces holding true for different types of excitable cells of the body: excitable cells respond to external stimuli either "yes" or "no". More precisely the cell does not respond to stimuli of a subthreshold value, but it responds to stimuli of any suprathreshold value by its full amplitude (it is true for neurons, muscle units, ...).

All this speaks of the fundamental importance of Boolean algebra of logic and Boolean functions for computer science and control in living bodies. On the basis of joint using Boolean algebra there is possible a mutual enrichment of algebraic biology and many other sciences: computer technologies, spectral logic, logical holography, etc. Boole dreamed of reproducing thinking logic through his algebra of human logic. His book was called "An investigation of the Laws of Thought". Our results show the importance of Boolean algebra of logic at the deepest biological level - genetic.

E.Schrodinger noted: *"from all we have learnt about the structure of living matter, we must be prepared to find it working in a manner that cannot be reduced to the ordinary laws of physics... because the construction is different from an anything we have yet tested in the physical laboratory»* [Schrödinger, 1944]. For comparison, the enzymes in biological organisms work in a million times more effectively than catalysts in the laboratory. What makes the enzyme in the body for 1 second, a catalyst in the laboratory can make only for 100 thousand years. We believe that such ultra-efficiency of enzymes in biological bodies is defined not only by laws of physics, but also by algebra-logical (computer-like) programs and algorithms of the geno-logic coding, and therefore - in line with Schrodinger - this ultra-efficiency cannot be reduced to the ordinary laws of physics.

10. 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. 2.2, 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. 10.1): $a=a_0+a_1i$, $b=b_0+b_1i$, $c=c_0+c_1i$, $d=d_0+d_1i$, $p=p_0+p_1i$, $q=q_0+q_1i$, $s=s_0+s_1i$, $r=r_0+r_1i$ where $i^2 = -1$ (the imagine unit of complex numbers).

a	b	c	d
b	a	d	c
p	q	s	r
q	p	r	s

Fig. 10.1. 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. 10.1. Taking into account that complex numbers $a = a_0 + a_1 i$ have their matrix representation by (2*2)-matrices $[a_0, a_1; -a_1, a_0]$, the (4*4)-matrix in Fig. 10.1 can be rewriting into the (8*8)-matrix in Fig. 10.2 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. 10.2. The matrix representation of 8-dimensional numbers of a special algebra (see explanation in the text).

In Fig. 10.2, 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].

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. 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 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 indicators (Fig. 2.1 and 2.2). This peculiarity of the alphabet is associated with thoughts about biological computers on the basis of binary-oppositional resonances of genetic molecules [Petoukhov, 2015, 2016a].

The author's study in the field of matrix genetics and algebraic biology is focused on the dictatorial influence of DNA and RNA on the whole organism. Obtained results, which are described in this and his other publications, define a special scientific direction in mathematical biology and lead to many new mathematical models, results and interesting hypothesizes (for example, the author puts forward the hypothesis about some connections of the genetic system with flicker noise, which is under testing now). Matrix approaches, proposed by the author for modeling the genetic system, show themselves as very effective and appropriate.

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