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

Sergey V. Petoukhov[1]

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

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Abstract. This article is devoted to the 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 binary 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 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 the key role of the named principle in genetic and other inherited physiological complexes. The author believes that further study of the algebraic relationships between the genetic system and inherited physiological complexes will increasingly reveal 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, root-complementarity.

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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 notion 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 of biological inheritance. This is essential for cell division during the 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, 2021a,b; 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 binary 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 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, the sequence GCATGAAGT is represented by binary sequence 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 the binary sequence 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 enumerated by binary symbols in line with the following principle. Entries of each column are enumerated 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 combinations “pyrimidine-purine-purine” and so this column is correspondingly enumerated 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 000000	CCA 000001	CAC 000010	CAA 000011	ACC 000100	ACA 000101	AAC 000110	AAA 000111
001	CCT 001000	CCG 001001	CAT 001010	CAG 001011	ACT 001100	ACG 001101	AAT 001110	AAG 001111
010	CTC 010000	CTA 010001	CGC 010010	CGA 010011	ATC 010100	ATA 010101	AGC 010110	AGA 010111
011	CTT 011000	CTG 011001	CGT 011010	CGG 011011	ATT 011100	ATG 011101	AGT 011110	AGG 011111
100	TCC 100000	TCA 100001	TAC 100010	TAA 100011	GCC 100100	GCA 100101	GAC 100110	GAA 100111
101	TCT 101000	TCG 101001	TAT 101010	TAG 101011	GCT 101100	GCG 101101	GAT 101110	GAG 101111
110	TTC 110000	TTA 110001	TGC 110010	TGA 110011	GTC 110100	GTA 110101	GGC 110110	GGA 110111
111	TTT 111000	TTG 111001	TGT 111010	TGG 111011	GTT 111100	GTG 111101	GGT 111110	GGG 111111

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 the tables is constructed in line with the principle of binary numeration of its columns and rows (see explanations in text).

One can see in Fig. 1, that all complementary *n*-plets are located inverse-symmetrically with respect to the center of the appropriate matrix. Correspondingly, the 2*n*-bit binary numbering of each *n*-plet is transformed into 2*n*-bit numbering of its complementary *n*-plet (that is, *n*-plet of the opposite strand of DNA) by the mutual interchanging of digits 0↔1 in it. For example, by this complementary operation, the numbering 001010 of the triplet CAT becomes the numbering 110101 of its complementary triplet GTA. This interchanging 0↔1 is called the complementary operation and is actively used below in the theme of a realization of the ancient principle "like begets like" in matrix genetics.

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 the 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):

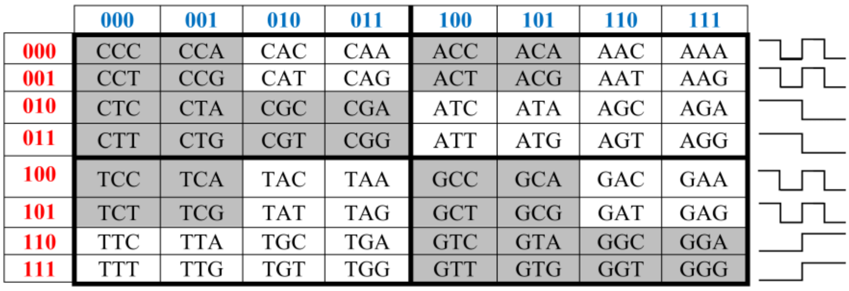
$$001, 000, 011, 010, 101, 100, 111, 110 \qquad (1)$$

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, 2021b]).

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 dyad-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].

$$s_0 = \begin{bmatrix} 1&0&0&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 0&0&1&0&0&0&0&0\\ 0&0&1&0&0&0&0&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&0&0&1&0\\ 0&0&0&0&0&0&1&0 \end{bmatrix} \quad s_1 = \begin{bmatrix} 0&0&-1&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&1&0&0&0 \end{bmatrix}$$

$$s_2 = \begin{bmatrix} 0&0&0&0&0&0&-1&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&-1&0&0&0\\ 0&0&0&0&-1&0&0&0\\ 0&0&-1&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0\\ -1&0&0&0&0&0&0&0\\ -1&0&0&0&0&0&0&0 \end{bmatrix} \quad s_3 = \begin{bmatrix} 0&0&0&0&1&0&0&0\\ 0&0&0&0&1&0&0&0\\ 0&0&0&0&0&0&-1&0\\ 0&0&0&0&0&0&-1&0\\ 1&0&0&0&0&0&0&0\\ 1&0&0&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0\\ 0&0&-1&0&0&0&0&0 \end{bmatrix}$$

*	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

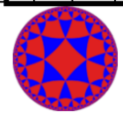


Fig. 4. The column dyadic-tensor-shift decomposition of the even-columns matrix (from Fig. 3 at left) into 4 sparse matrices s_0, s_1, s_2, s_3, whose set is closed relative to multiplication; s_0 plays a role of the identity matrix in this set. The multiplication table for this set is shown at right, 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.

$$p_0 = \begin{bmatrix} 0&1&0&0&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&0&0&1&0&0&0&0\\ 0&0&0&1&0&0&0&0\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&0&0&1\\ 0&0&0&0&0&0&0&1 \end{bmatrix} \quad p_1 = \begin{bmatrix} 0&0&0&-1&0&0&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&1&0&0 \end{bmatrix}$$

$$p_2 = \begin{bmatrix} 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&-1&0&0\\ 0&0&0&0&0&-1&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&-1&0&0&0&0&0&0\\ 0&-1&0&0&0&0&0&0 \end{bmatrix} \quad p_3 = \begin{bmatrix} 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&1&0&0\\ 0&0&0&0&0&0&0&-1\\ 0&0&0&0&0&0&0&-1\\ 0&1&0&0&0&0&0&0\\ 0&1&0&0&0&0&0&0\\ 0&0&0&-1&0&0&0&0\\ 0&0&0&-1&0&0&0&0 \end{bmatrix}$$

*	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

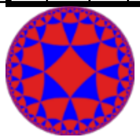


Fig. 5. The column dyadic-tensor-shift decomposition of the odd-columns matrix (from Fig. 3, at left) into 4 sparse matrices p_0, p_1, p_2, p_3, whose set is closed relative to multiplication; p_0 plays a role of the identity matrix inside this set. The multiplication table for this set is shown, which 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 to 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 the 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

$$\begin{matrix}1&0&0&0&0&0&0&0\\1&0&0&0&0&0&0&0\\0&0&1&0&0&0&0&0\\0&0&1&0&0&0&0&0\\0&0&0&0&1&0&0&0\\0&0&0&0&1&0&0&0\\0&0&0&0&0&0&1&0\\0&0&0&0&0&0&1&0\end{matrix}$$

v_1

$$\begin{matrix}0&1&0&0&0&0&0&0\\0&1&0&0&0&0&0&0\\0&0&0&1&0&0&0&0\\0&0&0&1&0&0&0&0\\0&0&0&0&0&1&0&0\\0&0&0&0&0&1&0&0\\0&0&0&0&0&0&0&1\\0&0&0&0&0&0&0&1\end{matrix}$$

v_2

$$\begin{matrix}0&0&-1&0&0&0&0&0\\0&0&-1&0&0&0&0&0\\1&0&0&0&0&0&0&0\\1&0&0&0&0&0&0&0\\0&0&0&0&0&0&-1&0\\0&0&0&0&0&0&-1&0\\0&0&0&0&1&0&0&0\\0&0&0&0&1&0&0&0\end{matrix}$$

v_3

$$\begin{matrix}0&0&0&-1&0&0&0&0\\0&0&0&-1&0&0&0&0\\0&1&0&0&0&0&0&0\\0&1&0&0&0&0&0&0\\0&0&0&0&0&0&0&-1\\0&0&0&0&0&0&0&-1\\0&0&0&0&0&1&0&0\\0&0&0&0&0&1&0&0\end{matrix}$$

v_4

$$\begin{matrix}0&0&0&0&1&0&0&0\\0&0&0&0&1&0&0&0\\0&0&0&0&0&0&-1&0\\0&0&0&0&0&0&-1&0\\1&0&0&0&0&0&0&0\\1&0&0&0&0&0&0&0\\0&0&-1&0&0&0&0&0\\0&0&-1&0&0&0&0&0\end{matrix}$$

v_5

$$\begin{matrix}0&0&0&0&0&1&0&0\\0&0&0&0&0&1&0&0\\0&0&0&0&0&0&0&-1\\0&0&0&0&0&0&0&-1\\0&1&0&0&0&0&0&0\\0&1&0&0&0&0&0&0\\0&0&0&-1&0&0&0&0\\0&0&0&-1&0&0&0&0\end{matrix}$$

v_6

$$\begin{matrix}0&0&0&0&0&0&-1&0\\0&0&0&0&0&0&-1&0\\0&0&0&0&-1&0&0&0\\0&0&0&0&-1&0&0&0\\0&0&-1&0&0&0&0&0\\0&0&-1&0&0&0&0&0\\-1&0&0&0&0&0&0&0\\-1&0&0&0&0&0&0&0\end{matrix}$$

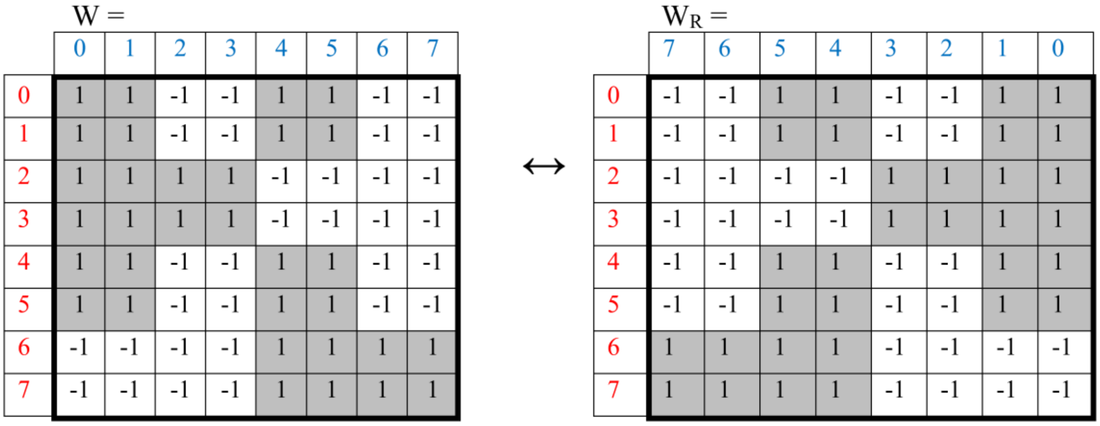
v_7

$$\begin{matrix}0&0&0&0&0&0&0&-1\\0&0&0&0&0&0&0&-1\\0&0&0&0&0&-1&0&0\\0&0&0&0&0&-1&0&0\\0&0&0&-1&0&0&0&0\\0&0&0&-1&0&0&0&0\\0&-1&0&0&0&0&0&0\\0&-1&0&0&0&0&0&0\end{matrix}$$

*	v_0	v_1	v_2	v_3	v_4	v_5	v_6	v_7
v_0	v_0	v_1	v_2	v_3	v_4	v_5	v_6	v_7
v_1	v_0	v_1	v_2	v_3	v_4	v_5	v_6	v_7
v_2	v_2	v_3	$-v_0$	$-v_1$	$-v_6$	$-v_7$	v_4	v_5
v_3	v_2	v_3	$-v_0$	$-v_1$	$-v_6$	$-v_7$	v_4	v_5
v_4	v_4	v_5	v_6	v_7	v_0	v_1	v_2	v_3
v_5	v_4	v_5	v_6	v_7	v_0	v_1	v_2	v_3
v_6	v_6	v_7	$-v_4$	$-v_5$	$-v_2$	$-v_3$	v_0	v_1
v_7	v_6	v_7	$-v_4$	$-v_5$	$-v_2$	$-v_3$	v_0	v_1

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.



$$W = \begin{array}{c|cccccccc} & 0 & 1 & 2 & 3 & 4 & 5 & 6 & 7 \\ \hline 0 & 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ 1 & 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ 2 & 1 & 1 & 1 & 1 & -1 & -1 & -1 & -1 \\ 3 & 1 & 1 & 1 & 1 & -1 & -1 & -1 & -1 \\ 4 & 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ 5 & 1 & 1 & -1 & -1 & 1 & 1 & -1 & -1 \\ 6 & -1 & -1 & -1 & -1 & 1 & 1 & 1 & 1 \\ 7 & -1 & -1 & -1 & -1 & 1 & 1 & 1 & 1 \end{array} \quad \leftrightarrow \quad W_R = \begin{array}{c|cccccccc} & 7 & 6 & 5 & 4 & 3 & 2 & 1 & 0 \\ \hline 0 & -1 & -1 & 1 & 1 & -1 & -1 & 1 & 1 \\ 1 & -1 & -1 & 1 & 1 & -1 & -1 & 1 & 1 \\ 2 & -1 & -1 & -1 & -1 & 1 & 1 & 1 & 1 \\ 3 & -1 & -1 & -1 & -1 & 1 & 1 & 1 & 1 \\ 4 & -1 & -1 & 1 & 1 & -1 & -1 & 1 & 1 \\ 5 & -1 & -1 & 1 & 1 & -1 & -1 & 1 & 1 \\ 6 & 1 & 1 & 1 & 1 & -1 & -1 & -1 & -1 \\ 7 & 1 & 1 & 1 & 1 & -1 & -1 & -1 & -1 \end{array}$$

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 generating 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	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

q_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

q_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

q_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

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 the 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 “–“:

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

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 has 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 palindrme. 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 the 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.

$$u_0 = \begin{bmatrix} 1&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&1&1&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&1&1&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&1&1\\ 0&0&0&0&0&0&0&0 \end{bmatrix} \quad u_1 = \begin{bmatrix} 0&0&-1&-1&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 1&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&-1&-1\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&1&1&0&0\\ 0&0&0&0&0&0&0&0 \end{bmatrix}$$

$$u_2 = \begin{bmatrix} 0&0&0&0&1&1&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&-1&-1\\ 0&0&0&0&0&0&0&0\\ 1&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&-1&-1&0&0&0&0\\ 0&0&0&0&0&0&0&0 \end{bmatrix} \quad u_3 = \begin{bmatrix} 0&0&0&0&0&0&-1&-1\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&-1&-1&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&-1&-1&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ -1&-1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0 \end{bmatrix}$$

*	u_0	u_1	u_2	u_3
u_0	u_0	u_1	u_2	u_3
u_1	u_1	$-u_0$	$-u_3$	u_2
u_2	u_2	u_3	u_0	u_1
u_3	u_3	$-u_2$	$-u_1$	u_0

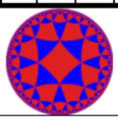


Fig. 10. The row dyadic-tensor-shift decomposition of the even-row matrix (from Fig. 9, at left) into 4 sparse matrices u_0, u_1, u_2, u_3, whose set is closed relative to multiplication; u_0 plays a role of the identity matrix in this set. The multiplication table for this set is shown at right, which 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.

$$a_0 = \begin{bmatrix} 0&0&0&0&0&0&0&0\\ 1&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&1&1&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&1&1&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&1&1 \end{bmatrix} \quad a_1 = \begin{bmatrix} 0&0&0&0&0&0&0&0\\ 0&0&-1&-1&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 1&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&-1&-1\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&1&1&0&0 \end{bmatrix}$$

$$a_2 = \begin{bmatrix} 0&0&0&0&0&0&0&0\\ 0&0&0&0&1&1&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&-1&-1\\ 0&0&0&0&0&0&0&0\\ 1&1&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&-1&-1&0&0&0&0 \end{bmatrix} \quad a_3 = \begin{bmatrix} 0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&-1&-1\\ 0&0&0&0&0&0&0&0\\ 0&0&0&0&-1&-1&0&0\\ 0&0&0&0&0&0&0&0\\ 0&0&-1&-1&0&0&0&0\\ 0&0&0&0&0&0&0&0\\ -1&-1&0&0&0&0&0&0 \end{bmatrix}$$

*	a_0	a_1	a_2	a_3
a_0	a_0	a_1	a_2	a_3
a_1	a_1	$-a_0$	$-a_3$	a_2
a_2	a_2	a_3	a_0	a_1
a_3	a_3	$-a_2$	$-a_1$	a_0

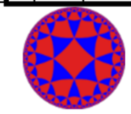


Fig. 11. The row dyadic-tensor-shift decomposition of the even-row matrix (from Fig. 9, at right) into 4 sparse matrices a_0, a_1, a_2, a_3, whose set is closed relative to multiplication; a_0 plays a role of the identity matrix in this set. The multiplication table for this set is shown at right, which 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.

5. Complementary replications and the matrix of 64 triplets under its twice-complementary transformation

This section continues research in the field of matrix genetics and phenomena of algebra-biological binary oppositions, aimed at demonstrating the key role of the principle "like begets like" and complementary replications in the genetic coding system including tensor families of genetic matrices.

For this additional research, let us consider a transformation of the Rademacher genetic matrix of 64 triplets from Fig. 2 under the simultaneous interchange of numbers 0↔1 in the binary numerating of its columns and rows with appropriate rearrangements of the columns and the rows. These rearrangements of numberings correspond to simultaneous molecular interchanges inside all pairs of complementary columns and also all pairs of complementary rows defined above by indicators of purine-pyrimidine endings and amino-keto endings in triplets. Fig. 12 shows a new Rademacher matrix B, which arises under such a twice-complementary transformation and which is conditionally called the twice-complementary matrix. This twice-complementary matrix B satisfies the following conditions: $B^2 = 4B$, $(B/2)^2 = B/2$, that is, the asymmetrical matrix B/2 is an oblique projector. The matrix B is the sum of two matrices: the odd-columns matrix and the even-columns matrix, which are shown in Fig. 12, at the bottom.

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

=

	7	6	5	4	3	2	1	0
7	1		1		-1		-1	
6	1		1		-1		-1	
5	-1		1		-1		1	
4	-1		1		-1		1	
3	-1		-1		1		1	
2	-1		-1		1		1	
1	-1		1		-1		1	
0	-1		1		-1		1	

+

	7	6	5	4	3	2	1	0
7		1		1		-1		-1
6		1		1		-1		-1
5		-1		1		-1		1
4		-1		1		-1		1
3		-1		-1		1		1
2		-1		-1		1		1
1		-1		1		-1		1
0		-1		1		-1		1

Fig. 12. The twice-complementary matrix B (at top), which is generated by the twice-complementary transformation from the Rademacher matrix of 64 triplets (from Fig. 2); its black cells correspond triplets with strong roots. This matrix B is the sum of the odd-columns matrix BOC and the even-columns matrix BEC, whose numberings of columns and rows are shown in decimal notations (at the bottom). Empty cells contain zeros. The matrices at the bottom present numbers of columns and rows in decimal notation.

It turns out that the odd-columns matrix BOC is the sum of 4 new sparse matrices $b_0 + b_1 + b_2 + b_3$, whose set is closed relative to multiplication and defines a multiplication table of the algebra of split-quaternions of Cockle as it is shown in Fig. 13 (compare with Figs. 4 and 5). This algebra is used in the Poincare conformal disk model of hyperbolic geometry.

$$\mathbf{b_0} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 1&0&0&0&0&0&0&0 \\ \hline 1&0&0&0&0&0&0&0 \\ \hline 0&0&1&0&0&0&0&0 \\ \hline 0&0&1&0&0&0&0&0 \\ \hline 0&0&0&0&1&0&0&0 \\ \hline 0&0&0&0&1&0&0&0 \\ \hline 0&0&0&0&0&0&1&0 \\ \hline 0&0&0&0&0&0&1&0 \\ \hline \end{array}$$

$$\mathbf{b_1} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&1&0&0&0&0&0 \\ \hline 0&0&1&0&0&0&0&0 \\ \hline -1&0&0&0&0&0&0&0 \\ \hline -1&0&0&0&0&0&0&0 \\ \hline 0&0&0&0&0&0&1&0 \\ \hline 0&0&0&0&0&0&1&0 \\ \hline 0&0&0&0&-1&0&0&0 \\ \hline 0&0&0&0&-1&0&0&0 \\ \hline \end{array}$$

$$\mathbf{b_2} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&0&0&-1&0&0&0 \\ \hline 0&0&0&0&-1&0&0&0 \\ \hline 0&0&0&0&0&0&1&0 \\ \hline 0&0&0&0&0&0&1&0 \\ \hline -1&0&0&0&0&0&0&0 \\ \hline -1&0&0&0&0&0&0&0 \\ \hline 0&0&1&0&0&0&0&0 \\ \hline 0&0&1&0&0&0&0&0 \\ \hline \end{array}$$

$$\mathbf{b_3} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&0&0&0&0&-1&0 \\ \hline 0&0&0&0&0&0&-1&0 \\ \hline 0&0&0&0&-1&0&0&0 \\ \hline 0&0&0&0&-1&0&0&0 \\ \hline 0&0&-1&0&0&0&0&0 \\ \hline 0&0&-1&0&0&0&0&0 \\ \hline -1&0&0&0&0&0&0&0 \\ \hline -1&0&0&0&0&0&0&0 \\ \hline \end{array}$$

*	**b_0**	**b_1**	**b_2**	**b_3**
b_0	**b_0**	**b_1**	**b_2**	**b_3**
b_1	**b_1**	**$-b_0$**	**$-b_3$**	**b_2**
b_2	**b_2**	**b_3**	**b_0**	**b_1**
b_3	**b_3**	**$-b_2$**	**$-b_1$**	**b_0**

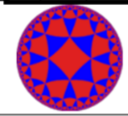


Fig. 13. The dyadic-tensor-shift decomposition of the odd-columns matrix BOC (from Fig. 12, at the bottom left) into 4 sparse matrix b_0, b_1, b_2, b_3, whose set is closed relative to multiplication and defines a multiplication table of the algebra of split-quaternions of Cockle (compare with Figs. 4 and 5). This split-quaternions algebra is used in the Poincare conformal disk model of hyperbolic geometry whose symbol is again presented.

It turns out also that the even-columns matrix BEC (from Fig. 12, at bottom right) is the sum of 4 new sparse matrix $k_0 + k_1 + k_2 + k_3$, whose set is closed relative to multiplication and defines a multiplication table of the algebra of split-quaternions of Cockle as well as it is shown in Fig. 14 (compare with the same multiplication table in Figs. 4, 5, and 13).

$$\mathbf{k_0} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&1&0&0&0&0&0&0 \\ \hline 0&1&0&0&0&0&0&0 \\ \hline 0&0&0&1&0&0&0&0 \\ \hline 0&0&0&1&0&0&0&0 \\ \hline 0&0&0&0&0&1&0&0 \\ \hline 0&0&0&0&0&1&0&0 \\ \hline 0&0&0&0&0&0&0&1 \\ \hline 0&0&0&0&0&0&0&1 \\ \hline \end{array}$$

$$\mathbf{k_1} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&0&1&0&0&0&0 \\ \hline 0&0&0&1&0&0&0&0 \\ \hline 0&-1&0&0&0&0&0&0 \\ \hline 0&-1&0&0&0&0&0&0 \\ \hline 0&0&0&0&0&0&0&1 \\ \hline 0&0&0&0&0&0&0&1 \\ \hline 0&0&0&0&0&-1&0&0 \\ \hline 0&0&0&0&0&-1&0&0 \\ \hline \end{array}$$

$$\mathbf{k_2} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&0&0&0&-1&0&0 \\ \hline 0&0&0&0&0&-1&0&0 \\ \hline 0&0&0&0&0&0&0&1 \\ \hline 0&0&0&0&0&0&0&1 \\ \hline 0&-1&0&0&0&0&0&0 \\ \hline 0&-1&0&0&0&0&0&0 \\ \hline 0&0&0&1&0&0&0&0 \\ \hline 0&0&0&1&0&0&0&0 \\ \hline \end{array}$$

$$\mathbf{k_3} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&0&0&0&0&0&-1 \\ \hline 0&0&0&0&0&0&0&-1 \\ \hline 0&0&0&0&0&-1&0&0 \\ \hline 0&0&0&0&0&-1&0&0 \\ \hline 0&0&0&-1&0&0&0&0 \\ \hline 0&0&0&-1&0&0&0&0 \\ \hline 0&-1&0&0&0&0&0&0 \\ \hline 0&-1&0&0&0&0&0&0 \\ \hline \end{array}$$

*	**k_0**	**k_1**	**k_2**	**k_3**
k_0	**k_0**	**k_1**	**k_2**	**k_3**
k_1	**k_1**	**$-k_0$**	**$-k_3$**	**k_2**
k_2	**k_2**	**k_3**	**k_0**	**k_1**
k_3	**k_3**	**$-k_2$**	**$-k_1$**	**k_0**

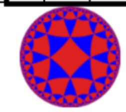


Fig. 14. The dyadic-tensor-shift decomposition of the even-columns matrix BEC (from Fig. 12) into 4 sparse matrix k_0, k_1, k_2, k_3, whose set is closed relative to multiplication and defines again a multiplication table of the algebra of split-quaternions of Cockle. The symbol of the Poincare conformal disk model of hyperbolic geometry is shown.

Twice-complementary matrix B (Fig. 12, at top) can be also presented as the sum of the odd-rows matrix BOR and the even-rows matrix BER as it is shown in Fig. 15.

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

=

	7	6	5	4	3	2	1	0
7	1	1	1	1	-1	-1	-1	-1
6								
5	-1	-1	1	1	-1	-1	1	1
4								
3	-1	-1	-1	-1	1	1	1	1
2								
1	-1	-1	1	1	-1	-1	1	1
0								

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	7	6	5	4	3	2	1	0
7								
6	1	1	1	1	-1	-1	-1	-1
5								
4	-1	-1	1	1	-1	-1	1	1
3								
2	-1	-1	-1	-1	1	1	1	1
1								
0	-1	-1	1	1	-1	-1	1	1

Fig. 15. The twice-complementary matrix B (at the top) is the sum of the odd-rows matrix BOR (at the bottom left) and the even-rows matrix BER (at the bottom right), whose numberings of columns and rows are shown in decimal notations (at the bottom). Empty cells contain zeros. Black cells correspond to triplets with strong roots. The matrices at the bottom present numbers of columns and rows in decimal notation.

The odd-rows matrix BOR (Fig. 15) is the sum of 4 sparse matrices $h_0 + h_1 + h_2$ the $+ h_3$, whose set is closed relative to multiplication and defines a multiplication table of the same algebra of split-quaternions of Cockle as it is shown in Fig. 16 (compare with the same multiplication table in Figs. 4, 5, 13, and 14).

$$\mathbf{h_0} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 1&1&0&0&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&1&1&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&0&0&1&1&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&0&0&0&0&1&1\\ \hline 0&0&0&0&0&0&0&0\\ \hline \end{array}$$

$$\mathbf{h_1} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&1&1&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline -1&-1&0&0&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&0&0&0&0&1&1\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&0&0&-1&-1&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline \end{array}$$

$$\mathbf{h_2} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&0&0&-1&-1&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&0&0&0&0&1&1\\ \hline 0&0&0&0&0&0&0&0\\ \hline -1&-1&0&0&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&1&1&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline \end{array}$$

$$\mathbf{h_3} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0&0&0&0&0&0&-1&-1\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&0&0&-1&-1&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline 0&0&-1&-1&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline -1&-1&0&0&0&0&0&0\\ \hline 0&0&0&0&0&0&0&0\\ \hline \end{array}$$

*	h_0	h_1	h_2	h_3
h_0	h_0	h_1	h_2	h_3
h_1	h_1	$-h_0$	$-h_3$	h_2
h_2	h_2	h_3	h_0	h_1
h_3	h_3	$-h_2$	$-h_1$	h_0

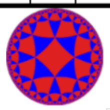

Fig. 16. The dyadic-tensor-shift decomposition of the odd-rows matrix BOR (from Fig. 15) into 4 sparse matrix h_0, h_1, h_2, h_3, whose set is closed relative to multiplication and defines a multiplication table of the algebra of split-quaternions of Cockle. The symbol of the Poincare conformal disk model of hyperbolic geometry, which is connected with this algebra, is shown.

The even-rows matrix BER (Fig. 15) is the sum of 4 sparse matrices $y_0 + y_1 + y_2 + y_3$, whose set is closed relative to multiplication and defines a multiplication table of the same algebra of split-quaternions of Cockle as it is shown in Fig. 1.8.6 (compare with the same multiplication table in Figs. 4, 5, 13, 14, and 16).

$$y_0 = \begin{array}{|c|c|c|c|c|c|c|c|}\hline 0&0&0&0&0&0&0&0\\\hline 1&1&0&0&0&0&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&1&1&0&0&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&1&1&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&0&0&1&1\\\hline \end{array} \quad y_1 = \begin{array}{|c|c|c|c|c|c|c|c|}\hline 0&0&0&0&0&0&0&0\\\hline 0&0&1&1&0&0&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline -1&-1&0&0&0&0&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&0&0&1&1\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&-1&-1&0&0\\\hline \end{array}$$

$$y_2 = \begin{array}{|c|c|c|c|c|c|c|c|}\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&-1&-1&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&0&0&1&1\\\hline 0&0&0&0&0&0&0&0\\\hline -1&-1&0&0&0&0&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&1&1&0&0&0&0\\\hline \end{array} \quad y_3 = \begin{array}{|c|c|c|c|c|c|c|c|}\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&0&0&-1&-1\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&0&0&-1&-1&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline 0&0&-1&-1&0&0&0&0\\\hline 0&0&0&0&0&0&0&0\\\hline -1&-1&0&0&0&0&0&0\\\hline \end{array}$$

*	y_0	y_1	y_2	y_3
y_0	y_0	y_1	y_2	y_3
y_1	y_1	$-y_0$	$-y_3$	y_2
y_2	y_2	y_3	y_0	y_1
y_3	y_3	$-y_2$	$-y_1$	y_0

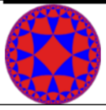

Fig. 17. The dyadic-tensor-shift decomposition of the even-rows matrix BER (from Fig. 15) into 4 sparse matrices y_0, y_1, y_2, y_3, whose set is closed relative to multiplication and defines a multiplication table of the algebra of split-quaternions of Cockle. The symbol of the Poincare conformal disk model of hyperbolic geometry, which is connected with this algebra, is shown.

6. Genetic matrices, root-complementarity, and hyperbolic numbers

The materials of sections 4 and 5 do not at all exhaust the vast topic of the implementation of the principle "like begets like" in matrix genetics based on binary oppositions in the structure of the genetic system, including complementary replications in the regular structuring of genetic matrices. This topic should be intensive and systematic studied in future. Here let us show only some additional examples of complementary interrelations in genetic matrices (that is, matrices built on the basis of binary-oppositional properties of the molecular ensembles of the genetic system).

It turns out that introduction of an additional notion of "root-complementarity" is useful for understanding and modeling the non-trivial structurization of a molecular genetic system. By definition, two *n*-bit binary numbers ($n = 3, 4, 5, \ldots$) form a root-complementary pair if they transfer each into other under the interchange of numbers 0↔1 only in their roots. For example, such interchanging transforms number 000 into number 110, that is, binary numbers 000 and 110 form the root-complementary pair. Correspondingly, in the genetic matrices, two columns (or rows) form a root-complementary pair if their binary numberings form a root-complementary pair. Below we show that this topic of the root-complementarity pairs is connected with algebra of 2-dimensional hyperbolic (double) numbers.

Let us return to the even-columns matrix in Fig. 5, at bottom left. It is the sum of two matrices shown in Fig. 18, at bottom. The first matrix contains only two non-zero columns, which are enumerated by root-complementary binary numbers 000 and 110 (that is, numbers 0 and 6 in decimal notation) and is denoted C_{06}. The second matrix contains only two non-zero columns, which are enumerated by root-complementary binary numbers 010 and 100 (that is, numbers 2 and 4 in decimal notation) and is denoted C_{24}.

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

+

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

Fig. 18. The decomposition of the even-columns matrix from Fig. 1.7.1 (at the bottom left) into the sum of matrices C_{06} (at left) and C_{24} (at right). Empty cells contain zeros. The matrices at the bottom present numbers of columns in decimal notation.

Fig. 19 shows that the first matrix C_{06} is decomposed into two matrices e_0 and e_1, whose set is closed relative to multiplication and defines the multiplication table of the 2-dimensional algebra of hyperbolic (or double) numbers $z = x + y\,j$, where x and y are real numbers, $j^2 = 1$, and $j \neq \pm 1$ [Kantor, Solodovnikov, 1989]. The multiplication table of bases elements of this algebra is shown in Fig. 19, at right.

e_0 =

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

e_1 =

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

*	**e_0**	**e_1**
e_0	**e_0**	**e_1**
e_1	**e_1**	**e_0**

Fig. 19. The decomposition of the matrix C_{06} (from Fig. 18) into the sum of two matrices $e_0 + e_1$, whose set is closed relative to multiplication. Their multiplication table is shown at right.

Fig. 20 shows that the second matrix C_{24} (from Fig. 18) is decomposed into the sum of two matrices g_0 and g_1, whose set is also closed relative to multiplication and defines the same multiplication table of 2-dimensional algebra of hyperbolic numbers.

$$\mathbf{g_0} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ \hline \end{array} \qquad \mathbf{g_1} = \begin{array}{|c|c|c|c|c|c|c|c|} \hline 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ \hline 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ \hline \end{array}$$

*	**g_0**	**g_1**
g_0	**g_0**	**g_1**
g_1	**g_1**	**g_0**

Fig. 20. The decomposition of the matrix C_{24} (from Fig. 18) into the sum of two matrices $g_0 + g_1$, whose set is closed relative to multiplication. Their multiplication table, shown at right, corresponds to algebra of hyperbolic numbers.

Now let us turn to the odd-columns matrix in Fig. 3, at bottom right. It is the sum of two matrices shown in Fig. 24, at bottom. The first matrix contains only two non-zero columns, which are numerated by root-complementary binary numbers 001 and 111 (that is, numbers 1 and 7 in decimal notation) and is denoted K_{17}. The second matrix contains only two non-zero columns, which are numerated by root-complementary binary numbers 011 and 101 (that is, numbers 3 and 5 in decimal notation) and is denoted K_{35}.

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

=

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

+

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

Fig. 21. The decomposition of the odd-columns matrix from Fig. 3 (at bottom right) into the sum of matrices K_{17} (at left) and K_{35} (at right). Empty cells contain zeros. The matrices at the bottom present numbers of columns in decimal notation.

Fig. 22 shows that the first matrix K_{17} is decomposed into the sum of two matrices q_0 and q_1, whose set is closed relative to multiplication and defines the multiplication table of the 2-dimensional algebra of hyperbolic numbers.

q_0 =

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

q_1 =

0	0	0	0	0	0	-1	0
0	0	0	0	0	0	-1	0
0	0	0	0	0	0	-1	0
0	0	0	0	0	0	-1	0
0	1	0	0	0	0	0	0
0	1	0	0	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_0	**q_0**	**q_1**
q_1	**q_1**	**q_0**

Fig. 22. The decomposition of the matrix K_{17} (from Fig. 18) into the sum of two matrices $q_0 + q_1$, whose set is closed relative to multiplication. Their multiplication table, shown at right, corresponds to the algebra of hyperbolic numbers.

Fig. 23 shows that the second matrix K_{35} (from Fig. 21) is decomposed into the sum of two matrices h_0 and h_1, whose set is closed relative to multiplication and defines the same multiplication table of the 2-dimensional algebra of hyperbolic numbers.

h_0 =

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

h_1 =

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

*	**h_0**	**h_1**
h_0	**h_0**	**h_1**
h_1	**h_1**	**h_0**

Fig. 23. The decomposition of the matrix K_{35} (from Fig. 21) into the sum of two matrices $h_0 + h_1$, whose set is closed relative to multiplication. Their multiplication table, shown at right, corresponds to the algebra of hyperbolic numbers.

These results about the connection between the algebra of hyperbolic numbers and the root-complementary relations in the structural set of triplets are especial interesting if one takes into account many other data about the role of hyperbolic numbers in genetics [Petoukhov, 2020a,b, 2021a].

Some concluding remarks

This article shows connections of the ancient principle “like begets like” not only with double-stranded DNAs but also with holistic families of structural molecular ensembles of the genetic coding system in their algebraic-matrix presentations. The author believes that this principle plays a key role in genetics, and therefore, within the framework of algebraic biology, many features of inherited biological structures can and should be studied precisely in connection with this principle. These include, for example, the following: morphogenetic symmetries; biological fractal-like patterns; conformal-geometric features of the space of visual perception according to the works [Kienle, 1964; Luneburg, 1950]; the golden section, which since the Renaissance is regarded as a mathematical symbol of self-reproduction.

The described results show that the noted principle is essential for studying and modeling 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.

The newly received knowledge about the algebraic features of the genetic molecular systems opens new approaches to understanding 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 transmission to the 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.

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