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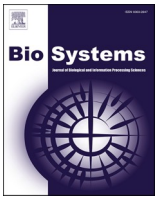

Binary oppositions, algebraic holography and stochastic rules in genetic informatics

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ABSTRACT

The article is devoted to the author's results of the algebraic analysis of molecular genetic systems, including a set of structured DNA alphabets and long nucleotide sequences in single-stranded DNA of eukaryotic and prokaryotic genomes. A connection of the system of DNA *n*-plets alphabets with principles of algebraic holography is shown, which concerns a popular theme of holography principles in genetically inherited physiology. In addition, a relation between DNA *n*-plets alphabets and the Poincaré disk model of Lobachevski hyperbolic geometry is revealed. This relation can explain known facts of the relationship of physiological phenomena with hyperbolic geometry. Considering long DNA sequences as a bunch of many parallel texts written in different *n*-plets alphabets led to the discovery of some universal rules of the stochastic organization of genomic DNAs. These rules are discussed concerning the general problem of the biological dualism "probability-vs-determinism". In general, the presented results give pieces of evidence in favor of the efficiency of a model approach to living organisms as quantum-informational algebraic-harmonic essences.

1. Introduction

Many authors supposed that living beings are molecular quantum computers and that natural laws are embedded in molecular texts of DNA for molecular controlling systems (see, for example, [Liberman and Minina, 1996; Liberman et al., 2001]).Speaking about the kinship of living organisms with computers that operate on trigger systems and binary numbers, it should be noted that the molecular genetic system is endowed with binary-oppositional traits that allow using binary numbers for descriptions of ensembles of genetic elements in a natural way. This article describes some of these genetic binary-oppositional traits, which lead to a family of square genetic matrices, which present DNA alphabets of nucleotide *n*-plets and whose columns and rows are enumerated by dyadic groups of binary numbers. Binary-oppositional features are typical not only for the molecular-genetic system (including complementary pairs of nucleobases in DNA double helix) but also for genetically inherited physiological systems. For example, a physiological "all-or-none" law for excitable tissues exists: a nerve cell or a muscle fiber gives only their answers "yes" or "no" under the action of various stimuli [Kalat, 2016].

Binary oppositions also play an important role in algebraic holography, where, for example, the method of the bit-reversible holography is well-known. This method is applied below in our genetic analysis. Here one can remind that holographic principles are very popular in physiology and cognitive research, as well as in modern physics with its concepts of the holographic universe. As it is known, holographic methods are widely used in storing and processing digital information as extremely effective. In particular, they have great perspectives in the field of creation of artificial intelligence devices. It should be noted that algebraic holography is based entirely on numerical algebraic methods and does not require special physical devices such as photosensitive plates and laser emitters, in contrast to physical holography.

Knowledge of binary oppositions in the structural organization of DNA alphabets helped to discover the universal rules for the stochastic (probabilistic) organization of genomic DNAs of higher and lower organisms [Petoukhov, 2022]. In this article, the list of universal rules of genomic DNAs is replenished by new rules of binary oppositions in the stochastic characteristics of these DNAs. The discovery of the universal rules of the stochastic organization of DNAs gives additional materials in favor of connections of the genetic system with quantum mechanics and quantum informatics, which are based on the ideology of probabilities.

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These connections are supposed by many authors (for example [Igamberdiev, 1993; Matsuno and Paton, 2000; Abbott et al., 2008; Petoukhov et al., 2019]).

The main purpose of the article is to draw attention to the proposed productive methods of algebraic analysis of the structural features of the system of genetic alphabets, as well as the stochastic organization of the DNA of the genomes of higher and lower organisms for the further development of algebraic and quantum biology.

2. Binary oppositions in DNA alphabets lead to a tensor family of genetic matrices

Informational DNA molecules possess the alphabet of 4 nucleotides (adenine A, cytosine C, guanine G, and thymine T), and their combinations, which form alphabets of 16 duplets, 64 triplets, 256 tetraplets, etc. The alphabet of 4 nucleotides A, C, G, and T is endowed with a system of binary-oppositional traits (or indicators):

1) two of the nucleotides are purines (A and G), and the other two (C and T) are pyrimidines. These oppositional indicators provide the following representation: C = T = 0, A = G = 1;
2) two of the nucleotides are keto molecules (T and G), and the other two (C and A) are amino molecules, which gives the representation C = A = 0, T = G = 1.

These binary oppositions give a possibility to represent DNA alphabets of 4 letters, 16 duplets and 64 triplets in the form of square tables, the columns of which are numbered with binary indicators “pyrimidine or purine” (C = T = 0, A = G = 1), and rows - with binary indicators “amino or keto "(C = A = 0, T = G = 1). In such tables, all monoplets, duplets, triplets, and other *n*-plets automatically take their strictly individual place (Fig. 1).

Fig. 1 shows a few examples of such tables of *n*-plet alphabets of DNA, which are not just tables but are the initial members of a single tensor family of matrices $[C, A; T, G]^{(n)}$, where the symbol (n) denotes the tensor power for $n = 1, 2, 3, 4, \ldots$. The second and third tensor (Kronecker) powers of the (2*2)-matrix [C, A; T, G] automatically give this (4*4)-matrix of the alphabet of 16 duplets and this (8*8)-matrix of the alphabet of 64 triplets in Fig. 1. The tensor product of matrices plays a great role in quantum informatics and quantum mechanics. The following quotation speaks about the meaning of the tensor product: «*This construction is crucial to understanding the quantum mechanics of multiparticle systems*» [Nielsen and Chuang, 2010, p. 71].

64 triplets encode 20 amino acids that make up the proteins of living bodies, as well as stop signals of protein synthesis (stop-codons). How are the 20 amino acids and stop signals of protein synthesis located in the matrix of 64 triplets (Fig. 1)? This arrangement cannot be predicted, since amino acids and nucleotides are completely different in structure. The number of variants of the arrangement of amino acids with some repetitions of them to fill the entire (8*8)-matrix is immense: » 10^{100} (for comparison, in physics, the lifetime of the Universe is estimated at 10^{17} s). Will this arrangement of amino acids be chaotic, or will it suddenly turn out to be regularly symmetrical?

It turns out that from an ocean of possibilities, nature has chosen an algebraically regular version of the repetition and arrangement of amino acids and stop signals in this matrix of 64 triplets, shown in Fig. 2 for the case of the Vertebrate Mitochondrial Genetic Code (this dialect of the genetic code is considered the most symmetrical and ancient [Frank--Kamenetskii, 1988]); in the theory of symmetry, it is customary to start the analysis with symmetric patterns, then move on to studying the case of violation of their symmetries). The shown matrix of encoded amino acids and stop signals consists of pairs of adjacent rows, identical in the composition of amino acids and stop-codons. This tensor-matrix regularity is one of the pieces of evidence of the deep connection of genetic coding with the formalisms of quantum informatics.

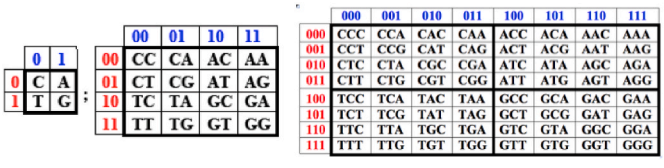


Fig. 1. Arrangement of DNA-alphabets of 4 nucleotides, 16 duplets, and 64 triplets in the tables based on binary-oppositional traits in the nucleotide alphabet C, A, T, G.

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 subalphabets: 32 triplets with strong roots (i.e. triplets starting with 8 doublets CC, CT, CG, AC, TC, GC, GT, GG) and 32 triplets with weak roots (i.e. triplets starting with other 8 doublets) [Rumer, 1968; Fimmel, Strü;ngmann, 2016]. In the constructed tensor family of matrices (Fig. 1) of DNA alphabets of 16 doublets, 64 triplets, and 256 tetraplets, we mark *n*-plets with strong roots in black (Fig. 3).

Fig. 3 shows that the noted phenomenological binary-oppositional separations of DNA-alphabets of *n*-plets ($n = 2, 3, 4, \ldots$) produce very symmetric mosaics in each of the genetic matrices:

- Left and right matrix halves are mirror-*anti*-symmetric to each other in their colors since any pair of cells, disposed of by the mirror-symmetrical manner in these halves, has opposite colors;
- Diagonal quadrants of the matrix are identical to each other from the viewpoint of their mosaic.
- The adjacent rows 1–2, 3–4, 5–6, 7–8 are identical to each other from the viewpoint of the mosaic, etc.;
- A sequence of black and white cells in each row has a meander-like character and corresponds to a form of one of Rademacher functions connected with the 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, 2021d]).

These mosaic genetic matrices are interested not only by their connection with binary-oppositional (Yin-Yang) principles but also by their connection to the method of the algebraic holography considered in the next section.

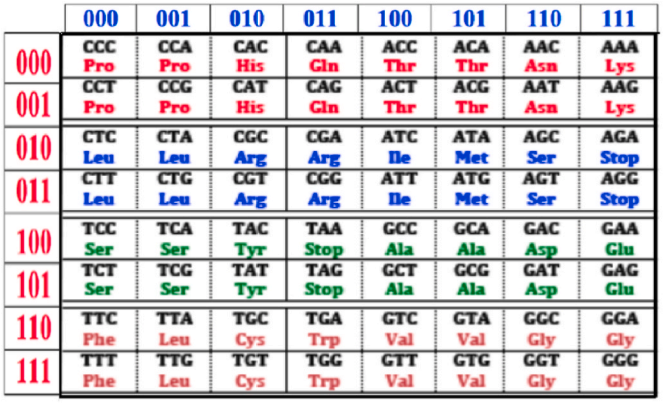
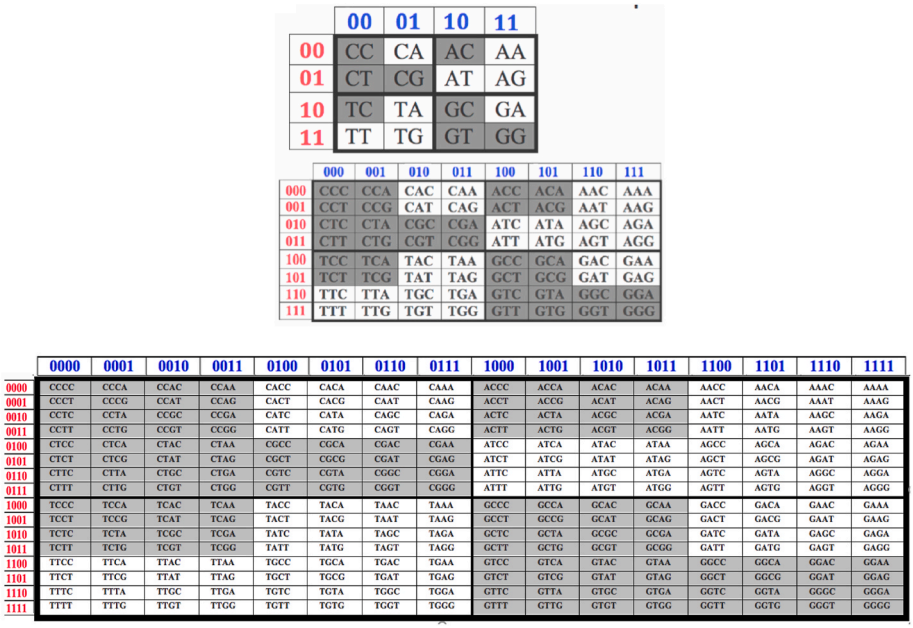


Fig. 2. The symmetrical arrangement of 20 amino acids and stop codons in the matrix of 64 triplets coding them. A case of the Vertebrate Mitochondrial Genetic Code is shown. The generally accepted abbreviations for these amino acids and stop codons (Stop) are used. Pairs of adjacent rows, identical in the composition of amino acids and stop codons, are highlighted in the same color.



	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
110	TTC	TTA	TGC	TGA	GTC	GTA	GGC	GGA
111	TTT	TTG	TGT	TGG	GTT	GTG	GGT	GGG

	0000	0001	0010	0011	0100	0101	0110	0111	1000	1001	1010	1011	1100	1101	1110	1111
0000	CCCC	CCCA	CCAC	CCAA	CACC	CACA	CAAC	CAAA	ACCC	ACCA	ACAC	ACAA	AACC	AACA	AAAC	AAAA
0001	CCCT	CCCG	CCAT	CCAG	CACT	CACG	CAAT	CAAG	ACCT	ACCG	ACAT	ACAG	AACT	AACG	AAAT	AAAG
0010	CCTC	CCTA	CCGC	CCGA	CATC	CATA	CAGC	CAGA	ACTC	ACTA	ACGC	ACGA	AATC	AATA	AAGC	AAGA
0011	CCTT	CCTG	CCGT	CCGG	CATT	CATG	CAGT	CAGG	ACTT	ACTG	ACGT	ACGG	AATT	AATG	AAGT	AAGG
0100	CTCC	CTCA	CTAC	CTAA	CGCC	CGCA	CGAC	CGAA	ATCC	ATCA	ATAC	ATAA	AGCC	AGCA	AGAC	AGAA
0101	CTCT	CTCG	CTAT	CTAG	CGCT	CGCG	CGAT	CGAG	ATCT	ATCG	ATAT	ATAG	AGCT	AGCG	AGAT	AGAG
0110	CTTC	CTTA	CTGC	CTGA	CGTC	CGTA	CGGC	CGGA	ATTC	ATTA	ATGC	ATGA	AGTC	AGTA	AGGC	AGGA
0111	CTTT	CTTG	CTGT	CTGG	CGTT	CGTG	CGGT	CGGG	ATTT	ATTG	ATGT	ATGG	AGTT	AGTG	AGGT	AGGG
1000	TCCC	TCCA	TCAC	TCAA	TACC	TACA	TAAC	TAAA	GCCC	GCCA	GCAC	GCAA	GACC	GACA	GAAC	GAAA
1001	TCCT	TCCG	TCAT	TCAG	TACT	TACG	TAAT	TAAG	GCCT	GCCG	GCAT	GCAG	GACT	GACG	GAAT	GAAG
1010	TCTC	TCTA	TCGC	TCGA	TATC	TATA	TAGC	TAGA	GCTC	GCTA	GCGC	GCGA	GATC	GATA	GAGC	GAGA
1011	TCTT	TCTG	TCGT	TCGG	TATT	TATG	TAGT	TAGG	GCTT	GCTG	GCGT	GCGG	GATT	GATG	GAGT	GAGG
1100	TTCC	TTCA	TTAC	TTAA	TGCC	TGCA	TGAC	TGAA	GTCC	GTCA	GTAC	GTAA	GGCC	GGCA	GGAC	GGAA
1101	TTCT	TTCG	TTAT	TTAG	TGCT	TGCG	TGAT	TGAG	GTCT	GTCG	GTAT	GTAG	GGCT	GGCG	GGAT	GGAG
1110	TTTC	TTTA	TTGC	TTGA	TGTC	TGTA	TGGC	TGGA	GTTC	GTTA	GTGC	GTGA	GGTC	GGTA	GGGC	GGGA
1111	TTTT	TTTG	TTGT	TTGG	TGTT	TGTG	TGGT	TGGG	GTTT	GTTG	GTGT	GTGG	GGTT	GGTG	GGGT	GGGG

Fig. 3. Black-and-white mosaics of matrices of DNA-alphabets (from Fig. 1) show the binary-oppositional separations of DNA-alphabets of *n*-plets into equal sub-alphabets of *n*-plets with strong roots (denoted by black) and sub-alphabets of *n*-plets with weak roots (an explanation in the text).

3. Genetic system and algebraic holography

The section shows a connection of DNA informatics with one of the principles of algebraic holography known in the technology of digital informatics under the term "bit-reversible holography". This kind of algebraic holography is connected, in particular, with noise-immunity coding and algorithms of fast Fourier transform [Karp, 1996; Lyons, 2010; Shishmintsev, 2012; Yang et al., 2013].

It has long been known that living organisms have properties that resemble those of holography with its non-local informatics. For example, in embryology, even 100 years ago, G. Driesch showed that by separating the blastomeres of sea urchin eggs from each other, it is possible to grow from one embryonic cell (blastomere) normal (albeit reduced) larvae with all their organs [Belousov, 2015]. Such "holographic" phenomena of distributed information have been repeatedly confirmed in many taxonomic groups of multicellular organisms - from sponges to mammals.

The book on the holographic principles of the brain emphasizes that holographic description is unmatched for explaining perceptual problems, especially imaging problems and fantastic recognition ability [Pribram, 1971]. There is a wealth of physiological data to support the holographic concept. For example, it is known that no matter which part of the rat's brain we remove, we can't destroy the memories of how to perform the complex actions that the rat learned before the operation [Lashley, 1929]. Many similar phenomena are described, for example, in the book [Talbot, 1996]. But all morphogenetic, brain, and other physiological structures are genetically inherited, and therefore it is natural to look for the algebraic holographic properties in a richly structured system of genetic coding when one considers organisms as computers.

The author found a consistency of DNA informatics with the bit-reversible holography method. Bit reversion means reading binary numbers in the opposite direction: for example, 001 becomes 100 (which corresponds to decimal numbers 1 and 5).

Fig. 4 shows a 512*512-pixel matrix, in which all columns and rows are sequentially numbered with binary numbers and in which the letter A is drawn. Reading each of these binary numbers in reverse order leads to renumbering columns and rows and to their new placement with the transformation of the entire image (the second frame in Fig. 4). If now

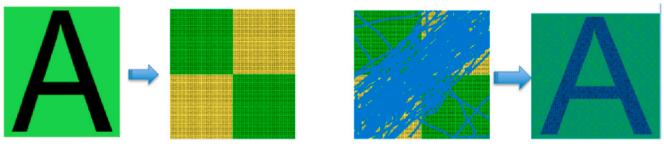


Fig. 4. An example of the bit-reversible holography (from https://habrahabr.ru/post/155471/).

part of this frame is painted over or deleted, then reapplying the reverse reading of the binary numbers with the permutation will restore the original image up to identifiable.

Now let us return to genetic mosaic matrices from the tensor family $[C, A; T, G]^{(n)}$ (Fig. 3) to study transformations of the matrix mosaics under the bit-revers in binary numberings of columns and rows of these matrices. This bit-reverse rearrangement of these binary numberings in the matrices in Fig. 3 generates a family of multi-block matrices whose mosaics consist of repetitions of the mosaic (4*4)-matrices of 16 doublets (Fig. 5).

Black and white cells of the matrices in Fig. 5 reflect the opposition of two sub-alphabets of *n*-plets with strong and weak roots and therefore can be represented by elements +1 and −1 in them. One can see those multi-block mosaics of all emerging numerical matrices of DNA alphabets have the form of "matrix crystals" since they consist of repetitions of a mosaic of the (4*4)-matrix of 16 doublets, which we conditionally term α-matrix (Fig. 5). Does this "universal" repeating block have a meaningful algebraic meaning? Yes, it has.

It turns out that this block is the sum of 4 sparse matrices, the set of which is closed under multiplication and determines the corresponding multiplication table, known as the multiplication table of the algebra of 4-dimensional split-quaternions of Cockle, known since 1849 (Fig. 7). Split-quaternions are used in the Poincaré disk model to describe hyperbolic motions in Lobachevsky's hyperbolic geometry [Karzel and Kist, 1985; https://en.wikipedia.org/wiki/Split-quaternion].

Using the symbol of the Poincaré disk model of hyperbolic geometry from Fig. 6, it is possible to present the obtained block mosaic matrices of structured DNA alphabets in an artistic form to facilitate heuristic associations (Fig. 8).

The family of block-unified matrices of DNA-alphabets (discovered

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

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

	0000	1000	0100	1100	0010	1010	0110	1110	0001	1001	0101	1101	0011	1011	0111	1111
0000	CCCC	ACCC	CACC	AACC	CCAC	ACAC	CAAC	AAAC	CCCA	ACCA	CACA	AACA	CCAA	ACAA	CAAA	AAAA
1000	TCCC	GCCC	TACC	GACC	TCAC	GCAC	TAAC	GAAC	TCCA	GCCA	TACA	GACA	TCAA	GCAA	TAAA	GAAA
0100	CTCC	ATCC	CGCC	AGCC	CTAC	ATAC	CGAC	AGAC	CTCA	ATCA	CGCA	AGCA	CTAA	ATAA	CGAA	AGAA
1100	TTCC	GTCC	TGCC	GGCC	TTAC	GTAC	TGAC	GGAC	TTCA	GTCA	TGCA	GGCA	TTAA	GTAA	TGAA	GGAA
0010	CCTC	ACTC	CATC	AATC	CCGC	ACGC	CAGC	AAGC	CCTA	ACTA	CATA	AATA	CCGA	ACGA	CAGA	AAGA
1010	TCTC	GCTC	TATC	GATC	TCGC	GCGC	TAGC	GAGC	TCTA	GCTA	TATA	GATA	TCGA	GCGA	TAGA	GAGA
0110	CTTC	ATTC	CGTC	AGTC	CTGC	ATGC	CGGC	AGGC	CTTA	ATTA	CGTA	AGTA	CTGA	ATGA	CGGA	AGGA
1110	TTTC	GTTC	TGTC	GGTC	TTGC	GTGC	TGGC	GGGC	TTTA	GTTA	TGTA	GGTA	TTGA	GTGA	TGGA	GGGA
0001	CCCT	ACCT	CACT	AACT	CCAT	ACAT	CAAT	AAAT	CCCG	ACCG	CACG	AACG	CCAG	ACAG	CAAG	AAAG
1001	TCCT	GCCT	TACT	GACT	TCAT	GCAT	TAAT	GAAT	TCCG	GCCG	TACG	GACG	TCAG	GCAG	TAAG	GAAG
0101	CTCT	ATCT	CGCT	AGCT	CTAT	ATAT	CGAT	AGAT	CTCG	ATCG	CGCG	AGCG	CTAG	ATAG	CGAG	AGAG
1101	TTCT	GTCT	TGCT	GGCT	TTAT	GTAT	TGAT	GGAT	TTCG	GTCG	TGCG	GGCG	TTAG	GTAG	TGAG	GGAG
0011	CCTT	ACTT	CATT	AATT	CCGT	ACGT	CAGT	AAGT	CCTG	ACTG	CATG	AATG	CCGG	ACGG	CAGG	AAGG
1011	TCTT	GCTT	TATT	GATT	TCGT	GCGT	TAGT	GAGT	TCTG	GCTG	TATG	GATG	TCGG	GCGG	TAGG	GAGG
0111	CTTT	ATTT	CGTT	AGTT	CTGT	ATGT	CGGT	AGGT	CTTG	ATTG	CGTG	AGTG	CTGG	ATGG	CGGG	AGGG
1111	TTTT	GTTT	TGTT	GGTT	TTGT	GTGT	TGGT	GGGT	TTTG	GTTG	TGTG	GGTG	TTGG	GTGG	TGGG	GGGG

Fig. 5. The result of the bit-reversible rearrangement in binary numberings of columns and rows of mosaic matrices of DNA alphabets from Fig. 3 is shown.

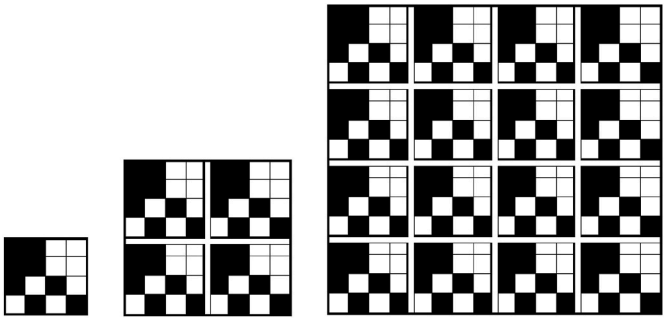


Fig. 6. Numerical representation of mosaic matrices of DNA alphabets from Fig. 5 is shown. The black and white cells of the matrices represent elements +1 and −1, respectively.

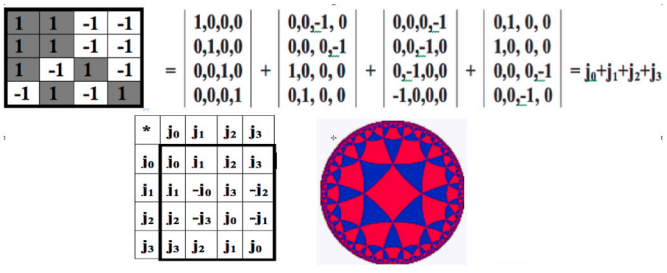


Fig. 7. Decomposition of the numerical (4 4)-matrix of the DNA-alphabet of 16 doublets (from Fig. 6) into 4 sparse matrices, whose set is closed concerning multiplication. The multiplication table for this set is shown, which matches with the multiplication table of the Cockle split-quaternion algebra used in the Poincaré disk model of hyperbolic geometry. The symbol for this model is shown from https://commons.wikimedia.org/wiki/Category:Poincar%C3%A9_disk_models.

by the method of bit-reversible holograph), whose blocks are conjugated with the disk model of hyperbolic geometry, unexpectedly echoes the theme of "holographic quantum error-correcting codes" developed at the California Institute of Technology in the USA in connection with the same disk model Poincaré and its tilings (see an online presentation [Preskill, 2016]). The topic also includes the consideration of space-time as a quantum error-correcting code [Pastawski et al., 2015]. The

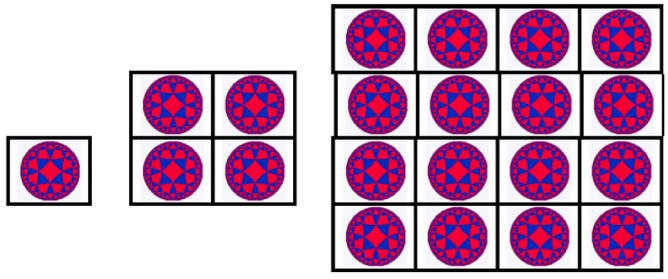


Fig. 8. "Crystals" of genetic matrices from Fig. 6 are presented in an artistic image.

following quotes from these works, which describe quantum error-correcting codes with a tensor network structure, clarify these parallels in more detail. "*The tensor network is* supported *on a uniform tiling of hyperbolic space, known as a hyperbolic tessellation. … We shall focus on examples based on tilings of two-dimensional hyperbolic space, which are specific realizations of uniform hyperbolic tilings known as hyperbolic tessellations*" [Pastawski et al., 2015]. "*Holographic quantum error-correcting codes are constructed by contracting perfect tensors according to a tilling of hyperbolic space by polygons*" [Preskill, 2016].

The bit-reversed analog of the initial matrix of 64 triplets from Fig. 2 also contains an impressive symmetrical arrangement of all the amino acids and stop-codons, which are encoded by the triplets, as Fig. 9 shows: the bit-reversed matrix has identical upper and lower halves in composition and arrangement of amino acids and stop-codons. So, genetic informatics is closely related to the principles of algebraic holography (see additional details in the preprint [Petoukhov, 2021d]).

Holographic principles have long been used for the physical understanding of the world. Thus, the famous physicist David Bohm believed that human consciousness is part of the universal hologram of the entire human race and that the entire Universe has a holographic structure. Bohm worked with K.Pribram [Pribram, 1971] on the theory that the brain works like a hologram following quantum mathematical principles and characteristics of wave patterns. Nobel laureate in physics Gerard t'Hooft put forward the principle of holography in the structure of the world, which is actively developed in modern physics by many authors (see for example [Shiva Meucci, 2020]).

Revealing the described connections of the genetic coding system with the Poincaré disk model of the Lobachevski hyperbolic geometry

	000	100	010	110	001	101	011	111
000	CCC Pro	ACC Thr	CAC His	AAC Asn	CCA Pro	ACA Thr	CAA Gln	AAA Lys
100	TCC Ser	GCC Ala	TAC Tyr	GAC Asp	TCA Ser	GCA Ala	TAA Stop	GAA Glu
010	CTC Leu	ATC Ile	CGC Arg	AGC Ser	CTA Leu	ATA Met	CGA Arg	AGA Stop
110	TTC Phe	GTC Val	TGC Cys	GGC Gly	TTA Leu	GTA Val	TGA Trp	GGA Gly
001	CCT Pro	ACT Thr	CAT His	AAT Asn	CCG Pro	ACG Thr	CAG Gln	AAG Lys
101	TCT Ser	GCT Ala	TAT Tyr	GAT Asp	TCG Ser	GCG Ala	TAG Stop	GAG Glu
011	CTT Leu	ATT Ile	CGT Arg	AGT Ser	CTG Leu	ATG Met	CGG Arg	AGG Stop
111	TTT Phe	GTT Val	TGT Cys	GGT Gly	TTG Leu	GTG Val	TGG Trp	GGG Gly

Fig. 9. The symmetrical arrangement of 20 amino acids and stop-codons in the bit-reversed matrix of 64 triplets. A case of the Vertebrate Mitochondrial Genetic Code is shown for comparison with Fig. 2. Identical colors mark the pairs of rows with identical compositions of amino acid and stop-codons.

indicates the genetic basis of the known facts of the relationship of physiological phenomena with hyperbolic geometry. Let us recall some. Articles on non-Euclidean geometry of the space of visual perception are published in different countries beginning with the pioneering work [Luneburg, 1950]. The author of the work, who carried out particularly careful experiments with the participation of 200 subjects and using 1300 visual patterns, summarized: "*Poincaré's model of hyperbolic space … shows fairly good agreement with the experimental results*" [Kienle, 1964].

The article on the results of 20 years of research by the author of the locomotions of many animals and humans states that the spatio-temporal organization of locomotions is associated with hyperbolic turns and the geometry of Minkowski [Smolyaninov, 2000]. In this regard, its author put forward the "locomotor theory of relativity" and wrote about the relativistic brain and relativistic biomechanics. A study of the regular rearrangements of phyllotaxis lattices during the growth of organisms led its author to the statement that living matter is structurally linked to the geometry of Minkowski [Bodnar, 1992, 1994].

One can add that each of the numeric matrices in Fig. 6 can be constructed from the α-matrix by the algorithm (1) based on its tensor product with the matrix [1, 1; 1, 1]:

$$[1,\ 1;1,\ 1]^{(n)} \otimes [1,1,-1,-1;\ 1,1,-1,-1;\ 1,-1,1,-1;\ -1,1,-1,1] \quad (1)$$

The matrix [1, 1; 1, 1] used in (1) is the matrix representation of a 2-dimensional hyperbolic number with unit coordinates. Deep structural connections of genetic informatics with 2^n-dimensional hyperbolic numbers are described in [Petoukhov, 2021a].

4. Biological dualism "probability-vs-determinism" and the stochastic organization of genomic DNA

Genetics as a science began with the discovery by G. Mendel of stochastic rules for the inheritance of traits in experiments on the crossing of organisms. Many processes in living bodies are stochastic and proceed against a background of noise or are accompanied by noise. For example, the expressions "gene noise" or "cell noise", which are known in biology, reflect the fact that even genetically identical cells within the same tissue exhibit different levels of protein expression, different sizes and structures due to the stochastic nature of interactions of individual molecules in cells [Chalancon et al., 2012; Horikawa et al., 2006; Raser and O'Shea, 2005]. This stochastic nature of genetic inheritance is manifested, in particular, in the fact that all people, even identical twins, have different fingerprints. In general, living bodies can be viewed as a mysterious phenomenon of a kind of block-stochastic organization, the structural features of which are subject to study. These features include genetically inherited multi-block structures of living bodies, in which individual blocks as a whole (globally) are similar to each other, although they differ significantly locally (like fingers in humans). It means that in living bodies stochastic-like phenomena are regularly connected with deterministic-like phenomena in some unknown ways. The article presented new phenomenological facts of the existence of regular connections between stochastic and deterministic properties at the level of the molecular-genetic system.

P. Jordan, who was one of the founders of quantum informatics and the author of the first article on quantum biology, stated: "*life's missing laws are the rules of chance and probability of the quantum world*" [McFadden and Al-Khalili, 2018]. In line with these phenomenological facts and Jordan's statement, the author studies possible probabilities rules in nucleotide sequences of single-stranded DNAs in eukaryotic and prokaryotic genomes. The first results of this study were described in articles [Petoukhov, 2020a, 2021a-d].

The mentioned results revealed the existence of universal rules of probabilities in percentage compositions of DNA sequences of genomes of higher and lower organisms. In particular, they generalize the well-known second Chargaff's rule about approximate equalities of the percent of adenine and thymine (%A ≈%T) and also the percent of cytosine and guanine (%C ≈ %G) in long single-stranded DNAs [Albrecht-Buehler, 2006; Chargaff, 1971; Prabhu, 1993].

The revealed universal probabilities rules of genomes provoke the following question: whether the probabilities rules of the stochastic organization of genomes are an independent class of genetic phenomena or are they structurally correlated with some other regular phenomena of the molecular-genetic system? This section describes the author's results about the multiple hidden connections of the named numeric rules of stochastic organization of genomes with the multilevel system of structured DNA alphabets and also with binary-oppositional molecular features of the nucleotides A, T, C, and G.

The presented results are based on the analysis of many genomic

DNA sequences, whose initial data were taken from the GenBank (https://www.ncbi.nlm.nih.gov/genbank/). In particular, the set of these analyzed genomes includes the following [Petoukhov, 2020]:

- 1) all 24 human chromosomes, which differ in their length, the quantity and type of genes, etc.;
- 2) all chromosomes of a fruit fly *Drosophila melanogaster*, all chromosomes of a house mouse *Mus musculus*, all chromosomes of a nematode *Caenorhabditis elegans*, all chromosomes of a plant *Arabidopsis thaliana*, and many other plants;
- 3) 19 bacterial genomes of different groups both from Bacteria and Archaea.

In this article, the stated results are demonstrated by numerical data regarding the single-stranded DNA sequence of the human chromosome №1, which contains about 250 million nucleotides A, T, C, and G.

Let us return to the DNA-alphabetical matrices in Fig. 1, which allow comfortable presentations of results of the study of probabilities rules in genomic DNAs. For this study, the author proposed the following effective method, which considers any long single-stranded DNA sequence as a multi-linguistic bunch of parallel *n*-texts, each of which is written in its *n*-plets alphabet (from the point of view of this method, any genomic DNA possesses many languages, is a polyglot). For example, the 1-textual representation shows a DNA sequence as a text written in the alphabet of 4 nucleotides (such as C-A-G-G-T-A- …); the 2-textual representation shows the same DNA sequence in a form of another text written in the alphabet of 16 duplets (such as CA-GG-TA- …); the 3-textual representation shows the same DNA sequence in a form of a text written in the alphabet of 64 triplets (such as CAG-GTA- …); and so on. The author has calculated the percent of each of the kinds of *n*-plets in corresponding *n*-textual representations of many genomic DNA sequences under $n = 1, 2, 3, 4$. For any analyzed DNA, the received percentage values of *n*-plets inside its *n*-texts are input into the appropriate cells of the family of *n*-alphabet matrices $[C, A; T, G]^{(n)}$ (such as in Fig. 1). As a result, numeric matrices of percentage values of *n*-plets appear, which characterize a stochastic organization of the analyzed genomic DNA. Fig. 10 shows such percentage matrices for the case of the DNA sequence of the human chromosome №1 (initial data of this DNA were taken from the GenBank: https://www.ncbi.nlm.nih.gov/nuccore/NC_000001.11).

At first glance, the sets of phenomenological percent in the different matrices in Fig. 10 have a chaotic character and are not numerically related to each other. In particular, the percentage of *n*-plets of the same letter composition depends on the sequence of letters and can differ several times: for example, %CG = 0.0103, and %GC = 0.0440.

But in this seeming chaos, there are many universal rules for *n*-plet groupings that are valid for all studied genomes. To clarify the unusualness of these genomic rules, consider, for example, the sequence ACTCGAGCAC of 10 nucleotides. Considering it as a text of 10 one-letter words, we have the text A-C-T-C-G-A-G-C-A-C, containing 4 nucleotides C, which gives %C = 0.4. Considering the same sequence in a form of a text of 5 two-letter words, we have the text AC-TC-GA-GC-AC, in which:

- 0 duplets with the first letter C, which gives the sum of their percentages Σ%CN = 0 (where N is any nucleotide A, T, C, G);
- 4 duplets with the second letter C, which gives the sum of their percentages Σ%NC = 0.8.

This example shows that, in the general case, in arbitrary sequences of nucleotides, the values of the probabilities %C, Σ%CN, Σ%NC are not at all equal. However, the stochastics of genomic DNAs obeys very special rules of a universal nature.

For example, *n*-texts of DNA of the human chromosome №1 give the following approximate equalities (2) of sums of *n*-plet percents in their compositions with high accuracy (though quantities and values of summands in these sums are essentially different):

$$\%C \approx \Sigma\%CN \approx \Sigma\%NC \approx \Sigma\%CNN \approx \Sigma\%NCN \approx \Sigma\%NNC \approx$$
$$\approx \Sigma\%CNNN \approx \Sigma\%NCNN \approx \Sigma\%NNCN \approx \Sigma\%NNNC \approx 0.2085;$$
$$\%G \approx \Sigma\%GN \approx \Sigma\%NG \approx \Sigma\%GNN \approx \Sigma\%NGN \approx \Sigma\%NNG \approx$$
$$\approx \Sigma\%GNNN \approx \Sigma\%NGNN \approx \Sigma\%NNGN \approx \Sigma\%NNNG \approx 0.2087;$$
$$\%A \approx \Sigma\%AN \approx \Sigma\%NA \approx \Sigma\%ANN \approx \Sigma\%NAN \approx \Sigma\%NNA \approx$$
$$\approx \Sigma\%ANNN \approx \Sigma\%NANN \approx \Sigma\%NNAN \approx \Sigma\%NNNA \approx 0.2910;$$
$$\%T \approx \Sigma\%TN \approx \Sigma\%NT \approx \Sigma\%TNN \approx \Sigma\%NTN \approx \Sigma\%NNT \approx$$
$$\approx \Sigma\%TNNN \approx \Sigma\%NTNN \approx \Sigma\%NNTN \approx \Sigma\%NNNT \approx 0.2918 \quad (2)$$

Correspondingly, for example, knowing a percent %C in a genomic DNA, it is possible to predict in this DNA with high accuracy values of the following sums of percentages: of 4 duplets having C at their first position; of 4 duplets having C at their second position; of 16 triplets having C at their first position; of 16 triplets having C at their second position; of 16 triplets having C at their third position; of 64 tetraplets having C at their first position; of 64 tetraplets having C at their second

	0	1
0	0.2085	0.2910
1	0.2918	0.2087

	00	01	10	11
00	0.05409	0.07274	0.05033	0.09504
01	0.07134	0.01031	0.07429	0.07137
10	0.06008	0.06312	0.04402	0.06008
11	0.09568	0.07286	0.05046	0.05419

	000	001	010	011	100	101	110	111
000	0.01385	0.01878	0.01524	0.01861	0.01183	0.01977	0.01447	0.03693
001	0.01853	0.00291	0.01789	0.02104	0.01622	0.00254	0.02375	0.01988
010	0.01758	0.01275	0.00251	0.00227	0.01317	0.01942	0.01441	0.02237
011	0.02009	0.02088	0.00259	0.00291	0.02388	0.01781	0.01614	0.01848
100	0.01588	0.01964	0.01103	0.01986	0.01255	0.01456	0.00962	0.01960
101	0.02226	0.00233	0.01939	0.01284	0.01437	0.00253	0.01327	0.01756
110	0.01972	0.01981	0.01457	0.01947	0.00956	0.01115	0.01256	0.01600
111	0.03725	0.01884	0.01988	0.01895	0.01445	0.01534	0.01185	0.01382

Fig. 10. Matrices of percent of *n*-plets in *n*-texts of the DNA of the human chromosome №1 ($n = 1, 2, 3$). The arrangement of the *n*-plets percentage values inside matrices corresponds to the *n*-plets arrangement in the tensor family of matrices in Fig. 1.

position; etc.

The following **positional rule of probabilities** in *n*-texts of long DNA sequences, which is a candidacy for the universal rule for genomes, can be formulated based on such results:

- All *n*-texts of a long DNA-sequence, each of which consists of a text of 4^n *n*-plets, has approximately the same sum of percentages of all those *n*-plets, which contain the considered nucleotide (C, G, A, or T) at a fixed *m*th position ($m \leq n$); here $n = 1, 2, 3, 4, \ldots$but is not too large compared to the length of DNA.

Rows	Percentage sums in matrix rows for 16 duplets
00	0.05409+0.07274+0.05033+0.09504 = **0.27220**
11	0.09568+0.07286+0.05046+0.05419 = **0.27319**
01	0.07134+0.01031+0.07429+0.07137 = **0.22731**
10	0.06008+0.06312+0.04402+0.06008 = **0.22730**

Rows	Percentage sums in matrix rows of 64 triplets
000	0.01385+0.01878+0.01524+0.01861+0.01183+0.01977+0.01447+0.03693 = **0.14946**
111	0.03725+0.01884+0.01988+0.01895+0.01445+0.01534+0.01185+0.01382 = **0.15039**
001	0.01853+0.00291+0.01789+0.02104+0.01622+0.00254+0.02375+0.01988 = **0.12275**
110	0.01972+0.01981+0.01457+0.01947+0.00956+0.01115+0.01256+0.01600 = **0.12285**
010	0.01758+0.01275+0.00251+0.00227+0.01317+0.01942+0.01441+0.02237 = **0.10448**
101	0.02226+0.00233+0.01939+0.01284+0.01437+0.00253+0.01327+0.01756 = **0.10456**
011	0.02009+0.02088+0.00259+0.00291+0.02388+0.01781+0.01614+0.01848 = **0.12277**
100	0.01588+0.01964+0.01103+0.01986+0.01255+0.01456+0.00962+0.01960 = **0.12273**

Rows	Percentage sums in matrix rows of 256 tetraplets
0000	0.0033+0.0055+0.0042+0.0044+0.0040+0.0056+0.0032+0.0070 + 0.0030+0.0042+0.0040+0.0053+0.0032+0.0059+0.0055+0.0149 = **0.0832**
1111	0.0150+0.0072+0.0055+0.0045 0.0059+0.0057+0.0043+0.0054+ 0.0055+0.0032+0.0040+0.0042+0.0032+0.0039+0.0030+0.0033 = **0.0838**
0001	0.0041+0.0010+0.0044+0.0058+0.0047+0.0010+0.0040+0.0044+ 0.0041+0.0005+0.0051+0.0054+0.0047+0.0006+0.0095+0.0071 = **0.0664**
1110	0.0073+0.0078+0.0038+0.0051+0.0037+0.0046+0.0042+0.0051+ 0.0030+0.0028+0.0029+0.0042+0.0023+0.0024+0.0030+0.0046 = **0.0668**
0010	0.0050+0.0029+0.0008+0.0006+0.0036+0.0039+0.0049+0.0059+ 0.0037+0.0032+0.0006+0.0006+0.0040+0.0070+0.0037+0.0066 = **0.0570**
1101	0.0077+0.0006+0.0063+0.0038+0.0049+0.0006+0.0045+0.0057+ 0.0038+0.0004+0.0032+0.0027+0.0042+0.0010+0.0034+0.0052 = **0.0580**
0011	0.0048+0.0058+0.0006+0.0009+0.0057+0.0047+0.0045+0.0058+ 0.0049+0.0044+0.0007+0.0007+0.0071+0.0057+0.0049+0.0047 = **0.0659**
1100	0.0051+0.0063+0.0034+0.0063+0.0041+0.0049+0.0031+0.0061+ 0.0023+0.0031+0.0017+0.0035+0.0031+0.0042+0.0023+0.0052 = **0.0647**
0100	0.0052+0.0057+0.0027+0.0038+0.0010+0.0006+0.0003+0.0006+ 0.0033+0.0045+0.0032+0.0063+0.0042+0.0049+0.0039+0.0078 = **0.0580**
1011	0.0068+0.0058+0.0006+0.0006+0.0070+0.0039+0.0032+0.0029+ 0.0037+0.0048+0.0006+0.0008+0.0041+0.0036+0.0036+0.0051 = **0.0571**
0101	0.0058+0.0009+0.0035+0.0028+0.0007+0.0003+0.0005+0.0008+ 0.0049+0.0005+0.0064+0.0035+0.0046+0.0007+0.0049+0.0059 = **0.0467**
1010	0.0057+0.0040+0.0005+0.0006+0.0030+0.0055+0.0026+0.0041+ 0.0032+0.0027+0.0006+0.0005+0.0025+0.0031+0.0032+0.0057 = **0.0475**
0110	0.0048+0.0036+0.0046+0.0051+0.0005+0.0004+0.0008+0.0006+ 0.0047+0.0056+0.0033+0.0050+0.0031+0.0037+0.0047+0.0057 = **0.0562**
1001	0.0057+0.0006+0.0051+0.0052+0.0037+0.0004+0.0056+0.0036+ 0.0047+0.0008+0.0033+0.0046+0.0030+0.0005+0.0046+0.0048 = **0.0562**
0111	0.0073+0.0044+0.0053+0.0058+0.0006+0.0010+0.0005+0.0010+ 0.0096+0.0040+0.0051+0.0044+0.0046+0.0047+0.0040+0.0041 = **0.0664**
1000	0.0046+0.0049+0.0042+0.0051+0.0024+0.0045+0.0028+0.0078+ 0.0030+0.0041+0.0029+0.0038+0.0023+0.0037+0.0029+0.0073 = **0.0663**

Fig. 11. The sums of percentages in pairs of rows with bit-inverted numberings from the percentage matrices of 16 duplets and 64 triplets (Fig. 10), and also 256 tetraplets in the case of DNA of the human chromosome №1. Bold frames highlight pairs of rows with bit-inverted numerations. In each frame, both amounts are practically the same, despite the strong difference in the values of the summands.

Now one can show other examples of universal equalities for the sums of percentages of n-plets in genomic DNAs, where binary oppositions also demonstrate their importance. Let us return to the tensor family of matrices of DNA-alphabets [C, A; T, G]$^{(n)}$ with binary numbered rows and columns (Fig. 1). It turns out that in these matrices any pair of rows and any pair of columns numbered with bit-inverted numbers (mutual inversion 0↔1) has, with high precision, the same sums of percentages of their *n*-plets within both rows of each pair, although separate percentages in these rows and columns differ significantly. Figs. 11 and 12 illustrate these equalities of percentage sums in such rows and columns from percentage matrices of 16 duplets and 64 triplets (from Fig. 10) and also of 256 tetraplets (from [Petoukhov,

Columns	Percentage sums in matrix columns for 16 duplets
00	0.05409+0.07134+0.06008+0.09568 = **0.28119**
11	0.09504+0.07137+0.06008+0.05419 = **0.28068**
01	0.07274+0.01031+0.06312+0.07286 = **0.21903**
10	0.05033+0.07429+0.04402+0.05046 = **0.21910**

Columns	Percentage sums in matrix columns in the case of 64 triplets
000	0.01385+0.01853+0.01758+0.02009+0.01588+0.02226+0.01972+0.03725 = **0.16516**
111	0.03693+0.01988+0.02237+0.01848+0.01960+0.01756+0.01600+0.01382 = **0.16464**
001	0.01878+0.00291+0.01275+0.02088+0.01964+0.00233+0.01981+0.01884 = **0.11594**
110	0.01447+0.02375+0.01441+0.01614+0.00962+0.01327+0.01256+0.01185 = **0.11607**
010	0.01524+0.01789+0.00251+0.00259+0.01103+0.01939+0.01457+0.01988 = **0.10310**
101	0.01977+0.00254+0.01942+0.01781+0.01456+0.00253+0.01115+ 0.01534 = **0.10312**
011	0.01861+0.02104+0.00227+0.00291+0.01986+0.01284+0.01947+0.01895 = **0.11595**
100	0.01183+0.01622+0.01317+0.02388+0.01255+0.01437+0.00956+0.01445 = **0.11603**

Columns	Percentage sums in matrix columns for 256 tetraplets
0000	0.0033+0.0041+0.0050+0.0048+0.0052+0.0058+0.0048+0.0073 + 0.0046+0.0057+0.0057+0.0068+0.0051+0.0077+0.0073+0.0150 = **0.0982**
1111	0.0149+0.0071+0.0066+0.0047+0.0078+0.0059+0.0057+0.0041 + 0.0073+0.0048+0.0057+0.0051+0.0052+0.0052+0.0046+0.0033 = **0.0980**
0001	0.0055+0.0010+0.0029+0.0058+0.0057+0.0009+0.0036+0.0044 + 0.0049+0.0006+0.0040+0.0058+0.0063+0.0006+0.0078+0.0072 = **0.0670**
1110	0.0055+0.0095+0.0037+0.0049+0.0039+0.0049+0.0047+0.0040 + 0.0029+0.0046+0.0032+0.0036+0.0023+0.0034+0.0030+0.0030 = **0.0671**
0010	0.0042+0.0044+0.0008+0.0006+0.0027+0.0035+0.0046+0.0053 + 0.0042+0.0051+0.0005+0.0006+0.0034+0.0063+0.0038+0.0055 = **0.0555**
1101	0.0059+0.0006+0.0070+0.0057+0.0049+0.0007+0.0037+0.0047 + 0.0037+0.0005+0.0031+0.0036+0.0042+0.0010+0.0024+0.0039 = **0.0556**
0011	0.0044+0.0058+0.0006+0.0009+0.0038+0.0028+0.0051+0.0058 + 0.0051+0.0052+0.0006+0.0006+0.0063+0.0038+0.0051+0.0045 = **0.0604**
1100	0.0032+0.0047+0.0040+0.0071+0.0042+0.0046+0.0031+0.0046 + 0.0023+0.0030+0.0025+0.0041+0.0031+0.0042+0.0023+0.0032 = **0.0602**
0100	0.0040+0.0047+0.0036+0.0057+0.0010+0.0007+0.0005+0.0006 + 0.0024+0.0037+0.0030+0.0070+0.0041+0.0049+0.0037+0.0059 = **0.0555**
1011	0.0053+0.0054+0.0006+0.0007+0.0063+0.0035+0.0050+0.0044 + 0.0038+0.0046+0.0005+0.0008+0.0035+0.0027+0.0042+0.0042 = **0.0555**
0101	0.0056+0.0010+0.0039+0.0047+0.0006+0.0003+0.0004+0.0010 + 0.0045+0.0004+0.0055+0.0039+0.0049+0.0006+0.0046+0.0057 = **0.0476**
1010	0.0040+0.0051+0.0006+0.0007+0.0032+0.0064+0.0033+0.0051 +
	0.0029+0.0033+0.0006+0.0006+0.0017+0.0032+0.0029+0.0040 = **0.0476**
0110	0.0032+0.0040+0.0049+0.0045+0.0003+0.0005+0.0008+0.0005 + 0.0028+0.0056+0.0026+0.0032+0.0031+0.0045+0.0042+0.0043= **0.0490**
1001	0.0042+0.0005+0.0032+0.0044+0.0045+0.0005+0.0056+0.0040 + 0.0041+0.0008+0.0027+0.0048+0.0031+0.0004+0.0028+0.0032 = **0.0488**
0111	0.0070+0.0044+0.0059+0.0058+0.0006+0.0008+0.0006+0.0010 + 0.0078+0.0036+0.0041+0.0029+0.0061+0.0057+0.0051+0.0054 = **0.0668**
1000	0.0030+0.0041+0.0037+0.0049+0.0033+0.0049+0.0047+0.0096 + 0.0030+0.0047+0.0032+0.0037+0.0023+0.0038+0.0030+0.0055 = **0.0674**

Fig. 12. The sums of percentages in pairs of columns with bit-inverted numberings from the percentage matrices of 16 duplets and 64 triplets (Fig. 10), and also 256 tetraplets in the case of DNA of the human chromosome №1. Bold frames highlight pairs of columns with bit-inverted numerations. In each frame, both amounts are practically the same, despite the strong difference in the values of the summands.

2021b,d]) in the case of DNA of the human chromosome №1.

The described rules can be termed rules of bit-inverted numerations. They testify that the stochastic organization of genomic DNAs is closely related to features of the deterministic system of DNA *n*-plet alphabets. Such discovered interrelations between stochastic and deterministic features in the molecular-genetic system seem to be useful for a deeper understanding of the interrelations of stochastic and deterministic properties in genetically inherited physiological systems. The received results give new abilities to develop quantum-information modeling genetic phenomena and for the creation of new approaches for artificial intelligence systems.

The whole set of equality relations between the percentage groupings of *n*-plets in genomic DNA *n*-texts, revealed by the author, indicates that the stochastic organization of genomic DNAs is the highly limited stochastic organization with many internal numeric interrelations among summary percentages of separate groupings.

The author believes that the genetic phenomena described in this article are closely connected with the published concept of multi-resonance genetics [Petoukhov, 2016; Petoukhov and Petukhova, 2017].

5. Some concluding remarks

The described author's results provide new opportunities for algebraic modeling of genetic structures and genetically inherited physiological phenomena, including from the standpoint of algebraic holography and formalisms of quantum informatics. They are correlated with the ideas of different authors about living beings as molecular quantum computers and can be useful for deeper understanding the cell language [Ji, 2017].

These results show new facets of the relationship of inherited physiological phenomena with the structures of genetic informatics. In particular, the known facts of conjugation of physiological phenomena with hyperbolic geometry exist in parallel with the connection of structured DNA alphabets with Poincaré's disk model of hyperbolic geometry.

The data presented indicate the effectiveness of the author's method of oligomeric sums when considering long DNA sequences as a bunch of parallel texts written in different *n*-plets alphabets. Figuratively speaking, in this consideration, any genomic DNA possesses many languages, is a polyglot! This method has led to the identification of universal rules and symmetries of the stochastic organization of DNAs in eukaryotic and prokaryotic genomes. These rules indicate limited stochasticity of DNA genomes, in which probabilities coexist with many deterministic relationships. They are discussed concerning the general problem of the biological dualism "probability-vs-determinism".

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

Abbott, D., Davies, P.C.W., Pati, A.K. (Eds.), 2008. *Quantum Aspects of Life*, Foreword by Sir Roger Penrose (2008). -13: 978-1-84816-253-2.

Albrecht-Buehler, G., 2006. Asymptotically increasing compliance of genomes with Chargaff's second parity rules through inversions and inverted transpositions. Proc. Natl. Acad. Sci. U.S.A. 103 (47), 17828–17833. https://doi.org/10.1073/pnas.0605553103.

Alexits, G., 1961. Convergence Problems of Orthogonal Series. Pergamon.

Belousov, L.V., 2015. Morphomechanics of Development. Springer International Publishing Switzerland. https://doi.org/10.1007/978-3-319-13990-6.

Bodnar, O.Ya, 1992. The Geometry of Phyllotaxis, №9. Reports of the Academy of Sciences of Ukraine, pp. 9–15.

Bodnar, O.Ya, 1994. Golden Ratio and Non-euclidean Geometry in Nature and Art. Lviv: Publishing House, Sweet.

Chalancon, G., Ravarani, ChN.J., Balaji, S., Martinez-Arias, A., Aravind, L., Jothi, R., Madan Babu, M., May 2012. Interplay between gene expression noise and regulatory network architecture. Trends Genet. 28 (5), 221–232. https://doi.org/10.1016/j.tig.2012.01.006.

Chargaff, E., 1971. Preface to a Grammar of Biology: a hundred years of nucleic acid research. Science 172, 637–642.

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

Frank-Kamenetskii, M.D., 1988. The Most Important Molecule. Nauka, Moscow (in Russian).

Horikawa, K., Ishimatsu, K., Yoshimoto, E., Kondo, S., Takeda, H., June 2006. Noise-resistant and synchronized oscillation of the segmentation clock. Nature 441 (7094), 719–723. https://doi.org/10.1038/nature04861.

Igamberdiev, A.U., 1993. Quantum mechanical properties of biosystems: a framework for complexity, structural stability, and transformations. *Biosystems*, v. 31 (1), 65–73.

Ji, S., 2017. The Cell Language Theory: Connecting Mind and Matter. WSPC (Europe), p. 610. -13: 978-1848166608.

Kalat, J.W., 2016. Biological Psychology, 12 ed. Australia, ISBN 9781305105409. OCLC 898154491.

Karp, A.H., 1996. Bit reversal on uniprocessors. SIAM Rev. 38 (1), 1–26. https://doi.org/10.1137/1038001. MR 1379039.

Karzel, H., Kist, G., 1985. Kinematic algebras and their geometries. In: Kaya, R., Plaumann, P., Strambach, K. (Eds.), Rings and Geometry, ISBN 90-277-2112-2, pp. 437–509.

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

Lashley R.S. Brain Mechanisms and Intelligence. University of Chicago Press. (January 1, 1929). ISBN-10: 1135563772, ISBN-13 : 978-1135563776.

Liberman, E.A., Minina, S.V., 1996. Cell molecular computers and biological information as the foundation of nature's laws. Biosystems 38, 173–177.

Liberman, E.A., Minina, S.V., Shklovskii-Kordi, N.E., 2001. Problems combining biology, physics, and mathematics. Ideas of the new science. Biophysics 46 (4.C), 767.

Luneburg, R., 1950. The metric of binocular visual space. J. Opt. Soc. Am. A 40, 627–642.

Lyons, R., 2010. Understanding Digital Signal Processing, third ed. Pearson. ISBN-10: 0137027419, ISBN-13: 978-0137027415.

Matsuno, K., Paton, R.C., 2000. Is there a biology of quantum information? Biosystems 55, 39–46.

Nielsen, M.A., Chuang, I.L., 2010. Quantum Computation and Quantum Information. Cambridge Univ. Press, New York. https://doi.org/10.1017/CBO9780511976667.

Pastawski, F., Yoshida, B., Harlow, D., Preskill, J., 2015. Holographic quantum error-correcting codes: toy models for the bulk/boundary correspondence. J. High Energy Phys. 149 https://doi.org/10.1007/JHEP06(2015)149. https://link.springer.com/article/10.1007%2FJHEP06%282015%29149#citeas.

Petoukhov, S.V., 2020. The Rules of Long DNA-Sequences and Tetra-Groups of Oligonucleotides, 6th version. arXiv:1709.04943v6.

Petoukhov, S.V., 2021. Algebraic rules for the percentage composition of oligomers in genomes. Preprints 2021 2021010360, 84. https://doi.org/10.20944/preprints202101.0360.v3, 3rd version, (2021c).

Petoukhov, S.V., 2021a. Modeling inherited physiological structures based on hyperbolic Numbers. Biosystems 199, 104285. https://doi.org/10.1016/j.biosystems.2020.104285. ISSN 0303-2647.

Petoukhov, S.V., 2021b. Algebraic harmony and probabilities in genomes. Long-range coherence in quantum code biology. *Biosystems*, v. 209, 104503 https://doi.org/10.1016/j.biosystems.2021.104503.

Petoukhov, S.V., 2021d. Tensor rules in the stochastic organization of genomes and genetic stochastic resonance in algebraic biology. Preprints 2021, 41. https://doi.org/10.20944/preprints202110.0093.v1, 2021100093.

Petoukhov, S.V., 2022. The stochastic organization of genomes and the doctrine of energy-information evolution based on bio-antenna arrays. Biosystems 104712. https://doi.org/10.1016/j.biosystems.2022.104712. ISSN 0303-2647.

Petoukhov, S.V., Petukhova, E.S., 2017. In: Burgin, M., Hofkirchner, W. (Eds.), Resonances and the Quest for Transdisciplinarity. - *Information Studies and the Quest for Transdisciplinarity*. World Scientific, pp. 467–487.

Petoukhov, S.V., Petukhova, E.S., Svirin, V.I., 2019. Symmetries of DNA alphabets and quantum informational formalisms. Symmetry: Culture Sci. 30 (No. 2), 161–179. https://doi.org/10.26830/symmetry_2019_2_161.

Prabhu, V.V., 1993. Symmetry observation in long nucleotide sequences. Nucleic Acids Res. 21, 2797–2800.

Preskill, J., 16 March 2016. Stability, Topology, Holography: the Many Facets of Quantum Error Correction. Presentation at American Physical Society. http://theory.caltech.edu/~preskill/talks/APS-March-2016-preskill.pdf.

Pribram, K., 1971. Languages of the Brain; Experimental Paradoxes and Principles in Neuropsychology. Prentice-Hall, Englewood Cliffs, N.J.

Raser, J.M., O'Shea, E.K., 2005. Noise in gene expression: origins, consequences, and control. Science 309 (5743), 2010–2013. https://doi.org/10.1126/science.1105891.

Rumer, YuB., 1968. Codon systematization in the genetic code. Dokl. Akad. Nauk SSSR 183 (1), 225–226.

Shishmintsev, S., 2012. Holographic properties of a bit-reversal permutation (in Russian). https://habrahabr.ru/post/155471/.

Shiva Meucci, 2020. Could a hologram from the holographic principle bend spacetime? https://www.quora.com/profile/Shiva-Meucci. https://www.quora.com/Could-a-hologram-from-the-holographic-principle-bend-spacetime/answer/Shiva-Meucci.

Smolyaninov, V.V., 2000. Spatio-temporal problems of locomotion control. Usp. Fiz. Nauk 170 (10), 1063–1128. https://doi.org/10.3367/UFNr.0170.200010b.1063.

Talbot, M., 1996. The Holographic Universe. HarperCollins Publishers Ltd., p. 352

Yang, Q., Ellis, J., Mamakani, K., Ruskey, F., 2013. In-place permuting and perfect shuffling using involutions. Inf. Process. Lett. 113 (10–11), 386–391. https://doi.org/10.1016/j.ipl.2013.02.017. MR 3037467.