Proceedings of the 2011 International Conference of Bioinformatics & Computational Biology (BIOCOMP 2011), (Ed. H.Arabnia, Quoc-Nam Tram), July 18-21, 2011, Las Vegas Nevada, USA, v. 2, CSREA Press, p. 589-595.

The Genetic Code, 8-Dimensional Hypercomplex Numbers and Dyadic Shifts

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Abstract - *The article is devoted to algebraic features of structural phenomena of molecular ensembles of the genetic code. Matrix forms of presentations of the genetic code allow showing deep relations of the genetic code with dyadic shifts and algebras of 8-dimensional hypercomplex numbers. Hadamard matrices and orthogonal systems of Rademacher and Walsh functions, which are well-known formalisms from discrete signal processing, participate in this discovery of hidden structural features of the genetic code. The described results are useful to understand a non-casual character of the genetic code systems, which has a deep algebraic nature. The results lead to new theoretical approaches in the field of algebraic biology.*

Keywords: Code, Hypercomplex Numbers, Dyadic Shifts

1 Introduction

A biological meaning of genetic informatics is reflected in the brief statement: "*life is a partnership between genes and mathematics*" [22]. We are trying to find math which is a partner of the genetic code. One of the possible directions of search is to use matrix forms of presentation and analysis of ensembles of molecular elements of the genetic code. Matrix representations and methods are widely and successfully used in the theory of error-correcting coding and processing of information, theoretical physics, computer science, the theory of hypercomplex numbers, etc. In this regard, a scientific field called "Matrix genetics" exists, which studies the matrix presentation of the genetic code, including through borrowing matrix methods from the field of digital signal processing [10, 11, 14, 15, 17]. Our results are a part of "algebraic biology", which gave rise to thematic conferences and international societies; the journal "Bulletin of Mathematical Biology" identifies this area as a separate category.

This article is devoted to author's results on algebraic features of structural phenomena of molecular ensembles of the genetic code. More precisely it shows relations of the genetic code with dyadic shifts, algebras of 8-dimensional hypercomplex numbers, Hadamard matrices, orthogonal systems of Rademacher and Walsh functions and the sequency theory by Harmuth [6-9].

BIOCOMP. Manuscript received March 9, 2011. This work was supported in part by the Russian Federal Agency of Science and Innovations (the contract № 02.740.11.0100) and by the Russian Federal Agency on Education (the contract № P377).

2 Genetic matrices, dyadic shifts, Rademacher functions and 8-dimensional hypercomplex numbers

The four letters of the genetic alphabet A (adenine), C (cytosine), G (guanine), U/T (uracil in RNA or thymine in DNA) represent specific poly-atomic constructions. The set of these four constructions bears the substantial symmetric system of distinctive-uniting attributes (or, more precisely, pairs of "attribute-antiattribute"). The system of such attributes divides the genetic four-letter alphabet into the following three pairs of letters, which are equivalent from a viewpoint of one of these attributes or its absence: 1) C = U & A = G (according to the binary-opposite attributes: "pyrimidine" or "non-pyrimidine", that is purine); 2) A = C & G = U (according to the attributes "keto" or "amino"); 3) C = G & A = U (according to the attributes: three or two hydrogen bonds are materialized in these complementary pairs). The possibility of such division of the genetic alphabet into three binary sub-alphabets is known from the work [12]. We utilize these known sub-alphabets in the field of matrix genetics which studies matrix forms of presentation of the genetic code. Let us mark these three kinds of binary-opposite attributes by numbers N = 1, 2, 3 and ascribe to each of the four genetic letters the symbol "0_N" (the symbol "1_N") in a case of presence (of absence correspondingly) of the attribute under number "N" in this letter. As a result we obtain the representation of the genetic four-letter alphabet in the system of its three "binary sub-alphabets corresponding to attributes" (Fig. 1).

	Symbols of a genetic letter from a viewpoint of binary-opposite attributes	**C**	**A**	**G**	**U/T**
№1	$\mathbf{0_1}$ – pyrimidines (one ring in a molecule); $\mathbf{1_1}$ – purines (two rings in a molecule)	$\mathbf{0_1}$	$\mathbf{1_1}$	$\mathbf{1_1}$	$\mathbf{0_1}$
№2	$\mathbf{0_2}$ – amino; $\mathbf{1_2}$ – keto	$\mathbf{0_2}$	$\mathbf{0_2}$	$\mathbf{1_2}$	$\mathbf{1_2}$
№3	$\mathbf{0_3}$ – a letter with three hydrogen bonds; $\mathbf{1_3}$ – a letter with two hydrogen bonds	$\mathbf{0_3}$	$\mathbf{1_3}$	$\mathbf{0_3}$	$\mathbf{1_3}$

Fig. 1. Three binary sub-alphabets according to three kinds of binary-opposite attributes in a set of nitrogenous bases C, A, G, U.

On the basis of the idea about a possible analogy between discrete signals processing in computers and in a genetic code system, one can present the genetic 4-letter alphabet in the following matrix form [C A; U G] (Fig. 2). Then the Kronecker family of matrices with such alphabetical kernel can be considered: $[C\ A;\ U\ G]^{(n)}$, where (n) means the integer Kronecker (or tensor) power [11, 14, 15, 17]. The matrix $[C\ A;\ U\ G]^{(3)}$ contains 64 triplets in a strict order (Fig. 2).

[C A; U G] =

	0	1
0	C 0	A 1
1	U 1	G 0

[C A; U G]$^{(3)}$ =

	000 (0)	001 (1)	010 (2)	011 (3)	100 (4)	101 (5)	110 (6)	111 (7)
000 (0)	CCC 000 (0)	CCA 001 (1)	CAC 010 (2)	CAA 011 (3)	ACC 100 (4)	ACA 101 (5)	AAC 110 (6)	AAA 111 (7)
001 (1)	CCU 001 (1)	CCG 000 (0)	CAU 011 (3)	CAG 010 (2)	ACU 101 (5)	ACG 100 (4)	AAU 111 (7)	AAG 110 (6)
010 (2)	CUC 010 (2)	CUA 011 (3)	CGC 000 (0)	CGA 001 (1)	AUC 110 (6)	AUA 111 (7)	AGC 100 (4)	AGA 101 (5)
011 (3)	CUU 011 (3)	CUG 010 (2)	CGU 001 (1)	CGG 000 (0)	AUU 111 (7)	AUG 110 (6)	AGU 101 (5)	AGG 100 (4)
100 (4)	UCC 100 (4)	UCA 101 (5))	UAC 110 (6)	UAA 111 (7)	GCC 000 (0)	GCA 001 (1)	GAC 010 (2)	GAA 011 (3)
101 (5)	UCU 101 (5)	UCG 100 (4)	UAU 111 (7)	UAG 110 (6)	GCU 001 (1)	GCG 000 (0)	GAU 011 (3)	GAG 010 (2)
110 (6)	UUC 110 (6)	UUA 111 (7)	UGC 100 (4)	UGA 101 (5)	GUC 010 (2)	GUA 011 (3)	GGC 000 (0)	GGA 001 (1)
111 (7)	UUU 111 (7)	UUG 110 (6)	UGU 101 (5)	UGG 100 (4)	GUU 011 (3)	GUG 010 (2)	GGU 001 (1)	GGG 000 (0)

Fig. 2. Genetic matrices [C A; U G] and [C A; U G]$^{(3)}$ with binary numerations of their columns and rows on the base of the binary sub-alphabets № 1 and № 2 from Fig. 1. Matrix cells contain a symbol of a multiplet, a dyadic-shift numeration of this multiplet and its expression in decimal notation. Decimal numerations of columns, rows and multiplets are written in brackets. Black and white cells contain triplets with strong and weak roots correspondingly (see the text).

All the columns and rows of the matrices on Fig. 2 are binary numerated and disposed in a monotonic order by the following algorithm which uses biochemical features of the genetic nitrogenous bases and which can be used in bio-computers of any organism really. Numerations of columns and rows are formed automatically if one interprets multiplets of each column from the viewpoint of the first binary sub-alphabet (Fig. 1) and if one interprets multiplets of each row from the viewpoint of the second binary sub-alphabet. For example, the column 010 contains all the triplets of the form "pyrimidine-purine-pyrimidine"; the row 010 contains all the triplets of the form “amino-keto-amino”. Each of the triplets in the matrix [C A; U G]$^{(3)}$ receives its dyadic-shift numeration by means of modulo-2 addition of binary numerations of its column and row. Here one should explain that this kind of addition is one of the main operations in digital signal processing; by definition the modulo-2 addition of two numbers written in binary notation is made in a bitwise manner in accordance with the following rules:

$$0 + 0 = 0,\ 0 + 1 = 1,\ 1 + 0 = 1,\ 1 + 1 = 0 \qquad (1)$$

For example, the triplet CAG receives its dyadic-shift numeration 010 (or 2 in decimal notation) because it belongs to the column 011 and the row 001. The series of binary numbers

$$000,\ 001,\ 010,\ 011,\ 100,\ 101,\ 110,\ 111 \qquad (2)$$

forms a diadic group, in which modulo-2 addition serves as the group operation [9]. The distance in this symmetry group is known as the Hamming distance. Since the Hamming distance satisfies the conditions of a metric group, the diadic group is a metric group. The modulo-2 addition of any two binary numbers from (2) always results in a new number from the same series. The number 000 serves as the unit element of this group. The reverse element for any number in this group is the number itself. Changes in the initial binary sequence (2), produced by modulo-2 addition of its members with any binary numbers (2), are termed diadic shifts [1, 9]. If any system of elements demonstrates its connection with diadic shifts, it indicates that the structural organization of its system is related to the logic of modulo-2 addition. This article gives some evidences that the genetic code is related to the logic of modulo-2 addition.

Black and white cells in the genomatrix [C A; U G]$^{(3)}$ reflect the following peculiarities of the genetic code. A combination of letters on the two first positions of each triplet is termed a “root” of this triplet; a letter on its third position is termed a “suffix”. The set of 64 triplets contains 16 possible variants of such roots. Taking into account properties of triplets, the set of 16 possible roots is divided into two subsets with 8 roots in each. The first of such octets contains roots CC, CU, CG, AC, UC, GC, GU, GG. These roots are termed "strong roots" [13] because each of them defines four triplets with this root, coding values of which are independent on their suffix. For example, four triplets CGC, CGA, CGU, CGG, which have the strong root CG, encode the same amino acid Arg, although they have different suffixes (Fig. 3). The second octet contains roots CA, AA, AU, AG, UA, UU, UG, GA. These roots are termed “weak roots” because each of them defines four triplets with this root, coding values of which depend on their suffix. An example of such a subfamily in Fig. 3 is represented by four triplets CAC, CAA, CAU and CAC, two of which (CAC, CAU) encode the amino acid His and the other two of which (CAA, CAG) encode the amino acid Gln.

THE STANDARD CODE	
8 subfamilies of triplets with strong roots (“black triplets”) and the amino acids, which are encoded by them	8 subfamilies of triplets with weal roots (“white triplets”) and the amino acids, which are encoded by them
CCC, CCU, CCA, CCG → Pro	CAC, CAU, CAA, CAG → His, His, Gln, Gln
CUC, CUU, CUA, CUG → Leu	AAC, AAU, AAA, AAG → Asn, Asn, Lys, Lys
CGC, CGU, CGA, CGG → Arg	AUC, AUU, AUA, AUG → Ile, Ile, Ile, Met
ACC, ACU, ACA, ACG → Thr	AGC, AGU, AGA, AGG → Ser, Ser, Arg, Arg
UCC, UCU, UCA, UCG → Ser	UAC, UAU, UAA, UAG → Tyr, Tyr, Stop, Stop
GCC, GCU, GCA, GCG → Ala	UUC, UUU, UUA, UUG → Phe, Phe, Leu, Leu
GUC, GUU, GUA, GUG → Val	UGC, UGU, UGA, UGG → Cys, Cys, Stop, Trp
GGC, GGU, GGA, GGG → Gly	GAC, GAU, GAA, GAG → Asp, Asp, Glu, Glu
THE VERTEBRATE MITOCHONDRIAL CODE	
CCC, CCU, CCA, CCG → Pro	CAC, CAU, CAA, CAG → His, His, Gln, Gln
CUC, CUU, CUA, CUG → Leu	AAC, AAU, AAA, AAG → Asn, Asn, Lys, Lys
CGC, CGU, CGA, CGG → Arg	AUC, AUU, AUA, AUG → Ile, Ile, Met, Met
ACC, ACU, ACA, ACG → Thr	AGC, AGU, AGA, AGG → Ser, Ser, Stop, Stop
UCC, UCU, UCA, UCG → Ser	UAC, UAU, UAA, UAG → Tyr, Tyr, Stop, Stop
GCC, GCU, GCA, GCG → Ala	UUC, UUU, UUA, UUG → Phe, Phe, Leu, Leu
GUC, GUU, GUA, GUG → Val	UGC, UGU, UGA, UGG → Cys, Cys, Trp, Trp
GGC, GGU, GGA, GGG → Gly	GAC, GAU, GAA, GAG → Asp, Asp, Glu, Glu

Fig. 3. The Standard Code and the Vertebrate Mitochondrial Code possess the basic scheme of the genetic code degeneracy with 32 triplets of strong roots and 32 triplets of weak roots (Initial data from http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi.)

How these two subsets of triplets with strong and weak roots are disposed in the genomatrix [C A; U G]$^{(3)}$ (Fig. 2) which was constructed formally on the base of the genetic alphabet and Kronecher multiplications without any mention about the degeneracy of the genetic code and about amino acids? Can one anticipate any symmetry in their disposition? It should be noted that the huge quantity $64! \approx 10^{89}$ of variants exists for dispositions of 64 triplets in the (8x8)-matrix. One can note for comparison, that the modern

physics estimates time of existence of the Universe in 10^{17} seconds. In such a situation an accidental disposition of the 20 amino acids and the corresponding triplets in a (8x8)-matrix will give almost never any symmetry in their disposition in matrix halves, quadrants and rows.

But it is phenomenological fact that the disposition of the 32 triplets with strong roots ("black triplets" in Fig. 2) and the 32 triplets with weak roots ("white triplets") has a symmetric character unexpectedly (see Fig. 2). For example 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, possesses the opposite colors. One can say that each row of this mosaic matrix corresponds to an odd function. In addition each row of the mosaic matrix $[C\ A;\ U\ G]^{(3)}$ has a meander-line character (the term "meander-line" means here that lengths of black and white fragments are equal to each other along each row). But the theory of discrete signal processing uses such odd meander functions for a long time under the name "Rademacher functions". Rademacher functions contain elements "+1" and "-1" only. Each of the matrix rows presents one of the Rademacher functions if each black (white) cell is interpreted such that it contains the number +1 (−1). Fig. 4 shows a transformation of the mosaic matrix $[C\ A;\ U\ G]^{(3)}$ (Fig. 2) into a numeric matrix in the result of such replacements of black and white triplets by means of numbers "+1" and "-1" correspondingly.

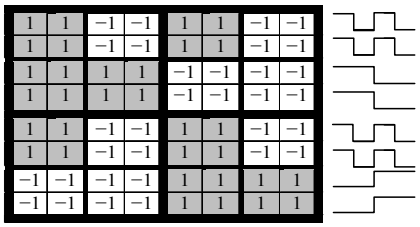

Fig. 4. Rademacher form R of presentation of the genomatrix $[C\ A;\ U\ G]^{(3)}$ from Fig. 2. A relevant system of Rademacher functions is shown at the right side.

The Rademacher form R of the genomatrix $[C\ A;\ U\ G]^{(3)}$ (Fig. 4) can be decomposed into sum of 8 sparse matrices r_0, r_1, r_2, r_3, r_4, r_5, r_6, r_7 (Fig. 5) in accordance with the principle of dyadic-shifts numerations of cells and triplets from Fig. 2. More precisely any sparse matrix r_k (k=0, 1, …, 7) contains entries "+1" or "-1" from the matrix R on Fig. 4 in those cells which correspond to cells with the same dyadic-shift numeration "k" of triplets on Fig. 2; all the other cells of the matrix r_k contain zero.

The author has revealed that this set of 8 matrices r_0, r_1,…, r_7 (where r_0 is identity matrix) is closed relative to multiplication and it satisfies the table of multiplication on Fig. 6.

The multiplication table on Fig. 6 is asymmetrical relative to the main diagonal and corresponds to the non-commutative associative algebra of 8-dimensional hypercomplex numbers. This matrix algebra is non-division algebra because it has zero divisors. It means that such non-zero hypercomplex numbers exist whose product is equal to zero. These genetic 8-dimensional hypercomplex numbers are different from Cayley's octonions (http://en.wikipedia.org/wiki/Octonion). The algebra of Cayley's octonions is non-associative algebra and correspondingly it does not possess a matrix form of its presentation (each of matrix algebras is an associative algebra). The known term "octonions" is not appropriate for the case of the multiplication table on Fig. 6 because this term is usually used for members of normed division non-associative algebra (http://en.wikipedia.org/wiki/Octonion).

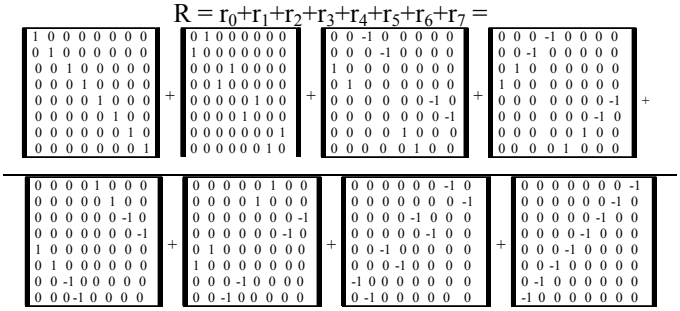

Fig. 5. The dyadic-shift decomposition of the Rademacher form R (Fig. 4) of the genomatrix $[C\ A;\ U\ G]^{(3)}$ into sum of 8 sparse matrices r_0, r_1,…, r_7.

	1	$\mathbf{r_1}$	$\mathbf{r_2}$	$\mathbf{r_3}$	$\mathbf{r_4}$	$\mathbf{r_5}$	$\mathbf{r_6}$	$\mathbf{r_7}$
1	**1**	$\mathbf{r_1}$	$\mathbf{r_2}$	$\mathbf{r_3}$	$\mathbf{r_4}$	$\mathbf{r_5}$	$\mathbf{r_6}$	$\mathbf{r_7}$
$\mathbf{r_1}$	$\mathbf{r_1}$	**1**	$\mathbf{r_3}$	$\mathbf{r_2}$	$\mathbf{r_5}$	$\mathbf{r_4}$	$\mathbf{r_7}$	$\mathbf{r_6}$
$\mathbf{r_2}$	$\mathbf{r_2}$	$\mathbf{r_3}$	**-1**	$\mathbf{-r_1}$	$\mathbf{-r_6}$	$\mathbf{-r_7}$	$\mathbf{r_4}$	$\mathbf{r_5}$
$\mathbf{r_3}$	$\mathbf{r_3}$	$\mathbf{r_2}$	$\mathbf{-r_1}$	**-1**	$\mathbf{-r_7}$	$\mathbf{-r_6}$	$\mathbf{r_5}$	$\mathbf{r_4}$
$\mathbf{r_4}$	$\mathbf{r_4}$	$\mathbf{r_5}$	$\mathbf{r_6}$	$\mathbf{r_7}$	**1**	$\mathbf{r_1}$	$\mathbf{r_2}$	$\mathbf{r_3}$
$\mathbf{r_5}$	$\mathbf{r_5}$	$\mathbf{r_4}$	$\mathbf{r_7}$	$\mathbf{r_6}$	$\mathbf{r_1}$	**1**	$\mathbf{r_3}$	$\mathbf{r_2}$
$\mathbf{r_6}$	$\mathbf{r_6}$	$\mathbf{r_7}$	$\mathbf{-r_4}$	$\mathbf{-r_5}$	$\mathbf{-r_2}$	$\mathbf{-r_3}$	**1**	$\mathbf{r_1}$
$\mathbf{r_7}$	$\mathbf{r_7}$	$\mathbf{r_6}$	$\mathbf{-r_5}$	$\mathbf{-r_4}$	$\mathbf{-r_3}$	$\mathbf{-r_2}$	$\mathbf{r_1}$	**1**

Fig. 6. The multiplication table of basic matrices r_0, r_1,… , r_7 (where r_0 is identity matrix) which corresponds to the 8-dimensional algebra over the field of real numbers. It defines the 8-dimensional numeric system of genetic R_{123}-octetons.

For this reason we term these hypercomplex numbers, which are revealed in matrix genetics, as "dyadic-shift genetic octetons" (or briefly "octetons"). In addition we term such kinds of matrix algebras, which are connected with dyadic-shift decompositions, as dyadic-shift algebras (or briefly DS-algebras). The author supposes that DS-algebras are important for genetic systems. All the basic matrices r_0, r_1,…, r_7 are disposed in the multiplication table (Fig. 6) in accordance with dyadic-shift numerations of cells on Fig. 2.

Below we will describe another variant of genetic octetons which is connected with Hadamard genomatrices. For this reason we term the first type of genooctetons (Fig. 4-6) as R_{123}-octetons (here R is the first letter of the name Rademacher; the index 123 means the order 1-2-3 of positions in triplets).

A general form of R_{123}-octetons (Fig. 5) is the following:

$$R_{123} = x_0*\mathbf{1} + x_1*\mathbf{r_1} + x_2*\mathbf{r_2} + x_3*\mathbf{r_3} + x4*\mathbf{r4} + x_5*\mathbf{r_5} + x_6*\mathbf{r_6} + x_7*\mathbf{r_7} \quad (4)$$

where coefficients x_0, x_1,.. , x_7 are real numbers. Here the first component x_0 is a scalar. Other 7 components $x_1*\mathbf{r_1}$,

x_2*$\mathbf{r_2}$, x_3*$\mathbf{r_3}$, x_4*$\mathbf{r_4}$, x_5*$\mathbf{r_5}$, x_6*$\mathbf{r_6}$, x_7*$\mathbf{r_7}$ are non-scalar units but imaginary units. Some properties of these octetons lead to the idea that for a system of genetic coding the main significance belong not to the entire set of possible real values of coordinates of 8-dimensional hypercomplex numbers but only to the subset of numbers 2^0, 2^1, 2^2,.., 2^n,.. [16]. It seems that for genetic systems DS-algebras are algebras of dichotomous biological processes.

3 Permutations and the DS-algebra

The theory of discrete signal processing pays a special attention to permutations of information elements. This paragraph shows that all the possible permutations of positions inside all the triplets lead to new mosaic genomatrices whose Rademacher forms of presentation are connected with the same DS-algebra (Fig. 6).

A simultaneous permutation of positions in triplets transforms the most of the triplets in cells of the initial genomatrix $[C\ A;\ U\ G]^{(3)}$. For example, in the case of the cyclic transformation of the order 1-2-3 of positions into the order 2-3-1, the triplet CAG is transformed into the triplet AGC, etc. Because each of the triplets is connected with the binary numeration of its column and row, these binary numerations are also transformed correspondingly; for example, the binary numeration 011 is transformed into 110. The six variants of the order of positions inside triplets are possible: 1-2-3, 2-3-1, 3-1-2, 3-2-1, 2-1-3, 1-3-2. The initial genomatrix $[C\ A;\ U\ G]_{123}^{(3)}$ is related with the first of these orders (Fig. 4). Other five genomatrices $[C\ A;\ U\ G]_{231}^{(3)}$, $[C\ A;\ U\ G]_{231}^{(3)}$, $[C\ A;\ U\ G]_{231}^{(3)}$, $[C\ A;\ U\ G]_{231}^{(3)}$, $[C\ A;\ U\ G]_{231}^{(3)}$, which correspond to other five orders, are shown on Fig. 7 (subscripts indicate the order of positions in triplets).

In these genomatrices on Fig. 7 black-and-white mosaics of each row corresponds again to one of Rademacher functions. The replacement of all the triplets with strong and weak roots by entries "+1" and "-1" correspondingly transforms these genomatrices into their Rademacher forms R_{231}, R_{312}, R_{321}, R_{213}, R_{132}. Each of the Rademacher forms R_{231}, R_{312}, R_{321}, R_{213}, R_{132} can be again decomposed into sum of 8 sparse matrices r_0, r_1, r_2, r_3, r_4, r_5, r_6, r_7 in accordance with dyadic-shift numerations of its cells (see details in [16]). Each of the 6 sets with eight sparse matrices r_0, r_1, r_2, r_3, r_4, r_5, r_6, r_7 is unique and different from other sets (r_0 is identity matrix in all the sets).

Unexpected facts are that, firstly, each of these sets is closed relative multiplication and, secondly, each of these sets corresponds to the same multiplication table from Fig. 6.

It means that this genetic DS-algebra of 8-dimensional hypercomplex numbers possesses at least 5 additional matrix forms of its presentation. Our results demonstrate that this DS-algebra of genetic R-octetons possesses a wonderful invariance relative not only to all the variants of positional permutations in triplets but also to some other permutations which are connected with Gray code and dyadic-shift transformations [16]. All the properties of R_{123}-octetons hold true in the cases of different matrix forms of presentation of R-octetons with the same multiplication table (Fig. 6).

$[C\ A;\ U\ G]_{231}^{(3)} =$

	000 (0)	010 (2)	100 (4)	110 (6)	001 (1)	011 (3)	101 (5)	111 (7)
000	CCC	CAC	ACC	AAC	CCA	CAA	ACA	AAA
(0)	000 (0)	010 (2)	100 (4)	110 (6)	001 (1)	011 (3)	101 (5)	111 (7)
010	CUC	CGC	AUC	AGC	CUA	CGA	AUA	AGA
(2)	010 (2)	000 (0)	110 (6)	100 (4)	011 (3)	001 (1)	111 (7)	101 (5)
100	UCC	UAC	GCC	GAC	UCA	UAA	GCA	GAA
(4)	100 (4)	110 (6)	000 (0)	010 (2)	101 (5)	111 (7)	001 (1)	011 (3)
110	UUC	UGC	GUC	GGC	UUA	UGA	GUA	GGC
(6)	110 (6)	100 (4)	010 (2)	000 (0)	111 (7)	101 (5)	011 (3)	001 (1)
001	CCU	CAU	ACU	AAU	CCG	CAU	ACG	AAG
(1)	001 (1)	011 (3)	101 (5)	111 (7)	000 (0)	010 (2)	100 (4)	110 (6)
011	CUU	CGU	AUU	AGU	CUG	CGG	AUG	AGG
(3)	011 (3)	001 (1)	111 (7)	101 (5)	010 (2)	000 (0)	110 (6)	100 (4)
101	UCU	UAU	GCU	GAU	UCG	UAG	GCG	GAG
(5)	101 (5)	111 (7)	001 (1)	011 (3)	100 (4)	110 (6)	000 (0)	010 (2)
111	UUU	UGU	GUU	GGU	UUG	UGG	GUG	GGG
(7)	111 (7)	101 (5)	011 (3)	001 (1)	110 (6)	100 (4)	010 (2)	000 (0)

$[C\ A;\ U\ G]_{312}^{(3)} =$

	000 (0)	100 (4)	001 (1)	101 (5)	010 (2)	110 (6)	011 (3)	111 (7)
000	CCC	ACC	CCA	ACA	CAC	AAC	CAA	AAA
(0)	000 (0)	100 (4)	001 (1)	101 (5)	010 (2)	110 (6)	011 (3)	111 (7)
100	UCC	GCC	UCA	GCA	UAC	GAC	UAA	GAA
(4)	100 (4)	000 (0)	101 (5)	001 (1)	110 (6)	010 (2)	111 (7)	011 (3)
001	CCU	ACU	CCG	ACG	CAU	AAU	CAU	AAG
(1)	001 (1)	101 (5)	000 (0)	100 (4)	011 (3)	111 (7)	010 (2)	110 (6)
101	UCU	GCU	UCG	GCG	UAU	GAU	UAG	GAG
(5)	101 (5)	001 (1)	100 (4)	000 (0)	111 (7)	011 (3)	110 (6)	010 (2)
010	CUC	AUC	CUA	AUA	CGC	AGC	CGA	AGA
(6)	010 (2)	110 (6)	011 (3)	111 (7)	000 (0)	100 (4)	001 (1)	101 (5)
011	UUC	GUC	UUA	GUA	UGC	GGC	UGA	GGC
(3)	110 (6)	010 (2)	111 (7)	011 (3)	100 (4)	000 (0)	101 (5)	001 (1)
001	CUU	AUU	CUG	AUG	CGU	AGU	CGG	AGG
(3)	011 (3)	111 (7)	010 (2)	110 (6)	001 (1)	101 (5)	000 (0)	100 (4)
111	UUU	GUU	UUG	GUG	UGU	GGU	UGG	GGG
(7)	111 (7)	011 (3)	110 (6)	010 (2)	101 (5)	001 (1)	100 (4)	000 (0)

$[C\ A;\ U\ G]_{321}^{(3)} =$

	000 (0)	100 (4)	010 (2)	110 (6)	001 (1)	101 (5)	011 (3)	111 (7)
000	CCC	ACC	CAC	AAC	CCA	ACA	CAA	AAA
(0)	000 (0)	100 (4)	010 (2)	110 (6)	001 (1)	101 (5)	011 (3)	111 (7)
100	UCC	GCC	UAC	GAC	UCA	GCA	UAA	GAA
(4)	100 (4)	000 (0)	110 (6)	010 (2)	101 (5)	001 (1)	111 (7)	011 (3)
010	CUC	AUC	CGC	AGC	CUA	AUA	CGA	AGA
(2)	010 (2)	110 (6)	000 (0)	100 (4)	011 (3)	111 (7)	001 (1)	101 (5)
110	UUC	GUC	UGC	GGC	UUA	GUA	UGA	GGC
(6)	110 (6)	010 (2)	100 (4)	000 (0)	111 (7)	011 (3)	101 (5)	001 (1)
001	CCU	ACU	CAU	AAU	CCG	ACG	CAU	AAG
(1)	001 (1)	101 (5)	011 (3)	111 (7)	000 (0)	100 (4)	010 (2)	110 (6)
101	UCU	GCU	UAU	GAU	UCG	GCG	UAG	GAG
(5)	101 (5)	001 (1)	111 (7)	011 (3)	100 (4)	000 (0)	110 (6)	010 (2)
011	CUU	AUU	CGU	AGU	CUG	AUG	CGG	AGG
(3)	011 (3)	111 (7)	001 (1)	101 (5)	010 (2)	110 (6)	000 (0)	100 (4)
111	UUU	GUU	UGU	GGU	UUG	GUG	UGG	GGG
(7)	111 (7)	011 (3)	101 (5)	001 (1)	110 (6)	010 (2)	100 (4)	000 (0)

$[C\ A;\ U\ G]_{213}^{(3)} =$

	000 (0)	001 (1)	100 (4)	101 (5)	010 (2)	011 (3)	110 (6)	111 (7)
000	CCC	CCA	ACC	ACA	CAC	CAA	AAC	AAA
(0)	000 (0)	001 (1)	100 (4)	101 (5)	010 (2)	011 (3)	110 (6)	111 (7)
001	CCU	CCG	ACU	ACG	CAU	CAU	AAU	AAG
(1)	001 (1)	000 (0)	101 (5)	100 (4)	011 (3)	010 (2)	111 (7)	110 (6)
100	UCC	UCA	GCC	GCA	UAC	UAA	GAC	GAA
(4)	100 (4)	101 (5)	000 (0)	001 (1)	110 (6)	111 (7)	010 (2)	011 (3)
101	UCU	UCG	GCU	GCG	UAU	UAG	GAU	GAG
(5)	101 (5)	100 (4)	001 (1)	000 (0)	111 (7)	110 (6)	011 (3)	010 (2)
010	CUC	CUA	AUC	AUA	CGC	CGA	AGC	AGA
(2)	010 (2)	011 (3)	110 (6)	111 (7)	000 (0)	001 (1)	100 (4)	101 (5)
011	CUU	CUG	AUU	AUG	CGU	CGG	AGU	AGG
(3)	011 (3)	010 (2)	111 (7)	110 (6)	001 (1)	000 (0)	101 (5)	100 (4)
110	UUC	UUA	GUC	GUA	UGC	UGA	GGC	GGC
(6)	110 (6)	111 (7)	010 (2)	011 (3)	100 (4)	101 (5)	000 (0)	001 (1)
111	UUU	UUG	GUU	GUG	UGU	UGG	GGU	GGG
(7)	111 (7)	110 (6)	011 (3)	010 (2)	101 (5)	100 (4)	001 (1)	000 (0)

$[C\ A;\ U\ G]_{132}^{(3)} =$

	000 (0)	010 (2)	001 (1)	011 (3)	100 (4)	110 (6)	101 (5)	111 (7)
000	CCC	CAC	CCA	CAA	ACC	AAC	ACA	AAA
(0)	000 (0)	010 (2)	001 (1)	011 (3)	100 (4)	110 (6)	101 (5)	111 (7)
010	CUC	CGC	CUA	CGA	AUC	AGC	AUA	AGA
(2)	010 (2)	000 (0)	011 (3)	001 (1)	110 (6)	100 (4)	111 (7)	101 (5)
001	CCU	CAU	CCG	CAG	ACU	AAU	ACG	AAG
(1)	001 (1)	011 (3)	000 (0)	010 (2)	101 (5)	111 (7)	100 (4)	110 (6)
011	CUU	CGU	CUG	CGG	AUU	AGU	AUG	AGG
(3)	011 (3)	001 (1)	010 (2)	000 (0)	111 (7)	101 (5)	110 (6)	100 (4)
100	UCC	UAC	UCA	UAA	GCC	GAC	GCA	GAA
(4)	100 (4)	110 (6)	101 (5)	111 (7)	000 (0)	010 (2)	001 (1)	011 (3)
110	UUC	UGC	UUA	UGA	GUC	GGC	GUA	GGA
(6)	110 (6)	100 (4)	111 (7)	101 (5)	010 (2)	000 (0)	011 (3)	001 (1)
101	UCU	UAU	UCG	UAG	GCU	GAU	GCG	GAG
(5)	101 (5)	111 (7)	100 (4)	110 (6)	001 (1)	011 (3)	000 (0)	010 (2)
111	UUU	UGU	UUG	UGG	GUU	GGU	GUG	GGG
(7)	111 (7)	101 (5)	110 (6)	100 (4)	011 (3)	001 (1)	010 (2)	000 (0)

Fig. 7. Five genomatrices $[C\ A;\ U\ G]_{231}^{(3)}$, $[C\ A;\ U\ G]_{312}^{(3)}$, $[C\ A;\ U\ G]_{321}^{(3)}$, $[C\ A;\ U\ G]_{213}^{(3)}$, $[C\ A;\ U\ G]_{132}^{(3)}$, which correspond to orders of positions in triplets 2-3-1, 3-1-2, 3-2-1, 2-1-3, 1-3-2 relative to the genomatrix $[C\ A;\ U\ G]_{123}^{(3)}$ on Fig. 2. Black and white cells contain triplets with strong and weak roots correspondingly. Binary numerations of columns and rows are shown.

The analysis of evolution of variants (or dialects) of the genetic code from the viewpoint of the DS-algebra of the R-octetons has allowed revealing two phenomenological rules [16]:

Rule #1. In all the organisms with sexual reproduction only those triplets can be involved in the evolutionary changing their correspondence to amino acids or to stop-signals, which possess dyadic-shift numerations 4, 5, 6, 7 in the genomatrix $[C\ A;\ U\ G]^{(3)}$ (Fig. 2); in other words, only

those triplets can be involved which are connected with the basic matrices r_4, r_5, r_6, r_7 (Fig. 5) of genetic R-octetons.

Rule #2. In all the dialects of the genetic code only triplets with dyadic-shift numerations 2, 6, 7 can be start-codons. In other words, only those triplets can be start-codons, which are connected with the basic matrices r_2, r_6, r_7 (Fig. 5) of genetic R-octetons.

4 Hadamard matrices and another DS-algebra

By definition a Hadamard matrix of dimension "n" is the (n*n)-matrix H(n) with elements "+1" and "-1". It satisfies the condition $H(n)*H(n)^T = n*I_n$, where $H(n)^T$ is the transposed matrix and I_n is the identity (n*n)-matrix. Rows of Hadamard matrices are termed Walsh functions. Hadamard matrices are widely used in error-correcting codes such as the Reed-Muller code and Hadamard codes; in the theory of compression of signals and images; in spectral analysis and multi-channel spectrometers with Hadamard transformations; in quantum computers with Hadamard gates; in a realization of Boolean functions by means of spectral methods; in the theory of planning of multiple-factor experiments and in many other branches of science and technology. The works [10, 14, 15] have revealed that Kronecker families of genetic matrices are related with some kinds of Hadamard matrices ("Hadamard genomatrices") by means of so termed U-algorithm. This paragraph describes that the dyadic-shift decompositions of Hadamard genomatrices lead to special 8-dimensional hypercomplex numbers. For the U-algorithm, phenomenological facts are essential that the letter U in RNA (and correspondingly the letter T in DNA) is a unique letter in the genetic alphabet in the two following senses:

- Each of three nitrogenous bases A, C, G has one amino-group NH_2, but the fourth basis U/T has not it. From the viewpoint of existence of the amino-group (which is very important for genetic functions) the letters A, C, G are identical to each other and the letter U is opposite to them;
- The letter U is a single letter in RNA, which is replaced in DNA by another letter T.

This uniqueness of the letter U can be utilized in genetic computers of organisms. Taking into account this unique status of the letter U, the author has revealed the existence of the following formal "U-algorithm", which demonstrates the close connection between Hadamard matrices and the matrix mosaic of the genetic code [10, 14, 15, 17].

By definition the U-algorithm contains two steps: 1) on the first step, each of the triplets in the black-and-white genomatrix (for example, in the genomatrix $[C\ A;\ U\ G]^{(3)}$ on Fig. 2) should change its own color into opposite color each time when the letter U stands in an odd position (in the first or in the third position) inside the triplet; 2) on the second step, black triplets and white triples are interpreted as entries "+1" and "-1" correspondingly. For example, the white triplet UUA (see Fig. 2) should become the black triplet (and its matrix cell should be marked by black color) because of the letter U in its first position; for this reason the triplet UUA is interpreted finally as "+1". Or the white triplet UUU should not change its color because of the letter U in its first and third positions (the color of this triplet is changed twice according to the described algorithm); for this reason the triplet UUU is interpreted finally as "-1".

H_{123} =

(0)	(1)	(2)	(3)	(4)	(5)	(6)	(7)
(1)	(0)	(3)	(2)	(5)	(4)	(7)	(6)
(2)	(3)	(0)	(1)	(6)	(7)	(4)	(5)
(3)	(2)	(1)	(0)	(7)	(6)	(5)	(4)
(4)	(5))	(6)	(7)	(0)	(1)	(2)	(3)
(5)	(4)	(7)	(6)	(1)	(0)	(3)	(2)
(6)	(7)	(4)	(5)	(2)	(3)	(0)	(1)
(7)	(6)	(5)	(4)	(3)	(2)	(1)	(0)

H_{231} =

(0)	(2)	(4)	(6)	(1)	(3)	(5)	(7)
(2)	(0)	(6)	(4)	(3)	(1)	(7)	(5)
(4)	(6)	(0)	(2)	(5)	(7)	(1)	(3)
(6)	(4)	(2)	(0)	(7)	(5)	(3)	(1)
(1)	(3)	(5)	(7)	(0)	(2)	(4)	(6)
(3)	(1)	(7)	(5)	(2)	(0)	(6)	(4)
(5)	(7)	(1)	(3)	(4)	(6)	(0)	(2)
(7)	(5)	(3)	(1)	(6)	(4)	(2)	(0)

H_{312} =

(0)	(4)	(1)	(5)	(2)	(6)	(3)	(7)
(4)	(0)	(5)	(1)	(6)	(2)	(7)	(3)
(1)	(5)	(0)	(4)	(3)	(7)	(2)	(6)
(5)	(1)	(4)	(0)	(7)	(3)	(6)	(2)
(2)	(6)	(3)	(7)	(0)	(4)	(1)	(5)
(6)	(2)	(7)	(3)	(4)	(0)	(5)	(1)
(3)	(7)	(2)	(6)	(1)	(5)	(0)	(4)
(7)	(3)	(6)	(2)	(5)	(1)	(4)	(0)

H_{321} =

(0)	(4)	(2)	(6)	(1)	(5)	(3)	(7)
(4)	(0)	(6)	(2)	(5)	(1)	(7)	(3)
(2)	(6)	(0)	(4)	(3)	(7)	(1)	(5)
(6)	(2)	(4)	(0)	(7)	(3)	(5)	(1)
(1)	(5)	(3)	(7)	(0)	(4)	(2)	(6)
(5)	(1)	(7)	(3)	(4)	(0)	(6)	(2)
(3)	(7)	(1)	(5)	(2)	(6)	(0)	(4)
(7)	(3)	(5)	(1)	(6)	(2)	(4)	(0)

H_{213} =

(0)	(1)	(4)	(5)	(2)	(3)	(6)	(7)
(1)	(0)	(5)	(4)	(3)	(2)	(7)	(6)
(4)	(5)	(0)	(1)	(6)	(7)	(2)	(3)
(5)	(4)	(1)	(0)	(7)	(6)	(3)	(2)
(2)	(3)	(6)	(7)	(0)	(1)	(4)	(5)
(3)	(2)	(7)	(6)	(1)	(0)	(5)	(4)
(6)	(7)	(2)	(3)	(4)	(5)	(0)	(1)
(7)	(6)	(3)	(2)	(5)	(4)	(1)	(0)

H_{132} =

(0)	(2)	(1)	(3)	(4)	(6)	(5)	(7)
(2)	(0)	(3)	(1)	(6)	(4)	(7)	(5)
(1)	(3)	(0)	(2)	(5)	(7)	(4)	(6)
(3)	(1)	(2)	(0)	(7)	(5)	(6)	(4)
(4)	(6)	(5)	(7)	(0)	(2)	(1)	(3)
(6)	(4)	(7)	(5)	(2)	(0)	(3)	(1)
(5)	(7)	(4)	(6)	(1)	(3)	(0)	(2)
(7)	(5)	(6)	(4)	(3)	(1)	(2)	(0)

Fig. 8. The Hadamard genomatrices H_{123}, H_{231}, H_{312}, H_{321}, H_{213}, H_{132} which are received from the genomatrices $[C\ A;\ U\ G]_{123}^{(3)}$, $[C\ A;\ U\ G]_{231}^{(3)}$, $[C\ A;\ U\ G]_{312}^{(3)}$, $[C\ A;\ U\ G]_{321}^{(3)}$, $[C\ A;\ U\ G]_{213}^{(3)}$, $[C\ A;\ U\ G]_{132}^{(3)}$ (Fig. 2 and 7) by means of the U-algorithm. Brackets contain dyadic-shift numerations of cells in decimal notation by analogy with matrices on Fig. 2 and 8. Black color and white color of cells mean entries "+1" and "-1" in these cells correspondingly.

By means of the U-algorithm, all the genomatrices $[C\ A;\ U\ G]_{123}^{(3)}$, $[C\ A;\ U\ G]_{231}^{(3)}$, $[C\ A;\ U\ G]_{312}^{(3)}$, $[C\ A;\ U\ G]_{321}^{(3)}$, $[C\ A;\ U\ G]_{213}^{(3)}$, $[C\ A;\ U\ G]_{132}^{(3)}$ (Fig. 2 and 7) are transformed into relevant numeric genomatrices H_{123}, H_{231}, H_{312}, H_{321}, H_{213}, H_{132} on Fig. 8.

One can make the dyadic-shift decomposition of each of these six Hadamard genomatrices H_{123}, H_{231}, H_{312}, H_{321}, H_{213}, H_{132} (Fig. 8) by analogy with the described decompositions of the genomatrices R_{123}, R_{231}, R_{312}, R_{321}, R_{213}, R_{132}. In the result six new different sets of 8 sparse matrices h_0, h_1, h_2, h_3, h_4, h_5, h_6, h_7 arise (where h_0 is identity matrix). It is unexpectedly but each of these six sets for Hadamard genomatrices is closed relative to multiplication. Moreover each of these sets h_0, h_1, h_2, h_3, h_4, h_5, h_6, h_7 corresponds to

the same multiplication table on Fig. 9 [16].

	1	h_1	h_2	h_3	h_4	h_5	h_6	h_7
1	**1**	h_1	h_2	h_3	h_4	h_5	h_6	h_7
h_1	h_1	**-1**	h_3	$-h_2$	h_5	$-h_4$	h_7	$-h_6$
h_2	h_2	h_3	**-1**	$-h_1$	$-h_6$	$-h_7$	h_4	h_5
h_3	h_3	$-h_2$	$-h_1$	**1**	$-h_7$	h_6	h_5	$-h_4$
h_4	h_4	h_5	h_6	h_7	**-1**	$-h_1$	$-h_2$	$-h_3$
h_5	h_5	$-h_4$	h_7	$-h_6$	$-h_1$	**1**	$-h_3$	h_2
h_6	h_6	h_7	$-h_4$	$-h_5$	h_2	h_3	**-1**	$-h_1$
h_7	h_7	$-h_6$	$-h_5$	h_4	h_3	$-h_2$	$-h_1$	**1**

Fig. 9. The multiplication table for the dyadic-shift decompositions of Hadamard genomatrices H_{123}, H_{231}, H_{312}, H_{321}, H_{213}, H_{132} (Fig. 8).

The existence of the multiplication table (Fig. 9) means that a new 8-dimensional DS-algebra or a new system of 8-dimensional hypercomplex numbers exists on the base of these Hadamard genomatrices which are connected with six different matrix forms of presentation of this hypercomplex system. We term these new 8-dimensional hypercomplex numbers as H-octetons (here "H" is the first letter in the name Hadamard) because they differ from R-octetons (Fig. 6) and Cayley's octonions. The six Hadamard genomatrices H_{123}, H_{231}, H_{312}, H_{321}, H_{213}, H_{132} are different matrix forms of presentation of the same H-octeton whose coordinates are equal to 1 ($x_0=x_1=\ldots=x_7=1$).

The DS-algebra of H-octetons (Fig. 9) is the non-commutative associative non-division algebra. It has zero divisors: for example (h_3+h_4) and (h_2-h_5) are non-zero H-octetons, but their product is equal to zero. The quantity and the disposition of signs "+" and "-" in the multiplication table on Fig. 9 are identical to their quantity and disposition in a Hadamard matrix. In addition, indexes of basic matrices are again disposed in the multiplication table (Fig. 9) in accordance with the dyadic-shift numeration on Fig. 2.

It should be noted that Hadamard matrices play important roles in many tasks of discrete signal processing; they are devoted to tens of thousands of publications (see a review in [19]). Only a few symmetrical Hadamard matrices are usually used in the field of discrete signal processing. But dyadic-shift decompositions of these "engineering" Hadamard matrices do not lead to any 8-dimensional hypercomplex numbers in contrast to the asymmetrical Hadamard genomatrices described in our article. Moreover the author knows no publications about the facts that Hadamard matrices can be the base for matrix forms of presentation of 8-dimensional hypercomplex numbers. It seems that the genetic code has led the author to discovering the new interesting fact in the field of the theory of Hadamard matrices about the unexpected relation of some Hadamard matrices with multidimensional DS-algebras and their systems of hypercomplex numbers. This fact can be useful for many applications of Hadamard genomatrices for simulating of bioinformation phenomena, for technology of discrete signal processing, etc. A great number of Hadamard (8x8)-matrices exists (according to some experts, their number is equal to approximately 5 billion). Perhaps, only the genetic Hadamard matrices, which represent a small subset of a great set of all the Hadamard matrices, are related with multidimensional DS-algebras but it is an open question now.

Why living nature uses just such the genetic code that is associated with Hadamard genomatrices? We suppose that its reason is related with solving in biological organisms the same information tasks which lead to a wide using of Hadamard matrices in digital signal processing and in physics.

5 Discussion

The author has revealed a close relation of the genetic code with 8-dimensional hypercomplex numbers (first of all, R-octetons and H-octetons) and with dyadic shifts and Hadamard matrices. This relation is interesting in many aspects. Some of them are the following.

Numeric presentations of genetic sequences are useful to study hidden genetic regularities [3, 4, 44, 17, etc.]. On the base of the described results, new approaches of numeric presentations of genetic sequences can be proposed for such aims taking into account additionally known applications of hypercomplex numbers to analysis of genetic sequences [2, 5, 20, 21, 23, etc.]. It seems appropriate to interpret genetic sequences as sequences of 8-dimensional vectors where genetic elements are replaced by their special numeric presentations which are connected with the described DS-algebras. Then Hadamard spectrums, dyadic distances and some other characteristics of these vector sequences can be studied. If the quantity of vector elements in a genetic sequence is not divisible by 8, the remaining short vector can be extended to an 8-dimensional vector by adding to its end of the required number of zeros by analogy with methods of digital signal processing.

Walsh functions play the main role in the fruitful sequency theory by Harmuth for signal processing [6-9]. Rows of Hadamard genomatrices correspond to special kinds of Walsh functions which define special variants of sequency analysis. The author believes that this "genetic" sequency analysis can be a key to understand important features not only of genetic informatics but also of many other inherited physiological systems (morphogenetic, sensori-motor, etc.). In comparison with spectral analysis by means of sine waves, which is applicable to linear time-invariant systems, the sequency analysis is based on non-sinusoidal waves and it is used to study systems which are changed in time (biological systems belong to such systems) [7, 9]. Genetic DS-algebras can also be useful in a realization of the famous idea by Boole on algebraic theory of laws of thinking. The author believes that mechanisms of biological morphogenesis are closely associated with spatial and temporal filters from the field of sequency analysis for genetic systems. Taking into account the sequency theory by Harmuth together with our data about Hadamard genomatrices and genetic H-octetons, one can assume that biological evolution can be interpreted largely like the evolution of physiological spatial and temporal filters of the sequency theory.

The notion "number" is the main notion of mathematics. In modern theoretical physics, systems of 8-dimensional

hypercomplex numbers (mainly, Cayley's octonions and split-octonions) are one of important objects. The discovery of the relation of the genetic code with special types of 8-dimensional hypercomplex numbers allows generating of heuristic associations between theoretical physics and mathematical biology. The described DS-algebras can be useful for development of algebraic biology [16].

Bioinformatics should solve many problems about inherited properties of biological bodies:

- Noise-immunity property of genetic coding;
- Management and synchronization of a huge number of inherited cyclic processes;
- Doubling of bio-information (mitosis, etc);
- Compression of inherited biological data;
- Spatial and temporal filtering of genetic information;
- Primary structure of proteins;
- Multi-channel informatics;
- Hidden rules of structural interrelations among parts of genetic systems;
- Laws of evolution of dialects of the genetic code, etc.

The principle of dyadic shifts and DS-algebras of genetic octetons can be useful for many of these problems.

In addition, one can mention about known facts of analogies between the genetic code and the symbolic system of ancient Chinese book "I Ching" (see a review in [17]). This symbolic system is a base of many branches of Oriental medicine including acupuncture, Tibetan pulse diagnostics, etc. which use ancient ideas of "I Ching" about inherited physiological systems. Using dyadic shifts for studying not only the genetic code but also the mysterious tables of "I Ching" reveals the hidden regularities and symmetrical patterns in this ancient system [16]. Results of matrix genetics give new approaches for better understanding the "I Ching".

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