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The principle "like begets like" in molecular and algebraic-matrix genetics

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Abstract. This article is devoted to results of in-depth analysis of the system of binary-oppositional structures in DNA *n*-plet alphabets and their algebraic-matrix representations. These results show that the molecular complementary replication of DNA strands is accompanied by the presence of an algebraic version of the principle "like begets like" in matrix representations of DNA alphabets having internal structures. This algebraic version is based on binary-oppositional structures in the genetic molecular system, which can be represented by bynary numbers and corresponding matrices of DNA alphabets. The received results allow thinking that the phenomenon "like begets like" (or a complementary replication in a wide sense) is a systemic in the genetic organization and is connected with algebraic features of biological organization. Correspondingly, the biological principle "like begets like" can be additionally modeled by algebraic-matrix methods and approaches. Such algebraic-matrix modeling of the genetic coding system gives new ways for studying and understanding a key role of the named principle in genetic and other inherited physiological complexes. The author believes that further study of the algebraic relationships of the genetic system and inherited physiological complexes will be increasingly revealing the key biological role of the ancient principle "like begets like" at different levels of biological organization.

Keywords: DNA strands, complementary replication, DNA alphabets, binary opposition, binary numbers, dyadic groups, matrices, algebras, split-quaternions.

Contents

1. Introduction

The DNA double helix model created by J.D. Watson and F. Crick in 1953 gave a powerful impetus to the development of genetic research. It showed the world a recursive algorithm for the complementary replication of DNA strands, which ensures the replication of the genetic information recorded on these strands. Before the complementary replication, DNA is separated in two complementary strands. Each strand of the original DNA molecule serves as a template for the production of its new complementary counterpart. This seminal work by Watson and Crick was perceived as the discovery of a key secret of life, corresponding to the ancient notions that "like begets like". Scientists were struck by how simple and beautiful this explanation of the replication and preservation of genetic information based on the mechanism of complementarity turned out to be. It was emphasized that it is this complementarity that provides the most important properties of DNA as a carrier of hereditary information (see, for example, [Chapeville, Haenni,1974]).

The complementary replication of DNA occurs in all living organisms acting as the most essential part for biological inheritance. This is essential for cell division during growth and repair of damaged tissues, while it also ensures that each of the new cells receives its own copy of the DNA. The cell possesses the distinctive property of division, which makes complementary replication of DNA essential. Complementary replication of DNA strands occurs at an astonishing speed rate. For example, the well-known bacteria E. coli has a speed of replication of over 1,000 bases per second [Bank, 2022].

The genetic information in DNA molecules is represented in the form of sequences of four types of nucleobases: adenine A, guanine G, cytosine C, and thymine T. Their set is often referred to as the 4-letter DNA alphabet. Along with it, other DNA alphabets exist: alphabets of 16 doublets, 64 triplets, 256 tetraplets, and other *n*-plets. In particular, the alphabet of 64 triplets is used in the genetic system to encode amino acids and termination signals of protein synthesis. Taking into account the existence of different alphabets of DNA *n*-plets turns out to be useful for revealing hidden regularities in the stochastic organization of genomic DNAs [Petoukhov, 2008, 2020, 2021; Petoukhov, He, 2010]. These DNA alphabets have binary-oppositional structures, which allow representing the alphabets in a comfortable form of (2^n*2^n)-matrices with dispositions - inside these matrices - of all corresponding *n*-plets in strict arrangements on the basis of their individual molecular peculiarities [Petoukhov, 2008; Petoukhov, He, 2010].

The purpose of this article is to describe the author's results of an in-depth analysis of the system of binary-oppositional structures in these DNA alphabets and their algebraic-matrix representations. These results show that the molecular complementary replication of DNA strands is accompanied by the presence of an

algebraic version of the principle "like begets like" in the named matrix representations of DNA alphabets. This algebraic version is based on binary-oppositional structures in the genetic molecular system, which can be represented by bynary numbers and corresponding matrices of DNA alphabets. The received results allow thinking that the phenomenon "like begets like" (or a complementary replication in a wide sense) is a systemic in the genetic organization and is connected with algebraic features of biological organization. Correspondingly, the biological principle "like begets like" can be additionally modeled by algebraic-matrix methods and approaches. Such algebraic-matrix modeling of the genetic coding system gives new ways for studying and understanding a key role of the named principle in genetic and other inherited physiological complexes.

2. Symmetries and binary principles in the molecular genetic system

The four nucleobases of DNA are interrelated by their their symmetrical peculiarities into the united molecular ensemble having the three pairs of binary-oppositional traits or indicators [Fimmel, Danielli, Strüngmann, 2013; Petoukhov, 2008; Petoukhov, He, 20010; Stambuk, 1999]:

- 1) Two letters are purines (A and G), and the other two are pyrimidines (C and T). From the standpoint of these binary-oppositional traits one can denote C = T = 0, A = G = 1. From the standpoint of these traits, any of the DNA-sequences are represented by a corresponding binary sequence. For example, GCATGAAGT is represented by 101011110;
- 2) Two letters are amino-molecules (A and C) and the other two are keto-molecules (G and T). From the standpoint of these traits one can designate A = C = 0, G = T = 1. Correspondingly, the same sequence, GCATGAAGT, as above, is represented by another binary sequence, 100110011;
- 3) The pairs of complementary letters, A-T and C-G, are linked by 2 and 3 hydrogen bonds, respectively. From the standpoint of these traits, one can designate C = G = 0, A = T = 1. Correspondingly, the same sequence, GCATGAAGT, is read as 001101101.

These three types of binary representations form a common logic set on the basis of logic operation of modulo-2 addition denoted by the symbol $\oplus$: modulo-2 addition of any two such binary representations of the DNA-sequence gives a sum, which is equal to the third binary representation of the same DNA-sequence: for example, 101011110 $\oplus$ 100110011 = 001101101. One can here remind the rules of the bitwise modulo-2 addition: $0 \oplus 0 = 0$; $0 \oplus 1 = 1$; $1 \oplus 0 = 1$; $1 \oplus 1 = 0$. (The logic operation of modulo-2 addition is actively used in computer informatics and quantum informatics).

It is convenient to represent DNA-alphabets of 4 nucleotides, 16 doublets, 64 triplets, …, 4^n *n*-plets in a form of appropriate square tables (Fig. 1), whose rows and columns are numerated by binary symbols in line with the following principle. Entries of each column are numerated by binary indicators "pyrimidine or purine" (C = T = 0, A = G = 1); for example, the triplet CAG and all other triplets in the same column are the combination “pyrimidine-purine-purine” and so this column is correspondingly numerated 011. By contrast, entries of each row are numerated by binary indicators "amino or keto "(C = A = 0, T = G = 1); for example, the same triplet CAG and all other triplets in the same row are the combination “amino-amino-keto” and so this row is

correspondingly numerated 001. In such tables (Fig. 1), each of 4 letters, 16 doublets, 64 triplets, … takes automatically its own individual place and all components of the alphabets are arranged in a strict order. This strict ordering of the relative positions of all members of the DNA alphabets proves useful in revealing hidden regularities and rules in the genetic coding system. As it is known, these three separate genetic tables (Fig. 1) form the joint tensor family of matrices $[C, A; T, G]^{(n)}$, where the symbol (n) refers to tensor power n, since they are interrelated by the known operation of the tensor (or Kronecker) product of matrices [Petoukhov, 2008].

	0	1
0	C	A
1	T	G

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

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

Fig. 1. The square tables of DNA-alphabets of 4 nucleotides, 16 doublets and 64 triplets with a strict arrangement of all components. Each of tables is constructed in line with the principle of binary numeration of its columns and rows (from [Petoukhov, 2008; Petoukhov, He, 2010]).

The presentation of ensembles of elements of the genetic coding system in the form of tensor families of genetic matrices has appeared as a useful tool to investigate structures of the genetic code from the viewpoint of their analogy with the theory of discrete signals processing, noise-immunity coding, quantum informatics, etc. The scientific direction, which deals with such matrix presentation of the ensembles of genetic elements and their numeric parameters, is named "matrix genetics' [Petoukhov, 2008; Petoukhov, He, 2010].

3. Complementary-replicated genetic matrices and an even-odd columns decomposition of the matrix of 64 triplets

As one can see from Fig. 1, binary numberings of columns and rows of the (2^n*2^n)-matrices of DNA alphabets belong to dyadic groups of binary numbers. For example, in the (8*8)-matrix of 64 triplets, its columns and rows are numerated by 3-bit binary numbers forming the corresponding dyadic group (1):

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

This series (1) is a partcular example of dyadic groups, in which modulo-2 addition serves as the group operation [Harmuth, 1989]. The distance in dyadic groups is known as the Hamming distance. Since the Hamming distance satisfies the conditions of a metric group, the dyadic group is a metric group. The modulo-2 addition of any two binary numbers from (1) always results in a new number from the same series. The number 000 serves as the unit element of this group: for example, 010 $\oplus$ 000 = 010. The reverse element for any number in this group is the number itself: for example, 010 $\oplus$ 010 = 000.

Two binary numbers that are converted into each other under inter-replacing 0↔1 will be called complementary. For example, in the dyadic group (1), the pairs of complementary numbers are the following: 000-111, 001-110, 010-101, 011-100 (in the decimal system, they correspond to pairs of numbers 0-7, 1-6, 2-5, 3-4). In a pair of complementary numbers, one of them is always even and the other is odd, that is, any pair of complementary numbers is the pair of even and odd numbers (or Yin and Yang numbers in line with ancient Chinese notions). Accordingly, any two columns (rows) that are enumerated by complementary binary numbers are called complementary. In the genetic matrices in Fig. 1, complementary columns are located mirror-symmetrical in the left and right halves of the matrices, and complementary rows are located mirror-symmetrical in the upper and lower halves.

One should emphasize that, in the matrix in Figs. 1 and 2, any column enumerated by even number contains only triplets ending by pyrimidines C or T; in contrast, any column enumerated by odd number contains only triplets ending by purines A or G. The mentioned numeric inter-replacing 0↔1 in numberings of columns symbolizes the molecular inter-replacing: it means the transition from columns with triplets ending in pyrimidines to columns with triplets ending in purines and vice versa. Similarity to this, any row enumerated by even number contains only triplets ending by amino-molecules A or C; in contrast, any row enumerates by odd number contains only triplets ending by keto-molecules G or T. The mentioned numeric inter-replacing 0↔1 in numberings of rows symbolizes the molecular inter-replacing: it means the transition from rows with triplets ending in amino-molecules to rows with triplets ending in keto-molecules and vice versa.

Let us remind one more phenomenological symmetry connected with the known binary-oppositional separation of the DNA alphabet of 64 triplets - according to their code properties - into two equal sub-alphabets: 32 triplets with strong roots (i.e. triplets starting with 8 strong duplets CC, CT, CG, AC, TC, GC, GT, GG) and 32 triplets with weak roots (i.e. triplets starting with other 8 duplets) [Rumer, 1968; Fimmel, Strüngmann, 2016]. Coding value of triplets with strong roots is independent of a letter on their third position. For example, the four triplets with the same strong root CGC, CGA, CGT, CGC encode the same amino acid Arg, though they have different letters on their third position. By contrary, the coding value of triplets with weak roots depends on a letter on their third position. For example, in the grouping of the four triplets with the same weak root CAC, CAT, CAA, and CAG, two triplets (CAC, CAT) encode the amino acid His and the other two (CAA, CAG) encode another amino acid Gln. In Fig. 2, which repeats Fig. 1 in some detail, all triplets with strong roots are marked by black color in contrast to triplets with weak roots denoted by white color.

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

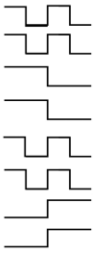

Fig. 2. Black-and-white mosaics of the matrix [C, A; T, G]$^{(3)}$ of 64 triplets from the tensor family [C,A; T,G]$^{(n)}$ (from Fig. 1) show the binary-oppositional separations of the alphabet of 64 triplets into the sub-alphabet of 32 triplets with strong roots (denoted by black) and the sub-alphabets of *n*-plets with weak roots. At the right of the matrix, Rademacher functions illustrate meander-like mosaics of its rows.

In the matrix in Fig. 2, a sequence of black and white cells in each row has a meander-like character: black fragments and white fragments have identical length. Such mosaic of each row corresponds to a meander-like form of one of Rademacher functions that take only two values «+1» and «-1» and whose examples are shown in Fig. 2. Rademacher functions are connected with the theory of orthogonal series and theory of probabilities. For example, every statement about the Rademacher functions can be interpreted from the point of view of the theory of probability (see details in [Alexits, 1961, §7; Petoukhov, 2021]).

Black and white cells of the symbolic matrices in Fig. 2 reflect the binary opposition of triplets with strong and weak roots and therefore can be represented by elements +1 and -1 in them. In this representation, a numeric matrix appears (Fig. 3, at top). Since this numerical matrix is closely related to the Rademacher functions, it is conventionally called Rademacher genetic matrix of 64 triplets. Does this Rademacher genetic matrix have any essential algebraic meaning? Yes, it has. Let us show this.

This Rademacher genetic matrix is a sum of two sparse matrices shown in Fig. 3 at bottom. One of these sparse matrices, called as an even-columns matrix, contains only columns with even numberings; the second sparse matrix, called as an odd-columns matrix, contains only columns with odd numberings.

	000	001	010	011	100	101	110	111
000	+1	+1	-1	-1	+1	+1	-1	-1
001	+1	+1	-1	-1	+1	+1	-1	-1
010	+1	+1	+1	+1	-1	-1	-1	-1
011	+1	+1	+1	+1	-1	-1	-1	-1
100	+1	+1	-1	-1	+1	+1	-1	-1
101	+1	+1	-1	-1	+1	+1	-1	-1
110	-1	-1	-1	-1	+1	+1	+1	+1
111	-1	-1	-1	-1	+1	+1	+1	+1

=

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

+

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

Fig. 3. The even-odd representation of the Rademacher genetic matrix of 64 triplets (from Fig. 2) as the sum of two sparse complementary matrices: at left, the even-columns matrix containing only non-zero columns having even numberings; at right, the odd-columns matrix containing only non-zero columns having odd numberings. Empty cells contain zero entries. Numbers in brackets are decimal values of binary numberings of columns and rows.

The even-columns (8*8)-matrix in Fig. 3 is the sum of 4 sparse (8*8)-matrices $s_0+s_1+s_2+s_3$ shown in Fig. 4 (such decomposition is conditionally called the column dyadic-tensor-shift decomposition since it is associated with the well-known dyado-shift decomposition of matrices [Ahmed, Rao, 1975], which has undergone a certain complication based on the tensor product). The set of these 4 matrices s_0, s_1, s_2, s_3 is closed relative to multiplication and corresponds to a certain multiplication table in Fig. 4, at right. This table matches to the multiplication table of the 4-dimensional algebra of Cockle split-quaternions [https://en.wikipedia.org/wiki/Split-quaternion], which is used in the Poincare conformal disk model of hyperbolic geometry [Karzel, Kist, 1985]. Some connections of hyperbolic geometry with structural peculiarities of inherited physiological systems were described in [Bodnar, 1992, 1994; Kienle, 1964; Petoukhov, 1989; Smolyaninov, 2000].

s_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	0

s_1 =

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

s_2 =

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

s_3 =

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

*	s_0	s_1	s_2	s_3
s_0	s_0	s_1	s_2	s_3
s_1	s_1	$-s_0$	s_3	$-s_2$
s_2	s_2	$-s_3$	s_0	$-s_1$
s_3	s_3	s_2	s_1	s_0

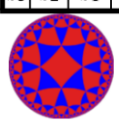

Fig. 4. The column dyadic-tensor-shift decomposition of the even-columns matrix (from Fig. 3 at left) into 4 sparse matrices s_0, s_1, s_2, s_3, whose set is closed relative to multiplication; s_0 plays a role of the identity matrix in this set. The multiplication table for this set is shown at right, which matches with the multiplication table of the 4-dimensional algebra of Cockle split-quaternions used in the Poincare conformal disk model of hyperbolic geometry. The symbol of this model is presented.

Analogically, the odd-columns matrix (Fig. 3, at right) is the sum of 4 sparse matrices $p_0+p_1+p_2+p_3$ shown in Fig. 5. The set of these 4 matrices p_0, p_1, p_2, p_3 is closed regarding multiplication and defines the multiplication table in Fig. 5, at right. This multiplication table coincides with the multiplication table of the 4-dimensional algebra, which was received above for the even-columns matrix (Fig. 4). Both the even-columns matrix and the odd-columns matrix present Cockle's split-quaternions with unit coordinates (these split-quaternions have different forms of their matrix representations, with which these even-columns and odd-columns genetic matrices turn out to be associated). Correspondingly, both these genetic matrices are connected with the Poincare conformal disk model of hyperbolic geometry.

p_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	0
0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	1

p_1 =

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

p_2 =

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

p_3 =

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

*	p_0	p_1	p_2	p_3
p_0	p_0	p_1	p_2	p_3
p_1	p_1	$-p_0$	p_3	$-p_2$
p_2	p_2	$-p_3$	p_0	$-p_1$
p_3	p_3	p_2	p_1	p_0

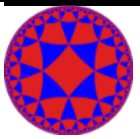

Fig. 5. The column dyadic-tensor-shift decomposition of the odd-columns matrix (from Fig. 3, at left) into 4 sparse matrices p_0, p_1, p_2, p_3, whose set is closed relative to multiplication; p_0 plays a role of the identity matrix inside this set. The multiplication table for this set is shown, which matches the multiplication table of the Cockle split-quaternions algebra used in the Poincare conformal disk model of hyperbolic geometry. The symbol of this model is presented.

Now let us show that the summation of the even-columns and odd-columns matrices, which are complementary each other and connected with the 4-dimensional algebra, gives the combined matrix W as a new algebraic entity, which is connected already with the 8-dimensional algebra. This combined matrix (Figs. 3 and 5) - under its column dyadic-tensor-shift decomposition – is the sum of 8 sparse matrices $v_0+v_1+v_2+v_3+v_4+v_5+v_6+v_7$ shown in Fig. 6. The set of these matrices v_0, v_1, v_2, v_3, v_4, v_5, v_6, v_7 is closed relative to multiplication and matches to the multiplication table (Fig. 6 , at bottom) of a certain 8-dimensional algebra. This algebra has interesting properties, which were described in previous publications without a connection with the presented topic of complementary replications [Petoukhov, 2008a-c; Petoukhov, He, 2010].

v_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	0

v_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	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

v_2

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

v_3

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

v4

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

v5

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

v6

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

v7

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

*	**v0**	**v1**	**v2**	**v3**	**v4**	**v5**	**v6**	**v7**
v0	**v0**	**v1**	**v2**	**v3**	**v4**	**v5**	**v6**	**v7**
v1	**v0**	**v1**	**v2**	**v3**	**v4**	**v5**	**v6**	**v7**
v2	**v2**	**v3**	**-v0**	**-v1**	**-v6**	**-v7**	**v4**	**v5**
v3	**v2**	**v3**	**-v0**	**-v1**	**-v6**	**-v7**	**v4**	**v5**
v4	**v4**	**v5**	**v6**	**v7**	**v0**	**v1**	**v2**	**v3**
v5	**v4**	**v5**	**v6**	**v7**	**v0**	**v1**	**v2**	**v3**
v6	**v6**	**v7**	**-v4**	**-v5**	**-v2**	**-v3**	**v0**	**v1**
v7	**v6**	**v7**	**-v4**	**-v5**	**-v2**	**-v3**	**v0**	**v1**

Fig. 6 . The column dyadic-tensor-shift decomposition of the sum of the even-columns matrix and the odd-columns matrix (this summary matrix is shown in Fig. 3) into 8 sparse matrices v_0, v_1, v_2, v_3, v_4, v_5, v_6, v_7, whose set is closed relative to multiplication. The multiplication table for this set is shown at bottom.

This summary matrix W generates algorithmically its complementary-replicated analogue W_R by means of the interchange of numbers 0↔1 in the binary numerating of its columns with the corresponding rearrangement of the columns (that is, rearrangements of columns located mirror symmetrically in the left and right halves of the matrix). This interchanging algorithm 0↔1 in binary numbers provides interchange in any pair of complementary columns that differ from each other in the content of triplets with purine and pyrimidine endings, in some analogy with the complementarity of purines and pyrimidines in DNA double strands. For example, the column with number 110 (which corresponds to the nucleotide order "purine-purine-pyrimidine" in all its triplets) takes the place of the column with number 001 (which corresponds to the order "pyrimidine-pyrimidine-purine" in all its triplets). Fig. 7 shows the summary matrix W and its complementary-replicated analogue W_R, which is generated by this algorithm based on binary-oppositions in the DNA nucleobases alphabet and which is also connected by its meander like mosaic with meander-like Rademacher functions.

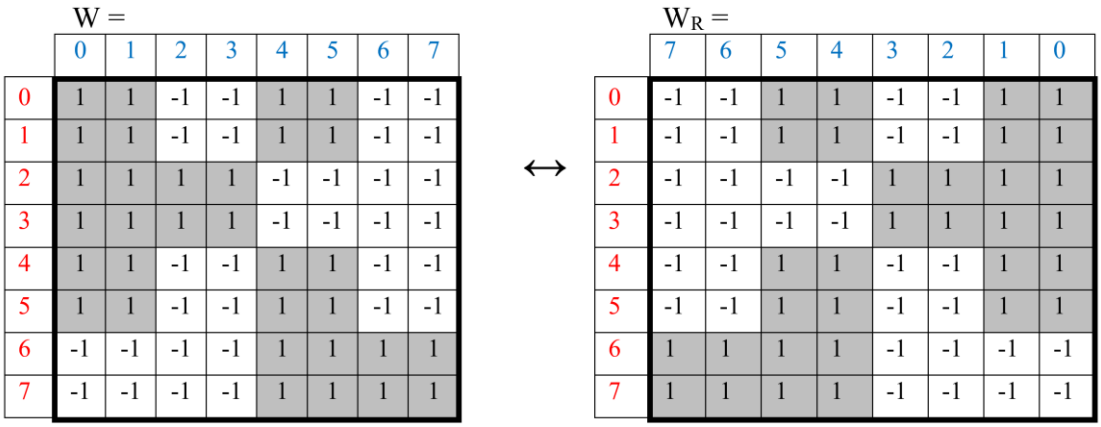

Fig. 7. The Rademacher genetic matrix W of 64 triplets (from Fig. 3, at top) and its complementary-replicated matrix W_R, which are transformed each to other by the interchanging algorithm based on binary-oppositions in the DNA nucleobases alphabet (the purine-pyrimidine transformation, see explanations in the text). Black cells containing entries +1 correspond to locations of triplets with strong roots. The numbering of columns and rows is shown in the decimal system.

Applying this complementary-replicating algorithm to the complementary-replicated matrix W_R generates the original Rademacher matrix W, that is, matrices W and W_R is mutual complementary-replicated matrices resembling two complementary strings of DNA. This algorithm is recursive and its applying allows generate such pairs of complementary-replicated matrices again and again. So, the ancient notions that "like begets like" surprisingly turn out to be realized in genetics not only for complementary strings of DNA but also for the phenomenological structure of the genetic matrix presented properties of the alphabet of 64 triplets. In other words, molecular complementary-replicated properties of DNA strings exist jointly with algebraic complementary-replicated properties of the considered alphabetical matrices of the genetic code. Both of these properties are parts of genetics of the whole organisms and so interrelated. These algebraic complementary-replicated properties of genetic matrices allow applying effective algebraic methods for further study of genetics to include it in the field of modern mathematical natural sciences in connection with multi-dimensional algebras, hyperbolic geometry, theory of resonances, etc.

The complementary-replicated matrix W_R – under its column dyadic-tensor-shift decomposition – is the sum of 8 sparse matrices $q_0+q_1+q_2+q_3+q_4+q_5+q_6+q_7$ shown in Fig. 8. The set of these matrices q_0, q_1, q_2, q_3, q_4, q_5, q_6, q_7 is closed relative to multiplication and matches to the multiplication table (Fig. 8, at bottom) of a certain 8-dimensional algebra. This new multiplication table is a complementary analogue of the multiplication table shown for the similar decompositions of the matrix W in Fig. 6 : in these multiplication tables, each value of the multiplication q_i*q_k is equal to the value v_i*v_k but taking with an opposite sign (here indexes i, k = 0, 1, 2, 3, 4, 5, 6, 7).

q_0

-1	0	0	0	0	0	0
-1	0	0	0	0	0	0
0	0	-1	0	0	0	0
0	0	-1	0	0	0	0
0	0	0	0	-1	0	0
0	0	0	0	-1	0	0
0	0	0	0	0	-1	0
0	0	0	0	0	-1	0

q_1

0	-1	0	0	0	0	0
0	-1	0	0	0	0	0
0	0	0	-1	0	0	0
0	0	0	-1	0	0	0
0	0	0	0	0	-1	0
0	0	0	0	0	-1	0
0	0	0	0	0	0	-1
0	0	0	0	0	0	-1

q_2

0	0	1	0	0	0	0
0	0	1	0	0	0	0
-1	0	0	0	0	0	0
-1	0	0	0	0	0	0
0	0	0	0	0	1	0
0	0	0	0	0	1	0
0	0	0	0	-1	0	0
0	0	0	0	-1	0	0

q_3

0	0	0	1	0	0	0
0	0	0	1	0	0	0
0	-1	0	0	0	0	0
0	-1	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	1
0	0	0	0	-1	0	0
0	0	0	0	-1	0	0

q_4

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

q_5

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

q_6

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

q_7

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

*	q_0	q_1	q_2	q_3	q_4	q_5	q_6	q_7
q_0	$-q_0$	$-q_1$	$-q_2$	$-q_3$	$-q_4$	$-q_5$	$-q_6$	$-q_7$
q_1	$-q_0$	$-q_1$	$-q_2$	$-q_3$	$-q_4$	$-q_5$	$-q_6$	$-q_7$
q_2	$-q_2$	$-q_3$	q_0	q_1	q_6	q_7	$-q_4$	$-q_5$
q_3	$-q_2$	$-q_3$	q_0	q_1	q_6	q_7	$-q_4$	$-q_5$
q_4	$-q_4$	$-q_5$	$-q_6$	$-q_7$	$-q_0$	$-q_1$	$-q_2$	$-q_3$
q_5	$-q_4$	$-q_5$	$-q_6$	$-q_7$	$-q_0$	$-q_1$	$-q_2$	$-q_3$
q_6	$-q_6$	$-q_7$	q_4	q_5	q_2	q_3	$-q_0$	$-q_1$
q_7	$-q_6$	$-q_7$	q_4	q_5	q_2	q_3	$-q_0$	$-q_1$

Fig. 8. The column dyadic-tensor-shift decomposition of the matrix W_R (Fig. 7) into 8 sparse matrices q_0, q_1, q_2, q_3, q_4, q, q_6, q_7, whose set is closed relative to multiplication. The multiplication table for this set is shown at bottom.

The action of complementary-replicated (8*8)-matrices W and W_R on an arbitrary 8-dimensional vector $\overline{X}$ generates two new vectors that are complementary to each other: the corresponding coordinates of both generated vectors are the same in their absolute values, but have opposite signs. A numerical example of this with a voluntary vector $\overline{X}$ = [1, 2, 3, 4, 5, 6, 7, 8] is shown by expression (2):

$$\overline{X}*W = [1, 2, 3, 4, 5, 6, 7, 8]*W = [6, 6, -22, -22, 22, 22, -6, -6] = \overline{Y}$$
$$\overline{X}*W_R = [1, 2, 3, 4, 5, 6, 7, 8]*W_R = [-6, -6, 22, 22, -22, -22, 6, 6] = -\overline{Y} \qquad (2)$$

Another interesting property of the Rademacher genetic complementary-replicated matrices W and W_R is that - by their repeated action on the emerging vectors (2) - one can generate as many complementary-replicated vectors as desired. In this case, the quadrupling of coordinate values in the vectors occurs, reminiscent of the quadrupling of genetic information during the meiosis division of germ cells, under which one cell generates 4 similar cells with a complete set of DNAs in each. The following example (3), using the denotations from (2), illustrates this quadrupling of coordinate values with a regular changing of signs "+" and "–":

$$\bar{Y}*W_R = -4*\bar{Y};\quad \bar{Y}*W_R^2 = 4^2*\bar{Y};\quad \bar{Y}*W_R^3 = -4^3*\bar{Y};\quad \bar{Y}*W_R^4 = 4^4*\bar{Y};\ \text{etc.} \qquad (3)$$

The expression (4) shows one more property of the Rademacher complementary-replicated matrices W and W_R:

$$W*W_R = W_R*W = -4W_R \qquad (4)$$

The matrix W/4 is an oblique projector since $(W/4)^2 = W/4$. In contrast, the matrix W_R corresponds to another condition: $(W_R/4)^2 = -W_R/4$.

Each of the resulting vectors $\overline{X}*W$ and $\overline{X}*W_R$ is always a complementary palindrome: the sequence of its coordinates, which is read in forward order, coincides with the sequence, which is read in reverse order and having coordinates with the opposite sign (see the example (2)). This algebraic feature of the action of complementary-replicated matrices on voluntary vectors is interesting, since in molecular genetics the problem of complementary palindromes has long been known. Here one should remind about the difference in notions of an ordinary palindrome and a complementary palindrome. By definition, an ordinary palindrome is a string that reads the same from beginning and from the end. By contrast, a complementary palindrome in molecular genetics is a fragment of a chain of DNA or RNA, which becomes an ordinary palindrome, if each symbol in one half of the fragment is replaced by its complementary symbol (A ↔ T, C ↔ G) [Gusfield,1997]. For instance, AGCTCGCGAGCT is a complementary palindrome. In nucleotide sequences of DNA and RNA, a great number of complementary palindromes and ordinary palindromes exists [Gusfield, 1997; Lehninger, 1982]. For instance, families of repetitive sequences occupy about one-third of the human genome. The importance of the problem of repeats in genetic sequences is reflected in the fact that during 20 years before 1991 on this subject was published 6000 articles [Gribskov, Devereux, 1991].

One should add that the theme of the complementary columns (and rows) in the described genetic matrices is also essential in connection with the universal rules of stochastic organization of DNA in genomes of higher and lower organisms [Petoukhov, 2022a,b]. These rules include approximate equalities of sums of probabilities of triplets belonging to the even column and the odd column of each pair of complementary columns (the same is true for each pair of complementary rows).

4. Complementary-replicated genetic matrices and an even-odd rows decomposition of the matrix of 64 triplets

Let us show that similar algebraic results arise in the case of "the rows dyadic-tensor-shift decomposition" of the same mosaic matrix of 64 triplets from Fig. 3. This matrix has pairs of complementary rows, which are located mirror-symmetrical in its top and bottom halves; as it was noted above, each of such pair contains one row with even

number and one row with odd number. Fig. 9 shows that the numeric presentation of this matrix, containing entries +1 and -1 (whose locations correspond to triplets with strong and weak roots), is the sum of two sparse matrices, one of which contains only non-zero rows enumerated by even numbers and the other contains only non-zero rows enumerated by odd numbers. Each of the pairs of complementary rows is separated among these two matrices. Correspondingly, the sparse matrix with even-numerated rows is conditionally called the even-rows matrix of the row type; all its non-zero rows correspond to triplets, which contain amino-molecules A or C at their ends (by this reason, this sparse matrix can be also called the amino-rows matrix). The sparse matrix with odd-numerated rows is called the odd-rows matrix; all its non-zero rows correspond to triplets, which contain keto-molecules G or T at their ends (by this reason, this sparse matrix can be also called the keto-rows matrix).

	000	001	010	011	100	101	110	111
000	+1	+1	-1	-1	+1	+1	-1	-1
001	+1	+1	-1	-1	+1	+1	-1	-1
010	+1	+1	+1	+1	-1	-1	-1	-1
011	+1	+1	+1	+1	-1	-1	-1	-1
100	+1	+1	-1	-1	+1	+1	-1	-1
101	+1	+1	-1	-1	+1	+1	-1	-1
110	-1	-1	-1	-1	+1	+1	+1	+1
111	-1	-1	-1	-1	+1	+1	+1	+1

=

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

+

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

Fig. 9. The even-odd presentation of the mosaic matrix of 64 triplets (from Fig. 3) as the sum of two sparse complementary matrices: the left matrix, called the even-rows matrix, contains only non-zero rows having even numberings; the matrix at right, called the odd-rows matrix, contains only non-zero rows having odd numberings. Empty cells contain zero entries. Numbers in brackets are decimal values of binary numberings of columns and rows.

The even-rows (8*8)-matrix in Fig. 9 is the sum of 4 sparse (8*8)-matrices $u_0+u_1+u_2+u_3$ shown in Fig. 10. The set of these 4 matrices u_0, u_1,u_2, u_3 is closed relative to multiplication and corresponds to a certain multiplication table in Fig. 10 at right. This table is again the multiplication table of the 4-dimensional algebra of Cockle split-quaternions, which we met above in Figs. 4, 5 and which is used in the Poincare conformal disk model of hyperbolic geometry.

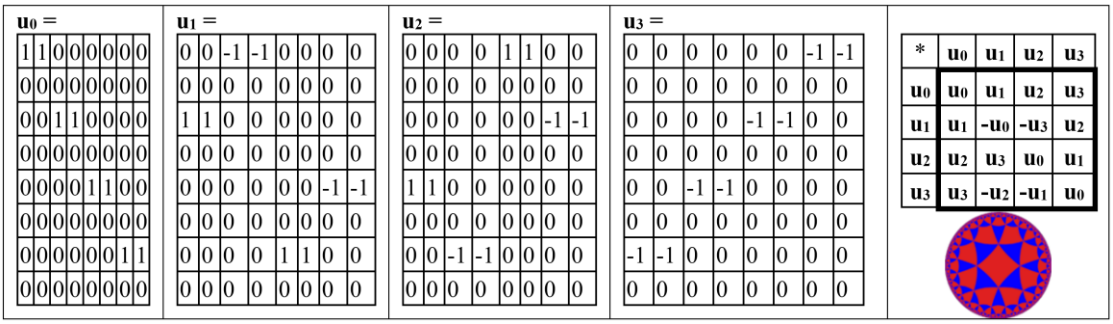

Fig. 10. The row dyadic-tensor-shift decomposition of the even-row matrix (from Fig. 9, at left) into 4 sparse matrices u_0, u_1, u_2, u_3, whose set is closed relative to multiplication; u_0 plays a role of the identity matrix in this set. The multiplication table for this set is shown at right, which matches with the multiplication table of the 4-dimensional algebra of Cockle split-quaternions used in the Poincare conformal disk model of hyperbolic geometry. The symbol of this model is presented.

Analogically, the odd-rows matrix (Fig. 9, at right) is the sum of 4 sparse matrices $a_0+a_1+a_2+a_3$ shown in Fig. 11. The set of these 4 matrices a_0, a_1, a_2, a_3 is closed regarding multiplication and defines the multiplication table in Fig. 11, at right. This multiplication table coincides with the multiplication table of the 4-dimensional algebra, which was received above for the even-rows matrix (Fig. 10) and for even-columns and odd-columns matrices (Figs. 4 and 5). Both the even-rows matrix and the odd-rows matrix represent Cockle's split-quaternions with unit coordinates, which are connected with the Poincare conformal disk model of hyperbolic geometry.

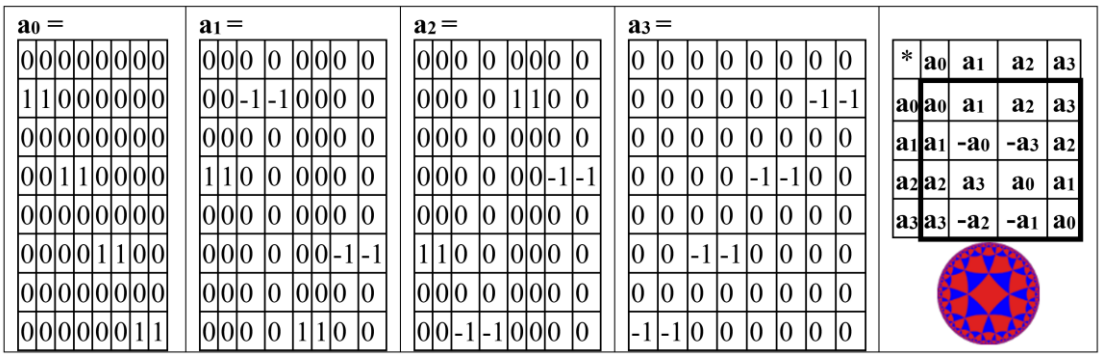

Fig. 11. The row dyadic-tensor-shift decomposition of the even-row matrix (from Fig. 9, at right) into 4 sparse matrices a_0, a_1, a_2, a_3, whose set is closed relative to multiplication; a_0 plays a role of the identity matrix in this set. The multiplication table for this set is shown at right, which matches with the multiplication table of the 4-dimensional algebra of Cockle split-quaternions used in the Poincare conformal disk model of hyperbolic geometry. The symbol of this model is presented.

The sum of the even-rows matrix and the odd-rows matrix gives the genetic matrix W in Fig. 3 at top, which was above analyzed jointly with its complementary-replicated analogue W_R (Figs. 6-8).

Similar approaches using even-odd structures and dyadic-tensor-shift decompositions are also appropriate to analyze complementary replicated properties of

Rademacher genetic matrices of higher orders, for example, the (16*16)-matrix of 256 tetraplets.

Different forms of implementation of the fundamental biological principle “like begets like” (or a complementary replication in a wide sense) can be seen at different levels of inherited biological organization. For example, in the brain of humans and animals, which has mirror complementary hemispheres (left and right), mirror neurons are known. A mirror neuron is a neuron that fires both when an animal acts and when the animal observes the same action performed by another. Thus, the neuron "mirrors" the behavior of the other, as though the observer were itself acting.

The theme of mirror neurons, whose functioning is based on one of the forms of the principle “like begets like”, provokes wide scientific researches and debates since it concerns cognitive functions, an origin of language, learning facilitation, automatic imitation, motor mimicry, autism, human capacity of emotions such as empathy, and many other problems (see for example [Morsella, Bargh, Gollwitzer, 2009; Rizzolatti, Sinigaglia, 2008]). In 2014, Philosophical Transactions of the Royal Society B published a special issue entirely devoted to mirror neuron research [Ferrari, Rizzolatti, 2014]. One of the arisen questions is the following: where do mirror neurons come from? [Heyes, 2010].

The above-described results of our studies in the field of matrix genetics give pieces of evidence that the system of mirror neurons and the system of DNAs complementary replication are not isolated parts of the organism, but they are particular parts of a bio-algebraic complex realizing inherited phenomena “like begets like”. Other examples of manifestation of this complex are, for example, structured DNA alphabets in their matrix representation forms, as well as universal rules for even-odd stochastic organization of genomic DNAs of higher and lower organisms [Petoukhov, 2022a,b]. Our body structure with its left and right halves, having left-and-right sensory-motor systems, also can be considered as one of the manifestations of this complementary-replicating complex. Another example is given by our visual perception whose optical system of the eye provides the transmission of the external image to the retina in complementary inverted and reduced forms. Although the image on the retina is inverted, we can see objects in a direct form by some complementary-replicating action of our brain.

Correspondingly, complementary replication is a systemic phenomenon in the genetic organization. It's not that the molecules of two strands of DNA randomly docked, formed a complementary pair and began to repeat the process of complementary replication at breakneck speed. Another point of view is proposed: the DNA filaments replication phenomenon is a part of a holistic bio-algebraic genetic complex of complementary replication, parts of which manifest themselves at different levels of organization of the living, up to the functioning of the brain with its mirror neurons and the ability to empathize and imitate external events. This bio-algebraic complex can be considered as responsible for the implementation of the ancient principle "like begets like" at different levels of biological organization in the course of biological evolution.

Some concluding remarks

The described results gives new materials for confirmation that the ancient principle “like begets like” plays important role in the structurization of genetic molecular system. Moreover, they show that this principle is essential for studying and modeling

of algebraic features of molecular ensembles of the genetic code including binary-oppositional properties among separate members and their groupings in these ensembles. New biological symmetries, connected with this principle, were revealed in the families of the genetic matrices. Complementary replication in a wide sense is a systemic phenomenon in the genetic organization concerning also algebraic features of molecular genetic ensembles.

The new received knowledge about the algebraic features of the genetic molecular systems opens new approaches to understand interconnections of the genetic system with structural peculiarities of inherited physiological systems. All physiological systems should be coordinated with the genetic code to be genetically encoded for their transmition to next generations. This determines the importance of studying the algebraic features of the molecular genetic system for understanding the origin and modeling of structures of inherited physiological complexes, and also for the development of evolutionary biology and genetic biomechanics. The author believes that further study of the structural relationships of the genetic system and inherited physiological complexes will be increasingly revealing the key biological role of the ancient principle "like begets like" at different levels of biological organization including phenomena of biological symmetries, brain functions, sensory-motor systems, morphogenesis, biological intelligence, etc.

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References.

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

Alexits G. *Convergence problems of orthogonal series*. Pergamon (1961).

Bank E. How Much Time Does It Take for a DNA Molecule to Replicate? - Sciencing, (8 November 2022), https://sciencing.com/much-time-dna-molecule-replicate-21660.html.

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

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

Chapeville F., Haenni A.-L. *Biosynthese des proteins*. Hermann Collection, Paris Methodes (1974, in French).

Ferrari P.F., Rizzolatti G. Mirror neuron research: the past and the future.- *Philos Trans R Soc Lond B Biol Sci.* **369** (1644): 20130169. (2014). doi:10.1098/rstb.2013.0169. PMC 4006175. PMID 24778369

Fimmel, E., Danielli A., Strüngmann L. On dichotomic classes and bijections of the genetic code. *J. Theor. Biol*., 336, 221–230 (2013). https://doi.org/10.1016/j.jtbi.2013.07.027

Fimmel E., Strüngmann L. Yury Borisovich Rumer and his 'biological papers' on the genetic code. *Phil. Trans. R. Soc. A*, 374: 20150228 (2016), http://dx.doi.org/10.1098/rsta.2015.0228

Gribskov M., Devereux J. *Sequence Analysis Primer*. New York: Stockton Press (1991).

Gusfield D. *Algorithms on String, Trees, and Sequences. Computer Science and Computational Biology*. Cambridge University Press (1997).

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

Heyes C. M. "Where do mirror neurons come from?". - *Neuroscience & Biobehavioral Reviews*, **34** (4): 575–583 (2010). doi*:*10.1016/j.neubiorev.2009.11.007. PMID 19914284. S2CID 2578537

Karzel H., Kist G. Kinematic Algebras and their Geometries. In: *Rings and Geometry*, R. Kaya, P. Plaumann, and K. Strambach editors, p. 437–509 (1985) ISBN 90-277-2112-2.

Kienle G. Experiments concerning the non-Euclidean structure of visual space. In: *Bioastronautics*. Pergamon Pree: New York, NY, USA, p. 386–400 (1964).

Lehninger A.L. (1982). *Principles of Biochemistry*. Vol. 3. Worth Publishers, Inc.

Morsella E., Bargh J.A., Gollwitzer P.M. (Eds.) Oxford Handbook of Human Action. New York: Oxford University Press (2009).

Petoukhov S.V. Non-Euclidean geometries and algorithms of living bodies. – *Computers & Mathematics with Applications*, v. 17, № 4-6, 1989, p. 505-534.

Petoukhov S.V. Matrix genetics, algebras of the genetic code, noise immunity, Moscow: RCD, 316 p., ISBN 978-5-93972-643-6 ((2008a, in Russian).

Petoukhov S.V. Matrix genetics, part 2: the degeneracy of the genetic code and the octave algebra with two quasi-real units (the genetic octave Yin-Yang-algebra). - Version 2 (14 May 2008b).

Petoukhov S.V. Matrix genetics, part 3: the evolution of the genetic code from the viewpoint of the genetic octave Yin-Yang-algebra. - arXiv:0805.4692, (30 May 2008c).

Petoukhov S.V. Tensor Rules in the Stochastic Organization of Genomes and Genetic Stochastic Resonance in Algebraic Biology. *Preprints* 2021, 2021100093, 41 pages (2021) (doi: 10.20944/preprints202110.0093.v1).

Petoukhov S.V., He M. *Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications*. IGI Global, USA (2010).

Rizzolatti G., Sinigaglia C. *Mirrors in the Brain. How We Share our Actions and Emotions*. Oxford (UK), Oxford University Press (2008).

Rumer Yu.B. Codon systematization in the genetic code. *Doklady Akademii Nauk SSSR*, 183(1), p. 225-226 (1968).

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

Stambuk N. Circular coding properties of gene and protein sequences. *Croatia Chemica Acta, 72*(4), p. 999-1008 (1999).