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BIOINFROMATICS: MATRIX GENETICS, ALGEBRAS OF THE GENETIC CODE AND BIOLOGICAL HARMONY

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Publications: Petoukhov S.V. (1981), *Biomechanics, Bionics and Symmetry*, Moscow, Nauka, 239 p.; (1988), *Geometries of Living Nature and Algorithms of Self-organization*, Moscow, Znanie, 48 p.; (1999) *Biosolitons. Foundations of Soliton Biology*, Moscow, 288 p.; (2001) *The Biperodic Table of Genetic Code and Numbers of Protons*, Moscow, 258 p. (in Russian)

***Abstract**: The article is devoted to algebraic properties of the genetic code. The investigations of the genetic code on the basis of matrix approaches ("matrix genetics") were described in many previous publications by the author. Their results revealed hidden interconnections, symmetries and evolutionary invariants in genetic code systems. They testified that genetic molecules are important part of specific maintenance of noise immunity and efficiency of discrete information transfer. New results in the field of the matrix genetics demonstrate a connection between the genetic code and special algebras. One of these algebras is the algebra of hypercomplex numbers, which are named hyperbolic matrions. Algebras with two quasi-real units are important also. They reflect binary-opposite features of the genetic code structures and are named "bisexual algebras" (or briefly "bisexes"). Bisexes are connected with the degeneration and with evolution of the genetic code. One of bisexual algebras is proposed as a mathematical model of a pre-code of the genetic code. Mathematical properties of bisexes are described briefly. A possible meaning of bisexes for informatics, theoretical biology and mathematical natural sciences is discussed.*

Keywords: genetic code, matrix, algebra, harmony, noise immunity

1. INTRODUCTION.

This article is devoted to algebraic properties of molecular systems of the genetic code in their matrix representations. The principles of investigations of genetic code systems from the viewpoint of matrix approaches were published in (Petoukhov, 2001-2005). These investigations are generalized under the name "matrix genetics". Their results, which were described in these publications, revealed hidden interconnections, symmetries and evolutionary invariants in genetic code systems. Simultaneously they testified that genetic molecules are important part of specific maintenance of noise immunity and efficiency of discrete information transfer. These molecular structures are related also with the general harmony of organism.

From an information viewpoint, living organisms are informational essences. They receive genetic information from their ancestors and transmit it to descendants. A conception of informational nature of living organisms is reflected in the words: "If you want to understand life, don't think about vibrant, throbbing dels and oozes, think about information technology" (Dawkins, 1986). Or another citation of a similar direction of thoughts: "Notions of "information" or "valuable information" are not utilized in physics of non-living nature because they are not needed there. On the contrary, in biology notions "information" and especially "valuable information" are main ones; understanding and description of phenomena in living nature are impossible without these notions. A specificity of "living matter" lies in them" (Chernavskiy, 2000). In particular from the bioinformatics, modern science hopes to receive deeper knowledge in the questions what is life and why life exists.

Mechanisms of genetic encoding provide high noise immunity of transmitting genetic information from a generation to next generation in spite of numerous quantities of noise and disturbances in biological medium. Investigations of these mechanisms should utilize achievements of the modern theory of noise immunity encoding from the field of digital information technology. In our opinion, many structural aspects of genetic code systems are determined by a demand of noise immunity of genetic information.

2. NOISE IMMUNITY OF GENETIC INFORMATION AND A MATRIX REPRESENTATION OF GENETIC CODE.

Genetic information is transferred by means of discrete elements: 4 letters of genetic alphabet, 64 amino acids, etc. General theory of processing of discrete signals utilizes encoding such signals by means of special mathematical matrices (Sklar, 2001; Ahmed, Rao, 1975, etc). A typical example of such matrices is the Kronecker family of Hadamard matrices. This family was utilized by the author to create the family of genetic matrices by analogy (this construction was described in (Petoukhov, 2005b)).

It is well-known, that multiplets are one of main peculiarities of genetic code. Really, the alphabet of genetic code is a set of four monoplets (nitrogenous bases): A (adenine), C (cytosine), G (Guanine), T/U (thymine in DNA or uracil in RNA); 64 triplets encode amino acids; each protein is encoded by more or less long multiplets (each protein with n amino acids is encoded by a 3n-plet). Due to the idea of a possible analogy between discrete signals processing in computers and in a genetic code system, the author has represented all sets of genetic multiplets as appropriate parts of a mutual family of symbolic square genomatrices $P^{(n)}$ (Fig.1), where brackets at exponent (n) mean the Kronecker exponentiation (Petoukhov, 2001-2005).

The alphabetic (2x2)-genomatrix P of this family is constructed from four letters A, C, G, T/U (Fig. 1). Each genomatrix $P^{(n)}$ contains a complete set of n-plets as its matrix elements. For example, the (8x8)-genomatrix $P^{(3)}$ contains all 64 triplets which encode 20 amino acids (for more details about this matrix presentation of genetic subsystems, see (Petoukhov, 2003a, 2005a)).

A quantity of variants of a disposition of 64 triplets in an (8x8)-matrix is equal to $64! = 10^{89}$. According to modern physics, all time of existence of our Universe is equal to 10^{30} sec. It means that, if a person takes 1 second to consider one of these 10^{89} variants of disposition, he can consider a very small amount of this quantity during all time of existence of our Universe. It is obvious that almost any variant of disposition of 64 triplets and of 20 amino acid in (8x8)-matrix has asymmetrical character. But the exclusive Kronecher variant of (8x8)-genomatrix $P^{(3)}$, which was constructed by a formal way (Fig.1), has unexpectedly a symmetrical character of this disposition in the case of a very important code. This case is the vertebrate mitochondrial genetic code,

which is considered mainly as the most ancient and "perfect" variant of the genetic code (Frank-Kamenetsky, 1988). Let us describe this essential moment in more detail.

P =

	1	0
1	C	A
0	U	G

; $P^{(2)}=P\otimes P=$

	11	10	01	00
11	CC 1111 15	CA 1110 14	AC 1101 13	AA 1100 12
10	CU 1011 11	CG 1010 10	AU 1001 9	AG 1000 8
01	UC 0111 7	UA 0110 6	GC 0101 5	GA 0100 4
00	UU 0011 3	UG 0010 2	GU 0001 1	GG 0000 0

$P^{(3)}=$

	111	110	101	100	011	010	001	000
111	CCC 111111 63	CCA 111110 62	CAC 111101 61	CAA 111100 60	ACC 111011 59	ACA 111010 58	AAC 111001 57	AAA 111000 56
110	CCU 110111 55	CCG 110110 54	CAU 110101 53	CAG 110100 52	ACU 110011 51	ACG 110010 50	AAU 110001 49	AAG 110000 48
101	CUC 101111 47	CUA 101110 46	CGC 101101 45	CGA 101100 44	AUC 101011 43	AUA 101010 42	AGC 101001 41	AGA 101000 40
100	CUU 100111 39	CUG 100110 38	CGU 100101 37	CGG 100100 36	AUU 100011 35	AUG 100010 34	AGU 100001 33	AGG 100000 32
011	UCC 011111 31	UCA 011110 30	UAC 011101 29	UAA 011100 28	GCC 011011 27	GCA 011010 26	GAC 011001 25	GAA 011000 24
010	UCU 010111 23	UCG 010110 22	UAU 010101 21	UAG 010100 20	GCU 010011 19	GCG 010010 18	GAU 010001 17	GAG 010000 16
001	UUC 001111 15	UUA 001110 14	UGC 001101 13	UGA 001100 12	GUC 001011 11	GUA 001010 10	GGC 001001 9	GGA 001000 8
000	UUU 000111 7	UUG 000110 6	UGU 000101 5	UGG 000100 4	GUU 000011 3	GUG 000010 2	GGU 000001 1	GGG 000000 0

Figure 1: The beginning of the family of symbolic genomatrices $P^{(n)}$ for n = 1, 2, 3. Here (n) means the Kronecker exponentiation. Binary and decimal numbers of multiplets are shown in the natural system of

numeration of multiplets (Petoukhov, 2001a).

3. GENOMATRICES OF THE VERTEBRATE MITOCHONDRIAL GENETIC CODE.

Fig. 2 shows the correspondence between the set of 64 triplets and the set of 20 amino acids with stop-signals (Stop) of protein synthesis in this code. The initial data are given, for example, on the web-site http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi.

8 subfamilies of "two-position" NN-triplets and amino acids, which are encoded by them	**8 subfamilies of "three-position" NN-triplets and amino acids, which are encoded by them**
CCC, **CC**A, **CC**U, **CC**G - **Pro**	**CA**C, **CA**A, **CA**U, **CA**G - **His**, **Gln**
CUC, **CU**A, **CU**U, **CC**G - **Leu**	**AA**C, **AA**A, **AA**U, **AA**G - **Asn**, **Lys**
CGC, **CG**A, **CG**U, **CG**G - **Arg**	**AU**C, **AU**A, **AU**U, **AU**G - **Ile**, **Met**
ACC, **AC**A, **AC**U, **AC**G - **Thr**	**AG**C, **AG**A, **AG**U, **AG**G - **Ser**, **Stop**
UCC, **UC**A, **UC**U, **UC**G - **Ser**	**UA**C, **UA**A, **UA**U, **UA**G - **Tyr**, **Stop**
GCC, **GC**A, **GC**U, **GC**G - **Ala**	**UU**C, **UU**A, **UU**U, **UU**G - **Phe**, **Leu**
GUC, **GU**A, **GU**U, **GU**G - **Val**	**UG**C, **UG**A, **UG**U, **UG**G - **Cys**, **Trp**
GGC, **GG**A, **GG**U, **GG**G - **Gly**	**GA**C, **GA**A, **GA**U, **GA**G - **Asp**, **Glu**

Fig. 2. The vertebrate mitochondrial genetic code.

The set of 64 triplets contains such 16 subfamilies of triplets, every of which contains 4 triplets with the same two letters on the first positions of each triplets (an example of such subsets is the case of four triplets CAC, CAA, CAU, CAG with the same two letters CA on their first positions). We shall name such subfamilies as the subfamilies of NN-triplets. In the case of the vertebrate mitochondrial code, the set of these 16 subfamilies of NN-triplets is divided into two equal subsets from the viewpoint of degeneration properties of the code (Fig.2). The first subset contains 8 subfamilies of so

named „two-position" NN-triplets, a coding value of which is independent on a letter on their third position. An example of such subfamilies is the four triplets CGC, CGA, CGU, CGC, all of which encode the same amino acid Arg, though they have different letters on their third position. All members of such subfamilies of NN-triplets are marked by black colour in the genomatrix $P^{(3)}$ on the Fig. 3 (top) and in other genomatrices on the Fig. 3.

The second subset contains 8 subfamilies of „three-position" NN-triplets, a coding value of which depends on a letter on their third position. An example of such subfamilies is the four triplets CAC, CAA, CAU, CAC, two of which (CAC, CAU) encode the amino acid His and other two (CAA, CAG) encode another amino acid Gln. All members of such subfamilies of NN-triplets are marked by white colour in the genomatrix $P^{(3)}$ on the Fig. 3 (top). So the genomatrix $P^{(3)}$ has 32 black triplets and 32 white triplets. By the way, such 1:1 division of the set of 64 triplets is connected with evolutionary invariants in relation to 17 variants of genetic codes, which are known in modern science (see details in (Petoukhov, 2001a,b; 2005a). Each subfamily of four NN-triplet is disposed in an appropriate (2x2)-subquadrant of the genomatrix $P^{(3)}$ due to the Kronecker algorithm of construction of genomatrix $P^{(3)}$ of triplets from the alphabet genomatrix P (Fig.1).

The black-and-white mosaic of genomatrix $P^{(3)}$ (or $P^{(3)}_{123}$ in Fig. 3, top) demonstrates a specificity of degeneration of the genetic code. It has a few interesting symmetrical peculiarities unexpectedly:

1. The left and right halves of the matrix mosaic are mirror-anti-symmetric to each other in its colors: any pair of cells, disposed by mirror-symmetrical manner in these halves, has opposite colors.

2. The genomatrix $P^{(3)}$ consists of four pairs of neighbor rows with even and odd numeration numbers in each pair: 1-2, 3-4, 5-6, 7-8. The rows of each pair are equivalent to each other from the viewpoint of a disposition of the same amino acids in their appropriate cells.

3. The black-white matrix mosaic has a symmetric figure of a diagonal cross: diagonal quadrants of the matrix are equivalent to each other from the viewpoint of their mosaic.

4. Mosaics of all rows have a meander-line character, which is connected with Rademacher functions from theory of discrete signals.

5. The turning of the genomatrix $P^{(3)}$ into a cylinder with an agglutination of its upper and lower borders reveals an ornamental pattern of a cyclic shift. This pattern is

CCC *PRO*	*CCA* *PRO*	*CAC* *HIS*	*CAA* *GLN*	*ACC* *THR*	*ACA* *THR*	*AAC* *ASN*	*AAA* *LYS*
CCU *PRO*	*CCG* *PRO*	*CAU* *HIS*	*CAG* *GLN*	*ACU* *THR*	*ACG* *THR*	*AAU* *ASN*	*AAG* *LYS*
CUC *LEU*	*CUA* *LEU*	*CGC* *ARG*	*CGA* *ARG*	*AUC* *ILE*	*AUA* *MET*	*AGC* *SER*	*AGA* *STOP*
CUU *LEU*	*CUG* *LEU*	*CGU* *ARG*	*CGG* *ARG*	*AUU* *ILE*	*AUG* *MET*	*AGU* *SER*	*AGG* *STOP*
UCC *SER*	*UCA* *SER*	*UAC* *TYR*	*UAA* *STOP*	*GCC* *ALA*	*GCA* *ALA*	*GAC* *ASP*	*GAA* *GLU*
UCU *SER*	*UCG* *SER*	*UAU* *TYR*	*UAG* *STOP*	*GCU* *ALA*	*GCG* *ALA*	*GAU* *ASP*	*GAG* *GLU*
UUC *PHE*	*UUA* *LEU*	*UGC* *CYS*	*UGA* *TRP*	*GUC* *VAL*	*GUA* *VAL*	*GGC* *GLY*	*GGA* *GLY*
UUU *PHE*	*UUG* *LEU*	*UGU* *CYS*	*UGG* *TRP*	*GUU* *VAL*	*GUG* *VAL*	*GGU* *GLY*	*GGG* *GLY*

CCC *PRO*	*CAC* *HIS*	*ACC* *THR*	*AAC* *ASN*	*CCA* *PRO*	*CAA* *GLN*	*ACA* *THR*	*AAA* *LYS*
CUC *LEU*	*CGC* *ARG*	*AUC* *ILE*	*AGC* *SER*	*CUA* *LEU*	*CGA* *ARG*	*AUA* *MET*	*AGA* *STOP*
UCC *SER*	*UAC* *TYR*	*GCC* *ALA*	*GAC* *ASP*	*UCA* *SER*	*UAA* *STOP*	*GCA* *ALA*	*GAA* *GLU*
UUC *PHE*	*UGC* *CYS*	*GUC* *VAL*	*GGC* *GLY*	*UUA* *LEU*	*UGA* *TRP*	*GUA* *VAL*	*GGA* *GLY*
CCU *PRO*	*CAU* *HIS*	*ACU* *THR*	*AAU* *ASN*	*CCG* *PRO*	*CAG* *GLN*	*ACG* *THR*	*AAG* *LYS*
CUU *LEU*	*CGU* *ARG*	*AUU* *ILE*	*AGU* *SER*	*CUG* *LEU*	*CGG* *ARG*	*AUG* *MET*	*AGG* *STOP*
UCU *SER*	*UAU* *TYR*	*GCU* *ALA*	*GAU* *ASP*	*UCG* *SER*	*UAG* *STOP*	*GCG* *ALA*	*GAG* *GLU*
UUU *PHE*	*UGU* *CYS*	*GUU* *VAL*	*GGU* *GLY*	*UUG* *LEU*	*UGG* *TRP*	*GUG* *VAL*	*GGG* *GLY*

CCC *PRO*	*CCA* *PRO*	*ACC* *THR*	*ACA* *THR*	*CAC* *HIS*	*CAA* *GLN*	*AAC* *ASN*	*AAA* *LYS*
CCU *PRO*	*CCG* *PRO*	*ACU* *THR*	*ACG* *THR*	*CAU* *HIS*	*CAG* *GLN*	*AAU* *ASN*	*AAG* *LYS*
UCC *SER*	*UCA* *SER*	*GCC* *ALA*	*GCA* *ALA*	*UAC* *TYR*	*UAA* *STOP*	*GAC* *ASP*	*GAA* *GLU*
UCU *SER*	*UCG* *SER*	*GCU* *ALA*	*GCG* *ALA*	*UAU* *TYR*	*UAG* *STOP*	*GAU* *ASP*	*GAG* *GLU*
CUC *LEU*	*CUA* *LEU*	*AUC* *ILE*	*AUA* *MET*	*CGC* *ARG*	*CGA* *ARG*	*AGC* *SER*	*AGA* *STOP*
CUU *LEU*	*CUG* *LEU*	*AUU* *ILE*	*AUG* *MET*	*CGU* *ARG*	*CGG* *ARG*	*AGU* *SER*	*AGC* *SER*
UUC	*UUA*	*GUC*	*GUA*	*UGC*	*UGA*	*GGC*	*GGA*

PHE	*LEU*	*VAL*	*VAL*	*CYS*	*TRP*	*GLY*	*GLY*
UUU	*UUG*	*GUU*	*GUG*	*UGU*	*UGG*	*GGU*	*GGG*
PHE	*LEU*	*VAL*	*VAL*	*CYS*	*TRP*	*GLY*	*GLY*
CCC	*ACC*	*CAC*	*AAC*	*CCA*	*ACA*	*CAA*	*AAA*
PRO	*THR*	*HIS*	*ASN*	*PRO*	*THR*	*GLN*	*LYS*
UCC	*GCC*	*UAC*	*GAC*	*UCA*	*GCA*	*UAA*	*GAA*
SER	*ALA*	*TYR*	*ASP*	*SER*	*ALA*	*STOP*	*GLU*
CUC	*AUC*	*CGC*	*AGC*	*CUA*	*AUA*	*CGA*	*AGA*
LEU	*ILE*	*ARG*	*SER*	*LEU*	*MET*	*ARG*	*STOP*
UUC	*GUC*	*UGC*	*GGC*	*UUA*	*GUA*	*UGA*	*GGA*
PHE	*VAL*	*CYS*	*GLY*	*LEU*	*VAL*	*TRP*	*GLY*
CCU	*ACU*	*CAU*	*AAU*	*CCG*	*ACG*	*CAG*	*AAG*
PRO	*THR*	*HIS*	*ASN*	*PRO*	*THR*	*GLN*	*LYS*
UCU	*GCU*	*UAU*	*GAU*	*UCG*	*GCG*	*UAG*	*GAG*
SER	*ALA*	*TYR*	*ASP*	*SER*	*ALA*	*STOP*	*GLU*
CUU	*AUU*	*CGU*	*AGU*	*CUG*	*AUG*	*CGG*	*AGG*
LEU	*ILE*	*ARG*	*SER*	*LEU*	*MET*	*ARG*	*STOP*
UUU	*GUU*	*UGU*	*GGU*	*UUG*	*GUG*	*UGG*	*GGG*
PHE	*VAL*	*CYS*	*GLY*	*LEU*	*VAL*	*TRP*	*GLY*

CCC	ACC	CCA	ACA	CAC	AAC	CAA	AAA
PRO	THR	PRO	THR	HIS	ASN	GLN	LYS
UCC	GCC	UCA	GCA	UAC	GAC	UAA	GAA
SER	ALA	SER	ALA	TYR	ASP	STOP	GLU
CCU	ACU	CCG	ACG	CAU	AAU	CAG	AAG
PRO	THR	PRO	THR	HIS	ASN	GLN	LYS
UCU	GCU	UCG	GCG	UAU	GAU	UAG	GAG
SER	ALA	SER	ALA	TYR	ASP	STOP	GLU
CUC	AUC	CUA	AUA	CGC	AGC	CGA	AGA
LEU	ILE	LEU	MET	ARG	SER	ARG	STOP
UUC	GUC	UUA	GUA	UGC	GGC	UGA	GGA
PHE	VAL	LEU	VAL	CYS	GLY	TRP	GLY
CUU	AUU	CUG	AUG	CGU	AGU	CGG	AGG
LEU	ILE	LEU	MET	ARG	SER	ARG	STOP
UUU	GUU	UUG	GUG	UGU	GGU	UGG	GGG
PHE	VAL	LEU	VAL	CYS	GLY	TRP	GLY

CCC	*CAC*	*CCA*	*CAA*	*ACC*	*AAC*	*ACA*	*AAA*
PRO	*HIS*	*PRO*	*GLN*	*THR*	*ASN*	*THR*	*LYS*
CUC	*CGC*	*CUA*	*CGA*	*AUC*	*AGC*	*AUA*	*AGA*
LEU	*ARG*	*LEU*	*ARG*	*ILE*	*SER*	*MET*	*STOP*
CCU	*CAU*	*CCG*	*CAG*	*ACU*	*AAU*	*ACG*	*AAG*
PRO	*HIS*	*PRO*	*GLN*	*THR*	*ASN*	*THR*	*LYS*
CUU	*CGU*	*CUG*	*CGG*	*AUU*	*AGU*	*AUG*	*AGG*
LEU	*ARG*	*LEU*	*ARG*	*ILE*	*SER*	*MET*	*STOP*
UCC	*UAC*	*UCA*	*UAA*	*GCC*	*GAC*	*GCA*	*GAA*
SER	*TYR*	*SER*	*STOP*	*ALA*	*ASP*	*ALA*	*GLU*
UUC	*UGC*	*AUU*	*AGU*	*CUG*	*CGG*	*GUA*	*GGA*
PHE	*CYS*	*ILE*	*SER*	*LEU*	*ARG*	*VAL*	*GLY*
UCU	*UAU*	*UCG*	*UAG*	*GCU*	*GAU*	*GCG*	*GAG*

SER	*TYR*	*SER*	*STOP*	*ALA*	*ASP*	*ALA*	*GLU*
UUU	*UGU*	*UUG*	*UGG*	*GUU*	*GGU*	*GUG*	*GGG*
PHE	*CYS*	*LEU*	*TRP*	*VAL*	*GLY*	*VAL*	*GLY*

Fig. 3. Six genomatrices which are differed from each other by an order of positions in triplets for the case of the vertebrate mitochondria code. Top-down: genomatrices $P^{(3)}_{123}$ (or $P^{(3)}$ in Fig.1), $P^{(3)}_{231}$, $P^{(3)}_{213}$, $P^{(3)}_{321}$, $P^{(3)}_{312}$ and $P^{(3)}_{132}$. Each matrix cell has a triplet and an amino acid (or stop-signal) coded by this triplet. The black-white mosaic presents a specificity of the degeneracy of this code.

demonstrated more clearly by a tessellation of a plane with this mosaic genomatrix (Fig. 4, left). The plane with this tessellation has the ornamental pattern with two pattern units which are identical in their forms, but contrary in their colors (black and white) and orientations (left and right).

The symmetry of a cyclic shift in the genomatrix $P^{(3)}_{123}$ puts forward questions about a possible genetic meaning of famous cyclic codes, which play important role in the theory of information processing. Whether principles of cyclic shifts have a certain meaning for genetic code structures? To investigate this question, let us take each cell of matrix $P^{(3)}_{123}$ with its triplet, which has an initial order 1-2-3 of its positions, and then replace this triplet by the triplet, which has the cyclic shift order 2-3-1 of the positions. For example, the triplet CAG is replaced by the triplets AGC. In a result of such changes, the new genomatrix $P^{(3)}_{231}$ is appeared (Fig. 3). The bottom index in the symbol of $P^{(3)}_{231}$ signifies an order of positions in the triplets of these genomatrix in a comparison with the initial genomatrix $P^{(3)}_{123}$. It is interesting that this "cyclic-generated" genomatrix $P^{(3)}_{231}$ has a symmetric character also:

1. All its (4x4)-quadrants are identical to each other by its mosaics;

2. The upper and the lower halves of $P^{(3)}_{231}$ are identical to each other from the viewpoint of dispositions of all amino acids and stop-signals;

Fig.4. At the left: a tessellation of a plane with the mosaic of genomatrix $P^{(3)}_{123}$ from Fig. 3.
At the right: a tessellation of a plane with the mosaic of genomatrix $P^{(3)}_{231}$ from Fig. 3

3. All rows of the (8x8)-genomatrix and its (4x4)-quadrants have a meander-line character again, which is connected with Rademacher functions;

4. The genomatrix $P^{(3)}_{231}$ has 4 pairs of identical rows again: 1-5, 2-6, 3-7, 4-8.

Note, that the mosaic of the initial (8x8)-genomatrix $P^{(3)}_{123}$ is reproduced in (4x4)-quadrants of this $P^{(3)}_{231}$ in a fractal manner: the coefficient of fractal ranging of areas is equal to 4. The tessellations of a plane by the mosaics of P_{123} and of $P^{(3)}_{231}$ demonstrate their fractal correspondence very clearly (Fig. 4). Such scale transformation of areas in the mosaics of the code degeneration will be named "tetra-reproduction" transformation. Due to this tetra-reproduction, the cyclic-generated genomatrix $P^{(3)}_{231}$ has the quantity of the pattern units 4 times more than the initial genomatrix $P^{(3)}_{123}$ (Fig. 3, 4).

It is interesting because an analogical tetra-reproduction or a tetra-division exist in the living nature always in a course of division of gametal cells which are transmitters of genetic information. In this mysterious act of meiosis, one gamete is divided into four new gametes. Described tetra-reproduction of mosaics of genomatrices can be utilized in formal models of meiosis.

4. GENOMATRICES AND PERMUTATIONS IN TRIPLETS.

Permutations of elements play an important role in the theory of signals processing. Six variants of permutations of positions in triplets are possible only: 123, 231, 312, 132, 213, 321. Genomatrices $P^{(3)}_{123}$ and $P^{(3)}_{231}$for the first two of these permutations were considered above. Let us consider other four variants which lead to genomatrices $P^{(3)}_{312}$, $P^{(3)}_{132}$, $P^{(3)}_{213}$, $P^{(3)}_{321}$. They are presented in Fig.3. It is unexpected phenomenological fact, that all of these genomatrices have symmetrical peculiarities, which are similar to symmetrical peculiarities of $P^{(3)}_{123}$ and $P^{(3)}_{231}$. The whole considered genetic code seems to be in agreement with these permutations and corresponding symmetries in the mosaics of these 6 genomatrices.

Why the nature has chosen just this variant of degeneracy of genetic code, which gives these mosaics? One can note that the more simple variants of mosaics exist

generally speaking. For example, the variant exists, which gives such mosaic of genomatrix $P^{(3)}_{123}$ that the left matrix half collects all black triplets and the right half collects all white triplets. Whether these 6 "triplets-permutations" genomatrices $P^{(3)}_{123}$, $P^{(3)}_{231}$, $P^{(3)}_{312}$, $P^{(3)}_{132}$, $P^{(3)}_{213}$, $P^{(3)}_{321}$ have such mutual mathematical properties that can be associated with famous biological facts of genetic inheritance? Yes, such mutual property exists and it is connected with a tetra-reproduction again. This property does not exist in the matrix with the simplest mosaic mentioned above and in many others.

Let us represent the black-and-white mosaic of each from these six genomatrices as a binary mosaic of numbers "+1" and "-1" by means of replacing black (white) color of each matrix cell by an element "+1" ("-1"). In the result, these genomatrices $P^{(3)}_{123}$, $P^{(3)}_{231}$, $P^{(3)}_{312}$, $P^{(3)}_{132}$, $P^{(3)}_{213}$, $P^{(3)}_{321}$ are transformed into the genomatrices B_{123}, B_{231}, B_{312}, B_{132}, B_{213}, B_{321} (Fig. 5). Unexpected mutual property of these six binary genomatrices on Fig.5 is the following one. The multiplication of each genomatrix with itself gives a phenomenon of its tetra-reproduction: four duplicates of the genomatrix are appeared. Really the following formulas take place: $(B_{123})^2 = 4*B_{123}$; $(B_{231})^2 = 4*B_{231}$; $(B_{312})^2 = 4*B_{312}$; $(B_{132})^2 = 4*B_{132}$; $(B_{213})^2 = 4*B_{213}$; $(B_{321})^2 = 4*B_{321}$.

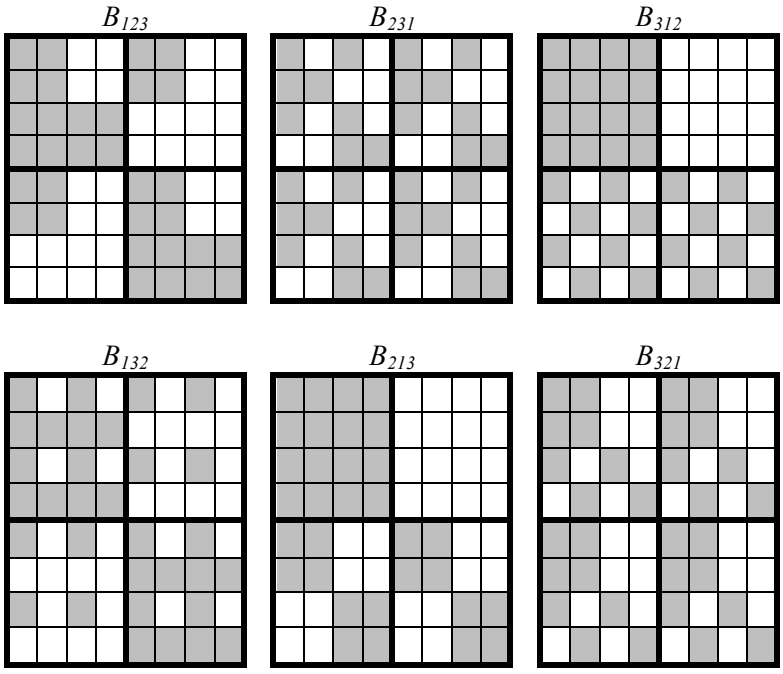

Fig. 5. Binary numeric genomatrices, in which each black cell means the element “+1”; each white cell means the element “-1”.

Such property is not a trivial one. If a voluntary (8x8)-matrix with 32 elements “+1” and 32 elements “-1” is raised to the second power, the resulting matrix almost invariably lose its binary character and its disposition of signs “+” and “-” at all. For example, the mentioned matrix with 32 elements “+1” in its left half and 32 elements “-1” in its right half gives the zero-matrix with 64 elements “0” in this case. The set of these six binary genomatrices has many other interesting properties (for instance, $B_{123}*B_{321}+B_{123}*B_{132} = B_{123}^2$, etc.), which generate heuristic associations with genetic phenomena, but they do not considered in this paper.

Presented materials of the matrix genetics lead us to questions of biological meaning. Really, we revealed unexpectedly that a simple algorithmic re-packing (re-arrangement) of elements in triplets by the cyclic shift is sufficient to receive new essential genomatrices with the fractal tetra-reproducing of mosaics of the code degeneration and with the properties of tetra-reproducing their binary analogues. Evidently, similar re-packing molecular elements in biological object can be sufficient also to provide foundations of a process of tetra-reproducing in some cases, first of all, in the case of meiosis. These and other considerations permit us to put forward a hypothesis of molecular re-packing. According to this hypothesis, the mysterious process of meiosis is based on a mechanism of algorithmic re-arrangement of molecular elements of gametes with a participation of algorithms of cyclic and dyadic shifts. In our opinion, re-packing of biological molecules and of their ensembles is an important general principle of biological self-organization. A meaning of this principle will be revealed more and more in the course of time. We will return to described mosaic genomatrices in the section about algebras with two quasi-real unities.

5. NUMERICAL GENOMATRICES AS MATRIX FORMS OF REPRESENTATIONS OF SPECIAL ALGEBRAS (HYPERBOLIC MATRIONS).

The theory of digital signals considers signals in a form of sequences of numeric values of their amplitudes in reference points. This theory represents discrete signals as vectors of many-dimensional spaces: a signal value on each time is interpreted as the value of one from coordinates of many-dimensional space of signals. In this reason, the theory of discrete signals has many mutual aspects with geometries of many-dimensional spaces.

A dimension of such space is equal to quantity of reference points of a considered signal. If we wish to utilize methods of the theory of signal processing in analysis of genetic code systems, we should learn to convert symbolic genomatrices to numeric genomatrices.

One of possible ways of such conversion is realized by means of replacements of symbols A, C, G, U/T with those quantitative parameters of these molecular "letters", which determine their physical-chemical role. For example, let us consider genomatrices of hydrogen bonds of nitrogen bases ("genetic letters") of genetic code. Hydrogen bonds of complementary pairs of genetic letters are suspected of information meanings long ago. The speech is about two and three hydrogen bonds, which connect letters in complementary pairs in molecules of heredity (C and G have 4 bonds; A and U/T have 2 bonds). Let us replace each multiplet in all genomatrices $P^{(n)}$ (Fig.1) by a product of numbers of hydrogen bonds of its nitrogen bases. In this case, for instance, the triplet CGA in the genomatrix $P^{(3)}$ will be replaced by a product 3*3*2=18. Multiplicative non-singular bisymmetrical genomatrices $P_{MULT}^{(n)}$ are produced in this case (Fig. 6).

The previous publications (Petoukhov, 2001-2005) have described that this Kronecker family of genomatrices $P_{MULT}^{(n)}$ has many interesting properties. For example, it has revealed the unexpected connection between genetic code and the golden section $\varphi = (1+5^{0.5})/2 = 1{,}618\ldots$. This family of genomatrices has demonstrated also its connection with Pythagorean musical scale, with the Ancient Chinese book "I-Ching", etc.

$$P_{MULT} = \begin{vmatrix} 3 & 2 \\ 2 & 3 \end{vmatrix};$$

$$P_{MULT}^{(2)} = \begin{vmatrix} 9 & 6 & 6 & 4 \\ 6 & 9 & 4 & 6 \\ 6 & 4 & 9 & 6 \\ 4 & 6 & 6 & 9 \end{vmatrix};$$

$$P_{MULT}^{(3)} = \begin{vmatrix} 27 & 18 & 18 & 12 & 18 & 12 & 12 & 8 \\ 18 & 27 & 12 & 18 & 12 & 18 & 8 & 12 \\ 18 & 12 & 27 & 18 & 12 & 8 & 18 & 27 \\ 12 & 18 & 18 & 27 & 8 & 12 & 12 & 18 \\ 18 & 12 & 12 & 8 & 27 & 18 & 18 & 12 \\ 12 & 18 & 8 & 12 & 18 & 12 & 27 & 18 \\ 12 & 8 & 18 & 12 & 18 & 12 & 27 & 18 \\ 8 & 12 & 12 & 18 & 12 & 18 & 18 & 27 \end{vmatrix}$$

Fig. 6. The beginning of the family of the multiplicative genomatrices $P_{MULT}^{(n)}$, which is based on products of numbers of hydrogen bonds (C=G=3, A=U=2).

In this paper we will show that these genomatrices $P_{MULT}^{(n)}$ are particular cases of the matrix forms of representation of special 2^n-dimensional hypercomplex numbers (or elements of special algebras). These hypercomplex numbers are constructed by means of an algorithmic generalization of so named double numbers proposed by Clifford in 1872 year: x_0***1** + x_1***e**$_1$, where $e_1^2 = +1$. This block-fractal algorithm of a generalization, proposed by the author, can be interpreted as a particular case of the doubling algorithm by Grassman-Clifford. This algorithm can be applied to generalize not only double numbers but also many types of hypercomplex numbers (complex numbers, dual numbers, quaternions by Hamilton, etc.). 2^n-dimensional numbers, which are constructed by such algorithm, were named "matrions" by the author because they were revealed in a course of the analysis of matrices of genetic code. It is known, that double numbers in their matrix form of representation (Fig. 7, left) are connected with a transformation of hyperbolic turning and Lorentz's transformations. In this reason, those matrions, which are the algorithmic generalization of double numbers, are named hyperbolic matrions. We could not find special investigations of these matrion kinds of hypercomplex numbers in literature. Sets of 2^n-dimensional hyperbolic matrions, determined over the algebraic field of real numbers, involve unitary matrices in a role of their units. They form rings and algebras with specific tables of multiplications of their basic elements. Since hyperbolic matrions present some structural properties of genetic code systems, double numbers, which are known long ago, assume new sides of their meaning in the fields of biology and physiology. For example, double numbers find themselves in a connection with the Pythagorean musical scale and with tables of the Chinese book "I-Ching", which was written a few thousands years ago.

In a course of construction of 2^n-dimensional hyperbolic matrions as generalizations of double numbers, each real elements x_0 and x_1 of the matrix form of presentation of double numbers (Fig. 7, left) is interpreted as (2x2)-matrix of a double number: $x_0=[y_0\ y_1;\ y_1\ y_0]$, $x_1=[y_2\ y_3;\ y_3\ y_2]$ (here we utilize the form of matrix presentation from the software MatLab). In a result of the substitution of these (2x2)-matrices into the initial (2x2)-matrix, we receive the (2^2x2^2)-matrix, which is the matrix form of presentation of 4-dimensional hyperbolic matrions. If we interpret each element of this new (4x4)-matrix as (2x2)-matrix of a double number ($y_0=[z_0\ z_1;\ z_1\ z_0]$, $y_1=[z_2\ z_3;\ z_3\ z_2]$, $y_2=[z_4\ z_5;\ z_5\ z_6]$, $y_3=[z_6\ z_7;\ z_7\ z_6]$), we receive (2^3x2^3)-matrix, which presents 8-dimensional hyperbolic matrions, etc. (Fig. 7).

All (2^nx2^n)-matrices of hyperbolic matrions are bisymmetrical ones: they are symmetrical in a relation to both diagonals. These (2^nx2^n)-matrices, which were

constructed by the local replacement of each element by a block matrix, have a global character of block matrices: their (2^{n-1}x2^{n-1})-quadrants, which are disposed along each diagonal, are identical to each other. In this reason, if we denote these quadrants as A_1 and A_2, we receive, that the whole matrix has a form of a matrix of double numbers for any "n": [A_1 A_2; A_2 A_1]. This property of identity along diagonals is also realized for its quadrants, sub-quadrants, sub-sub-quadrants, etc. In this sense, we have block fractals. The same algorithm of the construction of hyperbolic matrions can be presented in a form of the Kronecker multiplication of (2x2)-matrices of double numbers.

$$\begin{vmatrix} x0\ x1 \\ x1\ x0 \end{vmatrix} \Rightarrow \begin{vmatrix} y0\ y1 & y2\ y3 \\ y1\ y0 & y3\ y2 \\ y2\ y3 & y0\ y1 \\ y3\ y2 & y1\ y0 \end{vmatrix} \Rightarrow \begin{vmatrix} z0\ z1 & z2\ z3 & z4\ z5 & z6\ z7 \\ z1\ z0 & z3\ z2 & z5\ z4 & z7\ z6 \\ z2\ z3 & z0\ z1 & z6\ z7 & z4\ z5 \\ z3\ z2 & z1\ z0 & z7\ z6 & z5\ z4 \\ z4\ z5 & z6\ z7 & z0\ z1 & z2\ z3 \\ z5\ z4 & z7\ z6 & z1\ z0 & z3\ z2 \\ z6\ z7 & z4\ z5 & z2\ z3 & z0\ z1 \\ z7\ z6 & z5\ z4 & z3\ z2 & z1\ z0 \end{vmatrix} \Rightarrow \ldots$$

Fig. 7. The algorithmic construction of 2^n-dimensional hyperbolic matrions.

Each (2^nx2^n)-matrix of hyperbolic matrions can be realized as a sum of its basic matrices. For example, hyperbolic tetramatrion G_2 can be realized in the sum on Fig. 8. The first basic matrix in the right part of Fig. 8 is the unitary matrix, which can be denoted by the symbol **1**. Other three basic matrices on Fig. 8 can be denoted by the symbols e_1, e_2, e_3. They have the property: $e_1^2 = e_2^2 = e_3^2 = +1$. In the case of such symbolic designation, any 2^n-dimensional hyperbolic matrion receives a multilinear or vector form of its presentation (Fig. 9).

$$G_2 = \begin{vmatrix} X_0\ X_1\ X_2\ X_3 \\ X_1\ X_0\ X_3\ X_2 \\ X_2\ X_3\ X_0\ X_1 \\ X_3\ X_2\ X_1\ X_0 \end{vmatrix} = X_0 * \begin{vmatrix} 1\,0\,0\,0 \\ 0\,1\,0\,0 \\ 0\,0\,1\,0 \\ 0\,0\,0\,1 \end{vmatrix} + X_1 * \begin{vmatrix} 0\,1\,0\,0 \\ 1\,0\,0\,0 \\ 0\,0\,0\,1 \\ 0\,0\,1\,0 \end{vmatrix} +$$

$$+ X_2 * \begin{vmatrix} 0\,0\,1\,0 \\ 0\,0\,0\,1 \\ 1\,0\,0\,0 \\ 0\,1\,0\,0 \end{vmatrix} + X_3 * \begin{vmatrix} 0\,0\,0\,1 \\ 0\,0\,1\,0 \\ 0\,1\,0\,0 \\ 1\,0\,0\,0 \end{vmatrix}$$

Fig. 8. The presentation of hyperbolic tetramatrion as the sum of its basic matrices.

DIMENSIONS	***HYPERBOLIC MATRION***

2^1	$X_0*\boldsymbol{1} + X_1*\boldsymbol{E_1}$
2^2	$X_0*\boldsymbol{1} + X_1*\boldsymbol{E_1} + X_2*\boldsymbol{E_2} + X_3*\boldsymbol{E_3}$
2^3	$X_0*\boldsymbol{1} + X_1*\boldsymbol{E_1} + X_2*\boldsymbol{E_2} + X_3*\boldsymbol{E_3} + X_4*\boldsymbol{E_4} + X_5*E_5 + X_6*\boldsymbol{E_6} + X_7*\boldsymbol{E_7}$

Fig. 9. Vector presentations of hyperbolic matrions for the cases of 2-, 4-, 8-dimensional spaces.

The general rule of enclosure of vector forms exist for hyperbolic matrions of different dimensions. According to this rule that the well-ordered set of the first $2^n/2$ items in the vector form of a 2^n-dimensional hyperbolic matrion is the whole set of items in the vector form of 2^{n-1}-dimensional hyperbolic matrions. In other words, a matrion with the lesser dimension is enclosed in a matrion of a double dimension as its initial half. The realization of this rule is demonstrated by examples of Fig. 9. It means that hyperbolic matrions, as many-dimensional numbers, unite a set of analogous numbers of the lesser dimensions in a form of hierarchic ensembles. A similar rule of enclosure holds true for the table of multiplication of basic elements of hyperbolic matrions. Fig. 9 shows such multiplication table for 8-dimension hyperbolic matrions.

The left top corner of the table on Fig. 9 has (2x2)- and (4x4)-tables, which are denoted by bold lines. They are the tables of multiplications of basic elements for 2-dimensional and 4-dimensional hyperbolic matrions correspondingly. In the case of hyperbolic matrions we have the hierarchy of enclosures of appropriate algebras. The unique feature of hyperbolic matrions is that the structure of their multiplication table coincides with their own matrix structures. Really, if symbols of the multiplication table on Fig. 9 are interpreted as real numbers, the multiplication table becomes a hyperbolic matrion.

	1	**E_1**	**E_2**	**E_3**	**E_4**	**E_5**	**E_6**	**E_7**
1	**1**	**E_1**	**E_2**	**E_3**	**E_4**	**E_5**	**E_6**	**E_7**
E_1	**E_1**	**1**	**E_3**	**E_2**	**E_5**	**E_4**	**E_7**	**E_6**
E_2	**E_2**	**E_3**	**1**	**E_1**	**E_6**	**E_7**	**E_4**	**E_5**
E_3	**E_3**	**E_2**	**E_1**	**1**	**E_7**	**E_6**	**E_5**	**E_4**
E_4	**E_4**	**E_5**	**E_6**	**E_7**	**1**	**E_1**	**E_2**	**E_3**
E_5	**E_5**	**E_4**	**E_7**	**E_6**	**E_1**	**1**	**E_3**	**E_2**
E_6	**E_6**	**E_7**	**E_4**	**E_5**	**E_2**	**E_3**	**1**	**E_1**
E_7	**E_7**	**E_6**	**E_5**	**E_4**	**E_3**	**E_2**	**E_1**	**1**

Fig. 9. The table of multiplication of basic elements of hyperbolic octomatrions.

The multiplication tables of 2^n-dimensional matrions are symmetrical in a relation to the main diagonal that reflects a commutative property of these matrions. Hyperbolic matrions have an associative property also. A matrix of 2^n-dimensional matrions with non-zero components, in which all components are equal to each other, is singular one. It has no an inverse matrix. A matrix division can not be determined in such cases.

Non-singular hyperbolic matrions satisfy to the definition of metric tensors of Riemannian geometry. It permits to utilize them in an analysis of internal geometry of surfaces of biological bodies and in mathematical models of morphological heredity.

One can remark the additional numeric connection between hyperbolic matrions and the genomatrix $P^{(3}$ (Fig. 1) in the case of concatenation numbers of hydrogen bonds A=U=2, C=G=3. By definition, a triplet concatenation of hydrogen bonds is a sequence of quantities of hydrogen bonds of each genetic letter in the triplet; such sequence is interpreted as the whole three-digit number. For example, such concatenation number for the triplet CAG is 323. When 64 triplets are transformed in their concatenation presentation, we receive 8 concatenation numbers 232, 233, 322, 323, 332, 333, 222, 223. It is interesting that the 8 numbers of this sequence are comparable with the 8 numbers of the sequence 0, 1, …, 7 on the module 8. A sub-set of eight triplets is correspondent to each of these 8 concatenation numbers. For example, the sub-set of 8 triplets AAA, AAU, AUA, AUU, UAA, UAU, UUA, UUU is correspondent to the concatenation number 222. Fig.10 shows the transformation of the genomatrix $P^{(3)}$ in the case of the replacement of each triplet by its concatenation number. One can check that this numeric genomatrix is a hyperbolic matrion.

333 (5)	**332 (4)**	**323 (3)**	**322 (2)**	**233 (1)**	**232 (0)**	**223 (7)**	**222 (6)**
332 (4)	**333 (5)**	**322 (2)**	**323 (3)**	**232 (0)**	**233 (1)**	**222 (6)**	**223 (7)**
323 (3)	**322 (2)**	**333 (5)**	**332 (4)**	**223 (7)**	**222 (6)**	**233 (1)**	**232 (0)**
322 (2)	**323 (3)**	**332 (4)**	**333 (5)**	**222 (6)**	**223 (7)**	**232 (0)**	**233 (1)**
233 (1)	**232 (0)**	**223 (7)**	**222 (6)**	**333 (5)**	**332 (4)**	**323 (3)**	**322 (2)**
232 (0)	**233 (1)**	**222 (6)**	**223 (7)**	**332 (4)**	**333 (5)**	**322 (2)**	**323 (3)**
223 (7)	**222 (6)**	**233 (1)**	**232 (0)**	**323 (3)**	**322 (2)**	**333 (5)**	**332 (4)**
222 (6)	**223 (7)**	**232 (0)**	**233 (1)**	**322 (2)**	**323 (3)**	**332 (4)**	**333 (5)**

Fig. 10. The transformation of the genomatrix $P^{(3)}$ in the case of the replacement of each triplet by its concatenation number. Remainders of division of each concatenation numbers on 8 are shown in brackets.

6. HYPERBOLIC MATRIONS AND MATRICES OF DYADIC SHIFTS IN INFORMATICS.

Molecular-genetic system is investigated by us from the viewpoint of the theory of discrete signals and noise immunity encoding. Whether this theory knows bisymmetrical matrices of type of hyperbolic matrions? Our purposeful search revealed them. Such bisymmetrical matrices exist in this theory, and they are utilized due to their useful properties. They lie in bases of a few methods of signal processing, and they are named matrices of dyadic shifts (see, for example, (Ahmed, Rao, 1975)). In the fields of computer informatics, these matrices are constructed by means of an operation of logic addition on the module 2 (without the operation of Kronecker multiplication).

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

Fig.10. The octet matrix of dyadic shifts from the theory of digital signals.

Fig. 10 demonstrates an example of the (2^3x2^3)-matrix of dyadic shift. Numerical numbers of cells from the first matrix row are repeated in each row but in different orders. This specific numeration of all matrix cells by numbers from the sequence 0, 1, 2, .., 2^n-1 is defined by the algorithm of construction of (2^nx2^n)-matrix of dyadic shifts.

One can see from Fig. 7 and Fig. 11 that this matrix of dyadic shifts is an 8-dimensional hyperbolic matrion. The algorithm of the construction of (2^nx2^n)-matrices of dyadic shifts has the following operations. From the very beginning all rows and columns of a (2^nx2^n)-matrix are numerated in binary notation in the manner, which is demonstrated by Fig. 10. Then each matrix cell gets a number which is equal to a sum of binary numbers of its row and column; it is essential that this sum is calculated by logical bitwise addition of these binary numbers on the module 2 in accordance with the rules: 0+0=0, 0+1=1, 1+0=1, 1+1=1. For example, the cell, which belongs to the column 3 (=011) and to the row 2 (=010), gets the number 1 (=001) in the result of such addition

on the module 2. According to general features of hyperbolic matrions, matrices of dyadic shifts have a block structure: identical matrix blocks are disposed along each diagonal in the matrix, in its quadrants, in its sub-quadrants, etc. It gives a crosswise character to such matrices.

One can note that structures of many physiological and bioinformatics systems, which are defined genetically, demonstrate analogical crosswise characters. For example, the interface of hemispheres of a brain to halves of our body has such crosswise character: the left hemisphere serves the right half of body, and the right hemisphere serves the left half. Visual nervous ways from two eyes have the crosswise character also: these ways transfer the information from the right half of field of vision in the left hemisphere of a brain, and the information from the left half of field of vision - in the right hemisphere. This scheme holds true for the acoustic system. It is probably that these physiological phenomena are connected with hyperbolic matrions and with their crosswise structures to provide noise immunity encoding of genetic information. It generates many heuristic associations.

One can add that analogical fractal structure with crosswise block matrices is known during a few thousand years in a connection with a chessboard. If black cells of a chessboard are marked by number “a”, and its white cells – by number “b”, that the numeric matrix, which has arisen on a board, will appear a special case of hyperbolic matrions. The most ancient game in chess demonstrates a surprising survivability, which, according to the founder of analytical psychology C.Jung, one can explain by its intimacy to archetypes of unconscious. The given example of matrices of dyadic shifts is one of many examples, which confirm adequacy and perspectives of union of the matrion theory with computer and biological computer science. Additional materials to the theme of a connection among genetic systems, many-dimensional numbers and noise immunity encoding are included in a new book by the author, which is preparing for a publication.

7. GENETIC CODE AND ALGEBRAS WITH TWO QUASI-REAL UNITIES.

A development of theoretical biology needs in appropriate mathematical models of structural ensembles of genetic elements. One of such models is proposed below.

Fig. 1 shows that each triplet in the genomatrix $P^{(3)}$ has an individual number in the natural system of numeration of multiplets (Petoukhov, 2001a,b). This system of numeration was constructed by means of the system of three sub-alphabets of the genetic alphabet (in (Waterman, 1989, Chapter 6), they are named "two-letters nucleotide alphabets" -"purine-pyrimidine", "strong and weak hydrogen bonds", "keto-amino"). Each of these three sub-alphabets divides the set of 64 triplets into 8 sub-sets, each of which contains 8 triplets. Really, the sub-alphabet "purine–pyrimidine" divides the sets of 64 triplets into 8 sub-sets, which are corresponded to 8 columns of the genomatrix $P^{(3)}$ (Fig.1) with 8 triplets in each column. The sub-alphabet "keto-amino" divides the sets of 64 triplets into 8 sub-sets, which are corresponded to 8 rows of the genomatrix $P^{(3)}$ (Fig.1) with 8 triplets in each row. The sub-alphabet with 3 or 2 hydrogen bonds divides the sets of 64 triplets into the 8 sub-sets, each of which is correspondent to one of 8 concatenation numbers (Fig. 10). But these variants of division of set of 64 triplets into 8 octet sub-sets are not appropriate for its division into sub-sets of black and white triplets.

The author found the fourth variant of such division of the set of 64 triplets into 8 octet sub-sets, which satisfied to black-and-white mosaics of all genomatrices on Fig. 3 and which had the properties of binary genomatrices on Fig. 5. It was quite unexpectedly that this new division had a close connection with the algebras, basic elements of which had two quasi-real units and had not the real unit. The systems of many-dimensional numbers, which are connected with these algebras, were named the systems of "two-sexual" numbers (or briefly "bisexes") because of their relation with black and white colors in the genomatrices on Fig. 3. These two colors symbolize the binary-opposite attribute of the code degeneration (or its Yin and Yang, or "female" and "male" beginnings conditionally). Phenomena of binary-opposite attributes exist on many levels of biological organization. In our opinion, they are connected with male and female biological objects, which participate in genetic inheritance: male and female gametes, male and female chromosomes, etc. Results, which were received in the fields of matrix genetics, permitted to suppose that genomatrices with their ensembles of binary-opposites attributes could be modeled on a new language of special generalized numbers.

Below we demonstrate that the set of basic elements of 2n-dimensional bisexes does not contain the real unit in contrast to complex and hypercomplex numbers (which were constructed as generalizations of real numbers with the obligatory inclusion of the real unit in sets of their basic elements). So, one can speak about a new category of generalized numbers (elements of algebras with two quasi-real units). In our opinion, knowledge of this category of numbers is necessary for deep understanding of biological phenomena, and, perhaps, it will be useful for mathematical natural sciences in the whole.

Investigations of bisex numeric systems and their analogies with genetic structures testify in favor of a consideration of certain bisexes as the basis of the more fundamental code (pre-code) of genetic code. Mathematical theory of bisexes gives new formal and conceptual apparatus to model phenomena of reproduction, self-organization and self-development in living nature. The idea about existence and significance of bisexes is based on peculiarities of genetic code itself and on its mosaic genomatrix $P^{(3)}$. Let us describe some results of these investigations.

Bisexes will be denote by double letters (for example, BB) to distinguish them from traditional (complex and hypercomplex) numbers. The (8x8)-matrix on Fig. 11 (top), which is proposed by the author and which is a matrix form of presentation of the 8-dimensional bisex $BB_{\mathbf{8}}$, reproduces many peculiarities of the (8x8)-genomatrix $P^{(3)}$ (Fig. 3, top and Fig. 11, below). The index in the symbol $BB_{\mathbf{8}}$ means a dimension of the bisex. Coordinates $x_{\mathbf{0}}$, $x_{\mathbf{1}}$, …, $x_{\mathbf{7}}$ are real numbers. Cells with signs "+" are marked by black color and cells with signs "-" are marked by white color. Columns are numerated by numbers 0, 1, …, 7. In a comparison with its image on Fig. 1, the genomatrix $P^{(3)}$ on the Fig. 11 has bisex coordinates $x_{\mathbf{0}}$, $x_{\mathbf{1}}$, …, $x_{\mathbf{7}}$ and the reverse numbering of columns for its conformity of a traditional numbering of columns in matrices.

The binary genomatrix $B_{\mathbf{123}}$ (Fig. 5) is a particular case of the matrix BB8 (Fig. 11), proposed by the author to model the genomatrix $P^{(3)}$ with its specific mosaic of the degeneration of the genetic code. Other binary genomatrices $B_{\mathbf{231}}$, $B_{\mathbf{312}}$, $B1_{\mathbf{32}}$, $B_{\mathbf{213}}$, $B_{\mathbf{321}}$ are particular cases of genomatrices, which are constructed from BB_8 by appropriate permutations of its columns and rows and which do not considered in this paper.

Let us consider conditionally for a terminological convenience, that pyrimidines C and U/T are "female" genetic letters, and that purines A and G are "male" letters. Accordingly, those triplets, which have a female letter C or U (the female letter A or G) on the third position, we shall consider as female (male) triplets. In the case of the

binary opposition of the numbers 2 and 3 of hydrogen bonds of complementary genetic letters, we shall interpret the number 2 (3) as the female (male) number in accordance with the ancient tradition. Columns of matrices with even (odd) we shall consider also as female

$BB_8 =$

0	*1*	*2*	*3*	*4*	*5*	*6*	*7*
X_0	X_1	$-X_2$	$-X_3$	X_4	X_5	$-X_6$	$-X_7$
X_0	X_1	$-X_2$	$-X_3$	X_4	X_5	$-X_6$	$-X_7$
X_2	X_3	X_0	X_1	$-X_6$	$-X_7$	$-X_4$	$-X_5$
X_2	X_3	X_0	X_1	$-X_6$	$-X_7$	$-X_4$	$-X_5$
X_4	X_5	$-X_6$	$-X_7$	X_0	X_1	$-X_2$	$-X_3$
X_4	X_5	$-X_6$	$-X_7$	X_0	X_1	$-X_2$	$-X_3$
$-X_6$	$-X_7$	$-X_4$	$-X_5$	X_2	X_3	X_0	X_1
$-X_6$	$-X_7$	$-X_4$	$-X_5$	X_2	X_3	X_0	X_1

0	*1*	*2*	*3*	*4*	*5*	*6*	*7*
CCC PRO X_0	CCA PRO X_1	CAC HIS $-X_2$	CAA GLN $-X_3$	ACC THR X_4	ACA THR X_5	AAC ASN $-X_6$	AAA LYS $-X_7$
CCU PRO X_0	CCG PRO X_1	CAU HIS $-X_2$	CAG GLN $-X_3$	ACU THR X_4	ACG THR X_5	AAU ASN $-X_6$	AAG LYS $-X_7$
CUC LEU X_2	CUA LEU X_3	CGC ARG X_0	CGA ARG X_1	AUC ILE $-X_6$	AUA MET $-X_7$	AGC SER $-X_4$	AGA STOP $-X_5$
CUU LEU X_2	CUG LEU X_3	CGU ARG X_0	CGG ARG X_1	AUU ILE $-X_6$	AUG MET $-X_7$	AGU SER $-X_4$	AGG STOP $-X_5$
UCC SER X_4	UCA SER X_5	UAC TYR $-X_6$	UAA STOP $-X_7$	GCC ALA X_0	GCA ALA X_1	GAC ASP $-X_2$	GAA GLU $-X_3$
UCU SER X_4	UCG SER X_5	UAU TYR $-X_6$	UAG STOP $-X_7$	GCU ALA X_0	GCG ALA X_1	GAU ASP $-X_2$	GAG GLU $-X_3$
UUC PHE $-X_6$	UUA LEU $-X_7$	UGC CYS $-X_4$	UGA TRP $-X_5$	GUC VAL X_2	GUA VAL X_3	GGC GLY X_0	GGA GLY X_1
UUU PHE	UUG LEU	UGU CYS	UGG TRP	GUU VAL	GUG VAL	GGU GLY	GGG GLY

$-X_6$	$-X_7$	$-X_4$	$-X_5$	X_2	X_3	X_0	X_1

Fig. 11. Top: the matrix form of a presentation of octet bisex BB_8. Below: the octet genomatrix $P^{(3)}$ of the vertebrate mitochondria code, each cell of which contains a triplet, an amino acid, a coordinate of the bisex BB_8

(male) columns. Bisex coordinates with even indexes (for example, x_0, x_2, x_4, x_6) we shall believe female coordinates, and coordinates with odd indexes x_1, x_3, x_5, x_7 – male coordinates. Fig. 12 demonstrates main examples of a conformity between the bisex matrix BB_8 and the genomatrix $P^{(3)}$ from the Fig.11.

Let us analyze properties of the bisex matrix BB_8 in more detail. It can be presented as the sum (Fig. 13) of its 8 basic (8x8)-matrices (or 8 basic elements). Each of these basic matrices is appeared, if an appropriate coordinate x_k (k = 0, 1, …,7) of the matrix BB_8 is accepted to be equal to 1, and all other coordinates are accepted to be equal to 0.

We denote these basic matrices in their sequence by means symbols $\mathbf{1}^F_0$, $\mathbf{1}^M_1$, $\mathbf{i}^F_2$, $\mathbf{i}^M_3$, $\mathbf{e}^F_4$, $\mathbf{e}^M_5$, $\mathbf{e}^F_6$, $\mathbf{e}^M_7$. Lower indexes are corresponded to a serial number of a basic matrix, and upper indexes F and M are the initial letters of the words “female” and “male”. These upper indexes help to trace the binary-opposite structure realized in the bisex BB_8. By means of these symbols, the bisex BB_8 can be written in a vector form (7/1), which is known in the theory of hypercomplex numbers:

$$\mathbf{BB_8} = x_0*\mathbf{1}^F_0+x_1*\mathbf{1}^M_1+x_2*\mathbf{i}^F_2+x_3*\mathbf{i}^M_3+x_4*\mathbf{e}^F_4+x_5*\mathbf{e}^M_5+x_6*\mathbf{e}^F_6+x_7*\mathbf{e}^M_7 \quad \mathbf{(7/1)}$$

Multiplication of 8 matrixes with each other shows unexpectedly, that they form the closed set: the result of product of any of two of these matrices is a matrix from the same set. The corresponding multiplication table of basic matrixes for the bisex BB_8 is presented on Fig. 14. This table is not symmetric one relative to the main diagonal; it corresponds to non-commutative property of bisexes. This table gives the following information as well. The basic element $\mathbf{1}^F_0$ at squaring is equal to itself $(\mathbf{1}^F_0)^2 = \mathbf{1}^F_0$. By this property, the element $\mathbf{1}^F_0$ is similar to the real unit. But when this element $\mathbf{1}^F_0$ is multiplied with another basic element, the result can be equal to a new basic element, for example, $\mathbf{i}^M_3*\mathbf{1}^F_0 = \mathbf{i}^F_2$. It distinguishes cardinally an element $\mathbf{1}^F_0$ from the real unit, the result of multiplication on which always coincides with its factor. Due to these properties, the basic element $\mathbf{1}^F_0$ is named the quasi-real unit of the first type. The second basic element $\mathbf{1}^M_1$ possesses analogical peculiarities and it is named the quasi-real unit of the second type.

The basic elements with even serial numbers (even bottom indexes) $\mathbf{i}^F_2$, $\mathbf{e}^F_4$, $\mathbf{e}^F_6$ at their squaring give the quasi-real unit of the first type $\mathbf{1}^F_0$, which henceforth will be named the female quasi-real unit. The basic elements with odd serial numbers $\mathbf{i}^M_3$, $\mathbf{e}^M_5$, $\mathbf{e}^M_7$ at their squaring give the quasi-real unit of the second type $\mathbf{1}^M_1$, which henceforth will be named the male quasi-real unit. The upper indexes F and M at basic elements just mark

that a half of the quantity of basic elements forms the "female" part of the bisex BB_8, and the second half forms its "male" part.

THE OCTET GENOMATRIX $P^{(3)}$	**THE OCTET BISEX BB_8**
IT HAS THE BINARY MOSAIC OF SYMMETRICAL CHARACTER WITH 32 BLACK AND 32 WHITE TRIPLETS.	IT HAS THE SAME MOSAIC, WHICH CONTAINS 32 COORDINATES WITH THE SIGN "+" AND 32 COORDINATES WITH THE SIGNS "-".
THE NEIGHBORING ROWS IN EACH OF PAIRS 0-1, 2-3, 4-5, 6-7 ARE EQUIVALENT TO EACH OTHER BY A DISPOSITION OF IDENTICAL AMINO ACIDS.	THE NEIGHBORING ROWS IN EACH OF PAIRS 0-1, 2-3, 4-5, 6-7 ARE EQUIVALENT TO EACH OTHER BY A DISPOSITION OF IDENTICAL COORDINATES.
FEMALE TRIPLETS ARE PRESENTED IN EACH FEMALE COLUMN ONLY (WITH EVEN NUMBERS), AND MALE TRIPLETS ARE PRESENTED IN EACH MALE COLUMN ONLY.	FEMALE COORDINATES X_0, X_2, X_4, X_6 ARE PRESENTED IN EACH FEMALE COLUMN (WITH EVEN NUMBERS) ONLY, AND MALE COORDINATES X_1, X_3, X_5, X_7 ARE PRESENTED IN EACH MALE COLUMN ONLY.
PERMUTATIONS OF COLUMNS AND ROWS BECAUSE OF PERMUTATIONS OF POSITIONS IN TRIPLETS LEAD TO THE SET OF 6 DIFFERENT GENOMATRICES, EACH OF WHICH HAS A SYMMETRICAL CHARACTER OF A DISPOSITION OF 64 BLACK AND WHITE TRIPLETS.	ANALOGICAL PERMUTATIONS OF COLUMNS AND ROWS OF THE BISEX MATRIX BB_8 LEAD TO THE SET OF 6 DIFFERENT MATRICES, EACH OF WHICH IS AN OCTET BISEX MATRIX ALSO WITH THE SAME SYMMETRICAL CHARACTER OF A DISPOSITION OF 64 SIGNS "+" AND "-" OF ITS COORDINATES.
THE BINARY PRESENTATION OF EACH OF THOSE 6 INTERCONNECTED GENOMATRICES, WHICH ARE MENTIONED IN THE PREVIOUS ITEM, IS TETRA-REPRODUCED BY MULTIPLICATION OF EACH GENOMATRIX WITH ITSELF (§ 4).	THE BINARY PRESENTATION OF EACH OF THOSE 6 INTERCONNECTED MATRIX FORMS OF BISEXES, WHICH ARE MENTIONED IN THE PREVIOUS ITEM, IS TETRA-REPRODUCED BY MULTIPLICATION OF EACH BISEX MATRIX WITH ITSELF.
THE HALF OF KINDS OF AMINO ACIDS IS PRESENTED IN THE QUADRANTS ALONG THE MAIN MATRIX DIAGONAL ONLY (ALA, ARG, ASP, GLN, GLU, GLY, HIS, LEU, PRO, VAL). THE SECOND HALF OF KINDS OF AMINO ACIDS IS PRESENTED IN THE QUADRANTS ALONG THE SECOND DIAGONAL ONLY (ASN, CYS, ILE, LYS, MET, PHE, SER,THR, TRP, TYR).	THE HALF OF KINDS OF COORDINATES (X_0, X_1, X_2, X_3) IS PRESENTED IN THE QUADRANTS ALONG THE MAIN MATRIX DIAGONAL ONLY. THE SECOND HALF OF KINDS OF COORDINATES (X_4, X_5, X_6, X_7) IS PRESENTED IN THE QUADRANTS ALONG THE SECOND COORDINATES ONLY.

Fig. 12. Examples of conformity between the bisex matrix BB_8 and the mosaic genomatrix $P^{(3)}$ from Fig.11.

$$\mathbf{BB_8} = X_0 * \begin{bmatrix} 1&0&0&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 0&0&1&0&0&0&0&0\\ 0&0&1&0&0&0&0&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&0&0&1&0\\ 0&0&0&0&0&0&1&0 \end{bmatrix} + X_1 * \begin{bmatrix} 0&1&0&0&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&0&0&1&0&0&0&0\\ 0&0&0&1&0&0&0&0\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&0&0&1\\ 0&0&0&0&0&0&0&1 \end{bmatrix} +$$

$$+ X_2 * \begin{bmatrix} 0&0&-1&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&1&0&0&0 \end{bmatrix} + X_3 * \begin{bmatrix} 0&0&0&-1&0&0&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&1&0&0 \end{bmatrix} +$$

$$+ X_4 * \begin{bmatrix} 0&0&0&0&1&0&0&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&0&0&-1&0\\ 1&0&0&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0 \end{bmatrix} + X_5 * \begin{bmatrix} 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&0&0&-1\\ 0&1&0&0&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&0&0&-1&0&0&0&0 \end{bmatrix}$$

$$+ X_6 * \begin{bmatrix} 0&0&0&0&0&0&-1&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&-1&0&0&0\\ 0&0&0&0&-1&0&0&0\\ 0&0&-1&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0\\ -1&0&0&0&0&0&0&0\\ -1&0&0&0&0&0&0&0 \end{bmatrix} + X_7 \begin{bmatrix} 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&-1&0&0\\ 0&0&0&0&0&-1&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&-1&0&0&0&0&0&0\\ 0&-1&0&0&0&0&0&0 \end{bmatrix}$$

Fig.13. The presentation of the bisex matrix BB_8 as a sum of its basic matrices.

	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$	$\mathbf{E^F_4}$	$\mathbf{E^M_5}$	$\mathbf{E^F_6}$	$\mathbf{E^M_7}$
$\mathbf{1^F_0}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$	$\mathbf{E^F_4}$	$\mathbf{E^M_5}$	$\mathbf{E^F_6}$	$\mathbf{E^M_7}$
$\mathbf{1^M_1}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$	$\mathbf{E^F_4}$	$\mathbf{E^M_5}$	$\mathbf{E^F_6}$	$\mathbf{E^M_7}$
$\mathbf{I^F_2}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$	$\mathbf{-1^F_0}$	$\mathbf{-1^M_1}$	$\mathbf{-E^F_6}$	$\mathbf{-E^M_7}$	$\mathbf{E^F_4}$	$\mathbf{E^M_5}$
$\mathbf{I^M_3}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$	$\mathbf{-1^F_0}$	$\mathbf{-1^M_1}$	$\mathbf{-E^F_6}$	$\mathbf{-E^M_7}$	$\mathbf{E^F_4}$	$\mathbf{E^M_5}$
$\mathbf{E^F_4}$	$\mathbf{E^F_4}$	$\mathbf{E^M_5}$	$\mathbf{E^F_6}$	$\mathbf{E^M_7}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$
$\mathbf{E^M_5}$	$\mathbf{E^F_4}$	$\mathbf{E^M_5}$	$\mathbf{E^F_6}$	$\mathbf{E^M_7}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$
$\mathbf{E^F_6}$	$\mathbf{E^F_6}$	$\mathbf{E^M_7}$	$\mathbf{-E^F_4}$	$\mathbf{-E^M_5}$	$\mathbf{-I^F_2}$	$\mathbf{-I^M_3}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$
$\mathbf{E^M_7}$	$\mathbf{E^F_6}$	$\mathbf{E^M_7}$	$\mathbf{-E^F_4}$	$\mathbf{-E^M_5}$	$\mathbf{-I^F_2}$	$\mathbf{-I^M_3}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$

Fig. 14. The multiplication table of the basic elements of the bisex BB_8

Each column of the bisex table of multiplication (Fig. 14) contains only female or only male basic elements. In this aspect, each column of this table is a female column or a male column. One can see from Fig. 14 that all tabular columns with even serial numbers (including number 0) are female columns and all columns with odd serial numbers are male columns.

The set of basic elements of the female part of the bisex BB_8 has one female quasi-real unit $\mathbf{1^F_0}$; one female imaginary unit $\mathbf{i^F_2}$ with the property $(\mathbf{i^F_2})^2 = -\mathbf{1^F_0}$; two female elements $\mathbf{e^F_4}$ and $\mathbf{e^F_6}$ with the properties $(\mathbf{e^F_4})^2 = +\mathbf{1^F_0}$ and $(\mathbf{e^F_6})^2 = +\mathbf{1^F_0}$. Elements $\mathbf{e^F_4}$ and $\mathbf{e^F_6}$ and other elements with similar properties are named "semi-imaginary units" by us conditionally because they take a middle place between the real unit and imaginary units by their properties. The set of basic elements of the male part of the bisex BB_8 has also one male quasi-real unit $\mathbf{1^M_1}$; one male imaginary unit $\mathbf{i^M_3}$ with the property $(\mathbf{i^M_3})^2 = -\mathbf{1^M_1}$; two male semi-imaginary $\mathbf{e^M_5}$ and $\mathbf{e^M_7}$ with the properties $(\mathbf{e^M_5})^2 = \mathbf{1^M_1}$, $(\mathbf{e^M_7})^2 = \mathbf{1^M_1}$. The set of basic elements of the bisex forms a semigroup. Two squares are marked out by bold lines in the left top corner of the multiplication table on the Fig. 14. The first two basic elements $\mathbf{1^F_0}$ and $\mathbf{1^M_1}$ of the bisex BB_8 are disposed in the smaller (2x2)-square only. The greater (4x4)-square collects the four first basic elements $\mathbf{1^F_0}$, $\mathbf{1^M_1}$, $\mathbf{i^F_2}$, $\mathbf{i^M_3}$, which do not meet outside this square in the table also. These aspects say that sub-algebras BB_2 and BB_4 exist inside the algebra BB_8. We shall return to these sub-algebras later.

8. BISEXES AND EVOLUTION OF THE GENETIC CODE

Modern science knows 17 variants (or dialects) of the genetic code. All of them are presented on the web-site http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi. In a course of biological evolution, some triplets, which make a smaller part of the set of 64 triplets, can change their code meaning.

Why the nature has chosen these triplets for evolution? What differences exist between these variable triplets and other invariable triplets? How these variable triplets are disposed in the genomatrix $P^{(3)}$ on Fig.11? Whether has a genomatrix disposition of these variable triplets any connection with coordinates x_0, x_1, …, x_7 of the bisex BB_8 and with their disposition in its matrix on Fig. 11? Or these bisex coordinates have no relation to the evolution of genetic code and to a system disposition of the variable triplets in the genomatrix $P^{(3)}$?

If such connection exists, bisexes can be considered as an algebraic basis of the genetic code or as a candidate for the role of the mathematical system of genetic preceding code (or “pre-code”, that is the more fundamental code) relative to the genetic code. Really, from a traditional viewpoint, a code is an aggregate of symbols which corresponds to elements of information. In our bisex case, the speech is about the matrix system, symbols of which can be compared to triplets and to other elements of the genetic code. In other words, the genetic code can be encoded itself by bisex coordinates symbols. A revealing such bisex pre-code can help with sorting, ordering and deeper understanding of the genetic information. It can help also to develop new effective methods of processing and transfer of the information in many applied problems. Mathematical properties of such pre-code can explain evolutionary features of the genetic code due to features of this more fundamental mathematical system.

So, we put forward questions about existence of pre-code of the genetic triplet code and about the bisex BB_8 as a candidate on the role of a model of such pre-code system. The comparative analysis has revealed the expressed connection between a disposition of variable triplets in the genomatrix $P^{(3)}$ and the disposition of coordinates in the bisex matrix BB_8. Results of this analysis have permitted to formulate three phenomenological rules of the bisex pre-code and to show a validity of the bisex approach in bioinformatics.

The table 8/1 presents materials for such comparative analysis. Initial data about 17 variants of the genetic code were taken from the web-site of the National Center for

Biotechnology Information, USA (http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi). The second column of this table shows those triplets, which changed their code meaning in the code, indicated in the first column, in a comparison with the most ancient vertebrate mitochondria code (the code № 1). This code № 1 is utilized in this table as the standard of comparison of code meanings of triplets. Each row of the second column indicates that amino acid (or stop-signal Stop) after a triplet also, which is coded by this triplet in this code variant. In brackets one can see an amino acid (or stop-signal), which was encoded by this triplet in the vertebrate mitochondria code № 1. Each row of the second column is finished by that coordinate of the bisex BB_8, which corresponds to this triplet in the bisex matrix on Fig. 11. At last, the third column shows data about start-codons, which determine the beginning of protein synthesis in different variants of the genetic code. An appropriate coordinate of the bisex matrix BB_8 from Fig. 11 is indicated for each start-codon.

Table 8/1. Coordinates of the bisex BB_8 for variable triplets and for start-codons in 17 variants of the genetic code.

A NAME OF THE CODE	**VARIABLE TRIPLETS**	**START-CODONS**
1) THE VERTEBRATE MITOCHONDRIAL CODE		AUU, $-x_6$ AUC, $-x_6$ AUA, $-x_7$ AUG, $-x_7$ GUG, x_3
2) THE STANDART CODE	UGA, STOP (TRP), $-x_5$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	UUG, $-x_7$ CUG, x_3 AUG, $-x_7$
3) THE MOLD, PROTOZOAN, AND COELENTERATE MITOCHONDRIAL CODE AND THE MYCOPLASMA/ SPIROPLASMA CODE	AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	UUG, $-x_7$ UUA, $-x_7$ CUG, x_3 AUC, $-x_6$ AUU, $-x_6$ AUG, $-x_7$ AUA, $-x_7$ GUG, x_3
4) THE INVERTEBRATE MITOCHONDRIAL CODE	AGG, SER (STOP), $-x_5$ AGA, SER (STOP), $-x_5$	UUG, $-x_7$ AUU, $-x_6$ AUC, $-x_6$ AUA, $-x_7$ AUG, $-x_7$ GUG, x_3
5) THE ECHINODERM AND FLATWORM	AGG, SER (STOP), $-x_5$ AGA, SER (STOP), $-x_5$	AUG, $-x_7$ GUG, x_3

MITOCHONDRIAL CODE	AUA, ILE (MET), $-x_7$ AAA, ASN (LYS), $-x_7$	
6) THE EUPLOTID NUCLEAR CODE	UGA, CYS (TRP), $-x_5$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	AUG, $-x_7$
7) THE BACTERIAL AND PLANT PLASTID CODE	UGA, STOP (TRP), $-x_5$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	UUG, $-x_7$ CUG, x_3 AUC, $-x_6$ AUU, $-x_6$ AUA, $-x_7$ AUG, $-x_7$
8) THE ASCIDIAN MITOCHONDRIAL CODE	AGG, GLY (STOP), $-x_5$ AGA, GLY (STOP), $-x_5$	UUG, $-x_7$ AUA, $-x_7$ AUG, $-x_7$ GUG, x_3
9) THE ALTERNATIVE FLATWORM MITOCHONDRIAL CODE	UAA, TYR (STOP), $-x_7$ AGG, SER (STOP), $-x_5$ AGA, SER (STOP), $-x_5$ AUA, ILE (MET), $-x_7$ AAA, ASN (LYS), $-x_7$	AUG, $-x_7$
10) BLEPHARISMA NUCLEAR CODE	UGA, STOP (TRP), $-x_5$ UAG, GLN (STOP), $-x_7$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	AUG, $-x_7$
11) CHLOROPHYCEAN MITOCHONDRIAL CODE	UGA, STOP (TRP), $-x_5$ UAG, LEU (STOP), $-x_7$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	AUG, $-x_7$
12) TREMATODE MITOCHONDRIAL CODE	AGG, SER (STOP), $-x_5$ AGA, SER (STOP), $-x_5$ AAA, ASN (LYS), $-x_7$	AUG, $-x_7$ GUG, x_3
13) SCENEDESMUS OBLIQUUS MITOCHONDRIAL CODE	UGA, STOP (TRP), $-x_5$ UAG, LEU (STOP), $-x_7$ UCA, STOP (SER), x_5 AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	AUG, $-x_7$
14) THRAUSTOCHYTRIUM MITOCHONDRIAL CODE	UGA, STOP (TRP), $-x_5$ UUA, STOP (LEU), $-x_7$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	AUU, $-x_6$ AUG, $-x_7$ GUG, x_3

15) THE ALTERNATIVE YEAST NUCLEAR CODE	UGA, STOP (TRP), $-x_5$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$ CUG, SER (LEU), x_3	CUG, x_3 AUG, $-x_7$
16) THE YEAST MITOCHONDRIAL CODE	AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ CUG, THR (LEU), x_3 CUU, THR (LEU), x_2 CUA, THR (LEU), x_3 CUC, THR (LEU), x_2	AUA, $-x_7$ AUG, $-x_7$
17) THE CILIATE, DASYCLADACEAN AND HEXAMITA NUCLEAR CODE	UGA, STOP (TRP), $-x_5$ UAG, GLN (STOP), $-x_7$ UAA, GLN (STOP), $-x_7$ AGG, ARG (STOP), $-x_5$ AGA, ARG (STOP), $-x_5$ AUA, ILE (MET), $-x_7$	AUG, $-x_7$

8.1. About variable triplets.

Let us analyze data from the second column of the Table 8/1. There are 15 kinds of triplets, which have different code meanings in different genetic codes (or in different variants of the genetic code): AAA, AGA, AGA, AGG, AUA, CUA, CUC, CUG, CUG, CUU, UAA, UAG, UCA, UGA, UUA. Some of these triplets have a few meanings in different codes. For example, the triplet AGA encodes: Stop in the code №1; the amino acid Arg in the code №2; the amino acid Ser in the code №4; the amino acid Gly in the code №8. The triplet UAA encodes Stop in the code №1; Tyr - in the code №9; Gln – in the code №17, etc. Throughout the second column variable triplets happen 69 times.

One can see that two kinds of coordinates fit practically to all these cases of variable triplets only. These coordinates are two male coordinates with the minus: "$-x_5$" and "$–x_7$". More precisely from named 69 times, the coordinate "$-x_5$" meets 41 times (it is equal to 59,4%) and the coordinate "$–x_7$" meets 22 times (31,9 %). Both of them meet in more than 90% of cases. Besides the male coordinate "$+x_5$" is presented one time in the code №13. The male coordinates "$–x_7$", "$-x_5$" and "$+x_5$" are named "canonical bisex coordinates" conditionally to mark variable triplets in their disposition in the genomatrix $P^{(3)}$. Described statistics permits to formulate the following phenomenological rule.

The rule №1 of the bisex pre-code: in a course of evolution of genetic codes, those triplets change their code meanings, which correspond to canonical male coordinates "$–x_7$", "$-x_5$" and "$+x_5$" of the bisex matrix BB_8.

This rule holds true absolutely for all genetic codes, except for a case of yeast with its two yeast codes: the code №15, where the non-canonical male coordinate "$+x_3$" is appeared for the triplet CUG, and for the code №16, which has the following unique feature. Code meanings of those four triplets CUA, CUG, CUC, CUU, which begin from the same pair of letters CU, are changed simultaneously (no one of other codes has no such four triplets, which begin with an identical pair of letters and which change their code meanings simultaneously). These four triplets fit to non-canonical coordinates "x_2" and "x_3" of the matrix BB_8. The yeast is unicellular chemoorganotrophic fungi with asexual vegetative reproduction. Perhaps, these features of the yeast provide its deviation from the rule №1. An additional evidence of molecular-genetic originality of the yeast is that yeast has no histones H1 (http://drosophila.narod.ru/Review/histone.html).

The bisex matrix BB_8 has 4 cells with the canonical coordinate "$-x_5$" and 8 cells with the canonical coordinate "$–x_7$" only. All triplets, which are disposed in these 12 cells, change their code meanings with the exception of four triplets UGG, AAG, AUG и UUG. It is probably, that, if new variants of genetic codes are revealed in future, one or more from these four triplets will have changed code meanings there likewise to other triplets with the bisex coordinates "$–x_7$" and "$-x_5$".

8.2. About stop-codons.

Encoding of stop-signals of protein synthesis in the living nature is interesting specially. Stop-signals are coded by different stop-codons in different genetic codes. One can see from the third column of the Table 8/1, that 7 kinds of triplets play the role of stop-codons in 17 variants of genetic codes. Three of them UAA, UAG, UUA fit to the coordinate "$-x_7$" of the bisex matrix BB_8. Other three triplets AGA, AGG, UGA fit to the coordinate "$-x_5$". And the triplet UCA fits to the coordinate "$+x_5$". So, we have the following rule, which holds true for all 17 genetic codes without exceptions.

The rule №2 of the bisex pre-code: stop-codons fit always to canonical male coordinates "$–x_7$", "$-x_5$" and "$+x_5$" of the bisex matrix BB_8.

According to this rule, a function of stop-signal is the function of male coordinates always. A few triplets (for example, UUA and UGG) exist, which have the same coordinates "$–x_7$", "$-x_5$" and "$+x_5$" but which are not stop-codons in these codes. Whether will science reveal such genetic codes in future, where these triplets serve as stop-codons? The time will show.

8.3. About start-codons.

The third column of the Table 8/1 shows triplets, which play a role of start-signals of protein synthesis and which can differ in different variants of the genetic code. These start-codons were taken from the main sets of code meanings of 64 triplets of the 17 codes on the same web-site http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi.

8 kinds of triplets exist as start-codons there. Four of them (AUA, AUG, UUA, UUG) fit to the bisex coordinate "$-x_7$"; two triplets (AUC, AUU) fit to the bisex coordinate "$-x_6$"; two triplets (CUG, GUG) fit to the bisex coordinate "x_3". The most ancient code №1 has start-codons, which fit to all these three coordinates. These

materials demonstrate the existence of the following rule, which holds true absolutely for all 17 variants of the genetic code without exceptions.

The rule №3 of the bisex pre-code: start-codons fit to the coordinates "-x_7", "-x_6" and "x_3" of the bisex matrix BB_8.

8.4. About the bisex theory in molecular genetics.

From the viewpoint of the bisex matrix BB_8, each triplet, each amino acid and each stop-codon is "male" or "female" one depending on its belonging to a column with an odd or even number correspondingly. Due to this circumstance, molecular elements of the genetic code assume "sexual" character, and the bisex model plays a role of the molecular-sexual model.

According to this model for the case of the ancient code №1, the female amino acids are the low-degenerated acids Cys, Asp, Phe, His, Ile, Asn, Tyr, and the male amino-acids are the low-degenerated acids Glu, Lys, Met, Gln, Trp. The question about a sexual character of high-degenerated amino acids (which are encoded by 4 triplets or more) is more difficult because each such acid belongs to columns with even and odd numbers simultaneously (Fig.11). For example, the acid Arg belongs to the second and the third columns and it is female and male acid equally. Such amino acids are named androgynous acids. Pure androgynous acids are Ala, Arg, Gly, Pro, Thr, Val. The acid Ser is disposed in 4 cells of female columns and in 2 cells of male columns. In this reason, Ser is not the pure androgynous acid, but the androgynous-female acid with a prevalence of a female character. On the contrary, the acid Leu in the code №1 is the androgynous-male acid with a prevalence of a male character because it is disposed in 4 cells of the column №1 and in 2 cells of the column № 0 (Fig.11).

What occurs from the viewpoint of this bisex theory in a course of evolution of the genetic code, when dispositions of separate amino acids and stop-codons are changed? One can see from the Table 8/1 that the evolution of the genetic code appears as struggle of male and female substances (principles) at a molecular-genetic levels. It reminds a struggle between matriarchy and patriarchy in human history of change of social structures, and it reminds many other cases of a confrontation between male and female essences. More precisely, female substances force out male substances in the set of amino acids. But at the same time male substances increase their positions in a management of the beginning and the end of the protein synthesis.

Really, according to the rule №1, the evolution changes code meanings of male triplets of the code №1 only. An additional regularity is that, if such variable male triplet encodes a new amino acid in another code, this new amino acid is one of the female acids necessarily. In other words, an expansion of female amino acids (Asn, Cys, Ile, Tyr) into male columns exists, but never male amino acids come into female columns. In the result, the genomatrix $P^{(3)}$, which has equal quantities of male and female amino acids in the code №1, becomes more female in a relation to amino acids filling it in other codes. One can add that the androgynous acids Arg and Gly and the androgynous-male acid Leu force out male stop-signals in some codes also (they take their places in male columns of the initial genomatrix $P^{(3)}$). On the contrary, male triplets encode not only all stop-codons in all codes but the encoding of start-codons become the more male deal during the evolution: the single female coordinate "$-x_6$", which exists in the code №1, is removed in the most of other codes: the codes №№ 2, 5, 6, 8-13, 15-17 have no female bisex coordinates.

The molecular-bisex theory permits to classify many genetic elements (including proteins) according to their sexual characters. It gives new interesting opportunities to explain and predict many peculiarities of molecular-genetic systems. For example, this theory has permitted to put forward the hypothesis about a bisex attraction or a bisex interaction (as a new biophysical factor) between biomolecules with different sexual characters. The results of this theory will be published by the author separately.

9. ABOUT BISEX MATHEMATICS AND ITS IMPORTANCE.

Fig. 14 has demonstrated an existence of bisex sub-algebras BB_2 and BB_4 already. Fig. 15 shows the multiplication table of the bisex BB_2 with basic elements $\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$ and $\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$ and with two matrix forms of a presentation of BB_2. The multiplication table of the bisex BB_4 contains the basic elements $\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$ and $\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$ only**.** This bisex BB_4 coincides with the bisex-complex number $z_0*\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}+z_1*\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}+z_2*\mathbf{i}^{\mathbf{F}}_{\mathbf{2}}+z_3*\mathbf{i}^{\mathbf{M}}_{\mathbf{3}}$, which is a bisex generalization of a complex number (see below).

$$\begin{vmatrix} Z_0 & Z_1 \\ Z_0 & Z_1 \end{vmatrix}; \quad \begin{vmatrix} Z_0 & -Z_1 \\ -Z_0 & Z_1 \end{vmatrix};$$

	$\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$	$\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$
$\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$	$\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$	$\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$
$\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$	$\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$	$\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$

Fig. 15. Left: Two matrix forms of a presentation of the bisex BB_2. Right: the multiplication table of the basic elements of BB_2.

9.1. About the geometry of 2-dimensional bisexes.

It is known that complex numbers have been widely recognized only after finding of their geometrical interpretation on the plane of complex variables. This plane was named Gauss-Argan plane according to names of the mathematicians who introduced such plane. Whether it is possible to offer a substantial geometrical interpretation of the 2-dimensional bisex BB_2? Yes, it is possible. For this purpose we introduced the plane of bisex variables. It is an ordinary plane with a bisex system of Cartesian coordinates. This bisex system has the coordinate axises ***f*** and ***m***, which play a role of female and male axises. By analogy with the case of complex numbers, each 2-dimensional bisex is denoted on this bisex plane by a point or by a vector. A product of two bisex vectors (**XX**= x_0***1**$^{\mathbf{F}}_{\mathbf{0}}$ + x_1***1**$^{\mathbf{M}}_{\mathbf{1}}$ and **YY**= y_0***1**$^{\mathbf{F}}_{\mathbf{0}}$ + y_1***1**$^{\mathbf{M}}_{\mathbf{1}}$) has a geometric sense on such plane. Really, the result of non-commutative multiplication of such two bisex vectors is equal to the second vector with the scale coefficient, which is equal to the sum of coordinates of the first vector (Fig. 16, left). The same first vector-factor at multiplication with all other vectors of the plane or of a geometric figure leads to their identical scaling (Fig. 16, right).

XX*YY=(X_0***1**$^{\mathbf{F}}_{\mathbf{0}}$+$X_1$***1**$^{\mathbf{M}}_{\mathbf{1}}$)*($Y_0$***1**$^{\mathbf{F}}_{\mathbf{0}}$+$Y_1$***1**$^{\mathbf{M}}_{\mathbf{1}}$)=($X_O$+$X_1$)*($Y_0$***1**$^{\mathbf{F}}_{\mathbf{0}}$+$Y_1$***1**$^{\mathbf{M}}_{\mathbf{1}}$)
YY*XX=(Y_0***1**$^{\mathbf{F}}_{\mathbf{0}}$+$Y_1$***1**$^{\mathbf{M}}_{\mathbf{1}}$)*($X_0$***1**$^{\mathbf{F}}_{\mathbf{0}}$+ $_1$***1**$^{\mathbf{M}}_{\mathbf{1}}$)= ($Y_0$+$Y_1$)*($X_0$***1**$^{\mathbf{F}}_{\mathbf{0}}$+$X_1$***1**$^{\mathbf{M}}_{\mathbf{1}}$)

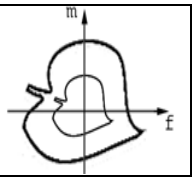

Fig. 16. Left: a multiplication of two bisex vectors. Right: a scaling of a geometric figure on the bisex plane.

It associates with the known biological phenomenon of volumetric growth of the living bodies, observed on the most different lines and branches of biological evolution. Biological bodies are capable to the mysterious volumetric growth, occuring in the cooperative way on all volume of the body or its growing part. It is one of sharp differences of living bodies from crystals with their surface growth occuring due to a local addition of new portions of substance on the surface of the crystal. In this connection, the bisex geometry is one of candidates on a role of the geometry of biological volumetric growth. Other details of the bisex geometry will be published later. It can be noted that an algorithm exists for a construction of matrix forms of presentations of 2^n-dimensional bisexes from a known matrix form of presentation of 2^{n-1}-dimensional bisexes.

9.2. Hypercomplex numbers and 2^n-dimensional bisexes.

Let us consider differences and algorithmic interconnections between bisexes and hypercomplex numbers. By definition, any hypercomplex number has the real unit in a set of its basic elements. On the contrary, bisexes are defined as generalized numbers (elements of special - bisex - algebras), which have not the real unit in their sets of basic elements at all but which have two quasi-real units $\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$ and $\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$ instead it with the properties $(\mathbf{1}^{\mathbf{F}}_{\mathbf{0}})^2 = \mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$, $(\mathbf{1}^{\mathbf{M}}_{\mathbf{1}})^2 = \mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$, $\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}*\mathbf{1}^{\mathbf{M}}_{\mathbf{1}} = \mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$, $\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}*\mathbf{1}^{\mathbf{F}}_{\mathbf{0}} = \mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$ (see Fig.14). So, bisexes are not hypercomplex numbers but they form a new category of generalized numbers. Bisexes can be considered as the generalization of hypercomplex numbers. Each 2^{n-1}-dimensional hypercomplex number can be transformed into a 2^n-dimensional bisex by a special algorithm. An inverse application of this algorithm to a 2^n-dimensional bisex permits to confront the bisex with an appropriate 2^{n-1}-dimensional hypercomplex number. According to this algorithm, if we have a $(2^n x 2^n)$-matrix, which represents a 2^n-dimensional hypercomplex number, we should replace each component of this matrix by a block (2x2)-matrix $[x_\kappa \quad x_{\kappa+1}; \quad x_\kappa \quad x_{\kappa+1}]$, which represents the bisex $\mathbf{XX}_2 = x_\kappa*\mathbf{1}^{\mathbf{F}}_{\mathbf{0}} + x_{\kappa+1}*\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$.

For example, if we have the (2x2)-matrix of the presentation of complex numbers, this algorithm transforms it into (4x4)-matrix of the presentation of 4-dimensional "bisex-complex" numbers KK_4 with a special multiplication table (Fig.17). Really, according to this algorithm, each component x_0 and x_1 of the initial matrix is replaced by a bisex matrix of the mentioned type: $x_0=[y_0 \ y_1; \ y_0 \ y_1]$, $x_1=[y_2 \ y_3; \ y_2 \ y_3]$. In the result we have bisex-complex numbers $\mathbf{KK}_4 = z_0*\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}+z_1*\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}+z_2*\mathbf{i}^{\mathbf{F}}_{\mathbf{2}}+z_3*\mathbf{i}^{\mathbf{M}}_{\mathbf{3}}$, where $\mathbf{1}^{\mathbf{F}}_{\mathbf{0}}$ and $\mathbf{1}^{\mathbf{M}}_{\mathbf{1}}$ are the

female and male quasi-real units; $\mathbf{i^F_2}$ и $\mathbf{i^M_3}$ are the female and male imaginary units with the properties $(\mathbf{i^F_2})^2 = -\mathbf{i^F_0}$, $(\mathbf{i^M_3})^2 = -\mathbf{i^M_1}$.

X_0	$-X_1$
X_1	X_0

;

Y_0	Y_1	$-Y_2$	$-Y_3$
Y_0	Y_1	$-Y_2$	$-Y_3$
Y_2	Y_3	Y_0	Y_1
Y_2	Y_3	Y_0	Y_1

;

	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$
$\mathbf{1^F_0}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$
$\mathbf{1^M_1}$	$\mathbf{1^F_0}$	$\mathbf{1^M_1}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$
$\mathbf{I^F_2}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$	$\mathbf{-1^F_0}$	$\mathbf{-1^M_1}$
$\mathbf{I^M_3}$	$\mathbf{I^F_2}$	$\mathbf{I^M_3}$	$\mathbf{-1^F_0}$	$\mathbf{-1^M_1}$

Fig. 17. The matrix forms of presentation of complex numbers (left) and bisex-complex numbers (in the middle). Right: the multiplication table for basic elements of the bisex-complex numbers.

By inverse application of this algorithm, one can receive a 4-dimensional hypercomplex number, which is correspondent to the 8-dimensional bisex BB_8. The bisex matrix BB_8 (Fig.11) contains 4 kinds of (2x2)-sub-quadrants, each of which has one of pairs of coordinates: x_0 and x_1; x_2 and x_3; x_4 and x_5; x_6 and x_7. One can replace each such subquadrant by a separate coordinate: $[x_0\ \ x_1;\ \ x_0\ \ x_1] = y_0$; $[x_2\ \ x_3;\ \ x_2\ \ x_3] = y_1$; $[x_4\ \ x_5;\ x_4\ \ x_5] = y_2$; $[x_6\ \ x_7;\ x_6\ \ x_7] = y_3$. In the result the (4x4)-matrix Q is appeared, which represents the 4-dimensional number $\mathbf{Q} = y_0\mathbf{*1} + y_1\mathbf{*i_1} + y_2\mathbf{*e_2} + y_3\mathbf{*e_3}$, where $i_1^2 = -1$, $e_2^2 = e_3^2 = +1$. Fig. 18 shows the matrix Q and the multiplication table for this hypercomplex number. The hypercomplex number Q reminds coquaternions (or split-quaternions, or para-quaternions, or hyperbolic quaternions), introduced by J.Cockle in 1849 year (http://en.Qikipedia.org/Qiki/Coquaternion), but their multiplication tables have differences. We name the number Q "genoquaternion of the first type". (A genoquaternion of the second type is produced by a special permutation of columns of the matrix Q, which is connected with a permutation of positions in genetic duplets).

$\mathbf{Q} =$

Y0	-Y1	Y2	-Y3
Y1	Y0	-Y3	-Y2
Y2	-Y3	Y0	-Y1
-Y3	-Y2	Y1	Y0

	1	$\mathbf{I_1}$	$\mathbf{E_2}$	$\mathbf{E_3}$
1	**1**	$\mathbf{I_1}$	$\mathbf{E_2}$	$\mathbf{E_3}$
$\mathbf{I_1}$	$\mathbf{I_1}$	**-1**	$\mathbf{-E_3}$	$\mathbf{E_2}$
$\mathbf{E_2}$	$\mathbf{E_2}$	$\mathbf{E_3}$	**1**	$\mathbf{I_1}$
$\mathbf{E_3}$	$\mathbf{E_3}$	$\mathbf{-E_2}$	$\mathbf{-I_1}$	**1**

Fig.18. The matrix form of presentation of the hypercomplex number Q (left) and its multiplication table (right).

The limited volume of the article does not permit to describe many other interesting results of the bisex mathematics and its correlation with genetic systems. We can

mention them briefly only. The section 3 has demonstrated (Fig. 3) that the 5 triplets-permutation genomatrices $P^{(3)}{}_{231}$, $P^{(3)}{}_{213}$, $P^{(3)}{}_{321}$, $P^{(3)}{}_{312}$, $P^{(3)}{}_{132}$ existed in addition to the genomatrix $P^{(3)}$. Each of these (8x8)-genomatrices is connected with its own bisex from the set of 8-dimensional bisexes $\mathbf{BB_{231}}$, $\mathbf{BB_{312}}$, $\mathbf{BB_{132}}$, $\mathbf{BB_{213}}$, $\mathbf{BB_{321}}$, which have their individual multiplication tables and their own vector notations:

$\mathbf{BB_{231}}= X_0*\mathbf{1}^{F}_{0}+X_1*\mathbf{I}^{F}_{1}+X_2*\mathbf{E}^{F}_{2}+X_3*\mathbf{E}^{F}_{2}+X_4*\mathbf{1}^{M}_{4}+X_5*\mathbf{I}^{M}_{5}+X_6*\mathbf{E}^{M}_{6}+X_7*\mathbf{E}^{M}_{7}$

$\mathbf{BB_{312}}= X_0*\mathbf{1}^{F}_{0}+X_1*\mathbf{E}^{F}_{1}+X_2*\mathbf{1}^{M}_{2}+X_3*\mathbf{E}^{M}_{3}+X_4*\mathbf{I}^{F}_{4}+X_5*\mathbf{E}^{F}_{5}+X_6*\mathbf{I}^{M}_{6}+X_7*\mathbf{E}^{M}_{7}$

$\mathbf{BB_{132}}= X_0*\mathbf{1}^{F}_{0}+X_1*\mathbf{I}^{F}_{1}+X_2*\mathbf{1}^{M}_{2}+X_3*\mathbf{I}^{M}_{3}+X_4*\mathbf{E}^{F}_{4}+X_5*\mathbf{E}^{F}_{5}+X_6*\mathbf{E}^{M}_{6}+X_7*\mathbf{E}^{M}_{7}$

$\mathbf{BB_{213}}= X_0*\mathbf{1}^{F}_{0}+X_1*\mathbf{1}^{M}_{1}+X_2*\mathbf{E}^{F}_{2}+X_3*\mathbf{E}^{M}_{3}+X_4*\mathbf{I}^{F}_{4}+X_5*\mathbf{I}^{M}_{5}+X_6*\mathbf{E}^{F}_{6}+X_7*\mathbf{E}^{M}_{7}$

$\mathbf{BB_{321}}= X_0*\mathbf{1}^{F}_{0}+X_1*\mathbf{E}^{F}_{1}+X_2*\mathbf{I}^{F}_{2}+X_3*\mathbf{E}^{F}_{3}+X_4*\mathbf{1}^{M}_{4}+X_5*\mathbf{E}^{M}_{5}+X_6*\mathbf{I}^{M}_{6}+X_7*\mathbf{E}^{M}_{7}$

A multiplication of bisex matrices with arbitrary vectors of appropriate dimensions has essential features. For example, an action of the bisex binary (8x8)-genomatrix B_{123} (Fig. 5) on an arbitrary 8-dimensional vector transforms it into the vector with interdependent values of coordinates: three different values exist for all 8 coordinates only. It means that, after such transformation, all arbitrary vectors belong to a 3-parametrical subspace of the initial 8-dimensional space. This subspace has the peculiarity that any ensemble of its vectors is transformed into itself with the increasing these vectors in 4 times in the result of each repeated action of the same bisex matrix B_{123}. It reminds the tetra-reproduction of gametal cells in a course of meiosis when the initial gamete reproducts four gametal cells, and all this occurs in the 3-dimensional space.

Bisexes permit to develop new class of mathematical models of self-reproduction systems. Interesting results are received from an analysis of algebraic bisex-equations, where variables and coefficients are bisexes. The author investigates bisex generalizations of known physical equations to find new results with a physical sense from there (it is the mathematical fact that known physical equations can be received from appropriate bisex equations by passage to the limit in values of appropriate bisex coordinates). One should note that algebras of polysexes (or n-sexes, where n = 3, 4, …) exist besides bisex algebras. Each n-sex algebra has not the real unit but has n quasi-real units and a corresponding matrix form of presentation. The algebraic theory of the genetic code can say many useful and unexpected things about an origin of the genetic code and about laws of living substances.

9.3. BISEXES AND MATHEMATICAL NATURAL SCIENCES.

It happens frequently, that a mathematician constructs a new beautiful abstract mathematics and then he searches for opportunities of its application in different areas of natural sciences. On the contrary, in our case the phenomenology of the genetic code has led the author unexpectedly to the new mathematics of bisex algebras. And we should investigate features of this mathematics on the second stage only.

The genetic code is the result of a gigantic experiment by the nature. This molecular code bears on itself the imprint of a great set of known and unknown laws of the nature. In this connection, algebraic features of genetic structures are very essential in a scientific choice of a perspective direction to develop algebraic bases of mathematical natural sciences in future. In our opinion, the bisex mathematics is the perspective one

not only for biology, but also for many other fields of mathematical natural sciences and for applied sciences like signals processing, mathematical economy, etc.

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