CYCLIC PHYSIOLOGY, CYCLIC CODES AND ALGEBRAIC-LOGIC PECULIARITIES OF THE GENETIC CODING SYSTEM, QUANTUM BIOINFORMATICS AND ANCIENT INDIAN PHILOSOPHY

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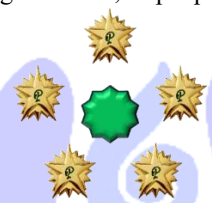

Five Star Paper

Abstract

This article presents the results of the author's research on the structural relationship of the genetic coding system and bioinformatics with cyclic and algebraic-logical features of genetically inherited physiological systems. There is shown that genetic informatics are connected with cyclic Gray codes, Karnaugh matrices and Boolean algebra of logic. The statement on the existence of a genetic n-plet code of Boolean functions, which is important for understanding the inherited logic of interactions between body parts, has been put forward and argued. Universal rules of statistical peculiarities of nucleotide sequences in single-stranded DNAs in genomes of higher and lower organisms are described. Revealing these rules gives pieces of evidence that harmony of living bodies is based on laws of probabilities in information genetic sequences. The presented results are discussed in connections with problems of evolutionary biology, quantum bioinformatics, and the doctrine of energy-information evolution based on bio-antenna arrays. Structural parallelisms between molecular genetic systems and provisions of ancient Indian philosophy are considered.

Keywords: genomic DNA, genetic coding, binary-opposition, cyclic physiology, Gray code, dichotomy, fractal, probability, quantum bioinformatics, Boolean functions.

1. Introduction

The creators of quantum mechanics, P. Jordan and E. Schrödinger, pointed out the key difference between living bodies and inanimate ones: inanimate objects are controlled by the average random movement of their millions of particles and the movement of individual particles is not significant for the whole object; on the contrary, in a living organism, selected – genetic – molecules have a dictatorial influence on the entire organism due to quantum enhancement (see the history of "quantum biology" [https://doi.org/10.1098/rspa.2018.0674]). In accordance with this, to reveal the secrets and patents of living nature, it is necessary to study the universal rules of DNA informatics. This article presents the results of the author's research on the structural relationship of the genetic coding system and bioinformatics with cyclic and algebraic-logical features of genetically inherited physiological systems. Any living organism is a huge chorus of genetically inherited cyclic processes. Since ancient times, chrono-medicine has believed that all diseases are the result of a violation of this coordination. Let me remind some examples on cyclic nature of bio-bodies. Our breathing, cardiac activity, locomotion, etc. are cyclical. Our body's proteins are involved in continuous life-death cycles of their assembling and disassembling into amino acids. For example, the half-life of the hormone insulin is 6-9 minutes, etc. In other words, genetically inherited parts of our body are constantly dying and reborn. Considering such phenomena, the renowned physiologist A.G. Gurvich claimed: "The main problem in biology is maintaining shape while constantly renewing the substrate" [Gurvich, 1977]. The energy costs for these cyclic events are taken from the universal source of energy for all biochemical processes of all living organisms on Earth: ATP (adenosine triphosphoric acid). The lifetime of one ATP molecule in humans is less than one minute. During the day, one ATP molecule goes through an average of 2000-3000 cycles of resynthesis (the human body synthesizes about 40 kg of ATP per day). Another illustrative example of cyclic organization in life is the metamorphosis of butterflies, consisting of the stages "butterfly-egg-caterpillar-pupa-butterfly". It is characteristic that no one teaches the butterfly how to get out of the pupa and begin to fly, but it gets out and begins to fly due to inherited cyclic movements of its wings (cyclic genetic biomechanics). Everything necessary for this is already available in its genomic code informatics. Many such facts suggest that the genetic coding system ensures the inheritance of coded cyclic processes since this system itself is based on some cyclic codes. But which of the many types of cyclic codes, known in mathematics,

corresponds to the structural organization of the genetic coding system? I have obtained some pieces of evidence about the important role of the family of cyclic Gray codes for the modeling of the genetic coding system. Received results allow me to introduce the following effective model postulate: living organisms are cyclically coded cyclic entities (see detail in [Petoukhov, 2024a,b]. A binary Gray code of order n is a sequence of 2^n n-bit numbers in which any two adjacent numbers differ by exactly one digit (Hamming distance between them is 1) [Beletsky, 2003; Gardner, 1986]. Gray codes of different orders form a hierarchical family, since a Gray code of order "n" is obtained from a Gray code of order "n-1" algorithmically. Gray codes are widely used in technology for information noise immunity, etc. For example, they are used in position controllers of rotating objects (encoders). Numbers in the Gray code are fundamentally different from binary numbers, although they also consist of sequences of zeros and ones. The decimal number 3 in binary notation is 011, but in Gray code it is 010.

Table 1. Comparison of three kinds of numbers: decimal, binary, and Gray code

Decimal	Binary	Gray code
0	000	000
1	001	001
2	010	011
3	011	010
4	100	110
5	101	111
6	110	101
7	111	100

The Genetic coding system, cyclic Gray codes, and Karnaugh matrices of Boolean algebra

In DNA, the alphabet of 4 nucleotides A (adenine), C (cytosine), G (guanine), and T (thymine) is the carrier of a system of binary-oppositional traits (or molecular indicators):

1. two of these nucleotides are purines (A and G), which have 2 rings in the molecule, and the other two (C and T) are pyrimidines, containing 1 ring, which gives a representation **C = T = 0, A = G = 1**;
2. two of these nucleotides are keto molecules (T and G), and the other two (C and A) are amino molecules, which gives a representation **C = A = 0, T = G = 1**.

Because of this, DNA alphabets of 4 letters, 16 duplets and 64 triplets are presented in the form of square tables, the columns of which are numbered with the opposition indicators "pyrimidine or purine" (**C = T = 0, A = G = 1**), and the rows - with the opposition indicators "amino or keto" (**C = A = 0, T = G = 1**). In these genetic tables, rows and columns are numbered by ordered numbers of n-bit Gray codes, similar to Karnaugh maps, a well-known method for simplifying Boolean algebra expressions. Such numeration was applied specially to search a possible communication of the genetic code system with Boolean algebra of logic.

	0	1
0	C 00 (0)	A 01 (1)
1	T 10 (3)	G 11 (2)

	00 (0)	01 (1)	11 (2)	10 (3)
00	CC 0000 (0)	CA 0001 (1)	AA 0011 (2)	AC 0010 (3)
01	CT 0100 (7)	CG 0101 (6)	AG 0111 (5)	AT 0110 (4)
11	TT 1100 (8)	TG 1101 (9)	GG 1111 (10)	GT 1110 (11)
10	TC 1000 (15)	TA 1001 (14)	GA 1011 (13)	GC 1010 (12)

	000 (0)	001 (1)	011 (2)	010 (3)	110 (4)	111 (5)	101 (6)	100 (7)
000 (0)	CCC 000000 (0)	CCA 000001 (1)	CAA 000011 (2)	CAC 000010 (3)	AAC 000110 (4)	AAA 000111 (5)	ACA 000101 (6)	ACC 000100 (7)
001 (1)	CCT 001000 (15)	CCG 001001 (14)	CAG 001011 (13)	CAT 001010 (12)	AAT 001110 (11)	AAG 001111 (10)	ACG 001101 (9)	ACT 001100 (8)
011 (2)	CTT 011000 (16)	CTG 011001 (17)	CGG 011011 (18)	CGT 011010 (19)	AGT 011110 (20)	AGG 011111 (21)	ATG 011101 (22)	ATT 011100 (23)
010 (3)	CTC 010000 (31)	CTA 010001 (30)	CGA 010011 (29)	CGC 010010 (28)	AGC 010110 (27)	AGA 010111 (26)	ATA 010101 (25)	ATC 010100 (24)
110 (4)	TTC 110000 (32)	TTA 110001 (33)	TGA 110011 (34)	TGC 110010 (35)	GGC 110110 (36)	GGA 110111 (37)	GTA 110101 (38)	GTC 110100 (39)
111 (5)	TTT 111000 (47)	TTG 111001 (46)	TGG 111011 (45)	TGT 111010 (44)	GGT 111110 (43)	GGG 111111 (42)	GTG 111101 (41)	GTT 111100 (40)
101 (6)	TCT 101000 (48)	TCG 101001 (49)	TAG 101011 (50)	TAT 101010 (51)	GAT 101110 (52)	GAG 101111 (53)	GCG 101101 (54)	GCT 101100 (55)
100 (7)	TCC 100000 (63)	TCA 100001 (62)	TAA 100011 (61)	TAC 100010 (60)	GAC 100110 (59)	GAA 100111 (58)	GCA 100101 (57)	GCC 100100 (56)

Fig. 1. Arrangements of 4 monoplets, 16 duplets and 64 triplets are shown in the genetic Karnaugh matrices with numbering of columns and rows according to Gray codes (the decimal equivalents of Gray numbers are given in parentheses).

In such tables, all monoplets, duplets and triplets automatically occupy a strictly individual place (Fig. 1). Each cell in these matrices, as well as the n-plet in it, is numbered by concatenation of the Gray code numberings of its row and column. We conventionally call such square tables as "genetic Karnaugh matrices".
How are the amino acids and stop codons they encode located in the matrix of 64 triplets constructed in this way? The number of options for the arrangement of amino acids with their repetitions to fill the entire (8*8)-matrix is immeasurable: >>10^100 (for comparison, in physics, the lifetime of the Universe is estimated at 10^17 seconds). Will this arrangement be chaotic or will it suddenly turn out to be naturally symmetrical? Fig. 2 shows the case of the Vertebrate Mitochondrial Genetic Code, which is considered in science to be the most ancient and symmetrical among the genetic code dialects.

It turns out that from the ocean of possibilities, nature chose a regular and symmetric variant of the repetition and arrangement of amino acids and stop codons in this matrix of 64 triplets (Fig. 2). The shown matrix of encoded amino acids and stop-codons consists of pairs of adjacent rows 0-1, 2-3, 4-5, 6-7, identical in composition of amino acids and stop-codons, shown in color. For example, rows 0 and 1 contain the same composition and arrangement of red amino acids **Pro**, **Gln**, **His**, **Asn**, **Lys**, **Thr**. The rows in each of the indicated pairs 0-1, 2-3, 4-5, 6-7 with repetition of amino acids and stop codons in them differ in that the sequence of 6-bit numbers of their 16 cells forms a cyclic sequence with unit Hamming distance between adjacent cells, if you read the binary Gray numbers of the cells in the top of the two rows from left to right, and the cell numbers of the second row reversely from right to left.

	000 (0)	001 (1)	011 (2)	010 (3)	110 (4)	111 (5)	101 (6)	100 (7)
000 (0)	CCC **Pro** 000000 (0)	CCA **Pro** 000001 (1)	CAA **Gln** 000011 (2)	CAC **His** 000010 (3)	AAC **Asn** 000110 (4)	AAA **Lys** 000111 (5)	ACA **Thr** 000101 (6)	ACC **Thr** 000100 (7)
001 (1)	CCT **Pro** 001000 (15)	CCG **Pro** 001001 (14)	CAG **Gln** 001011 (13)	CAT **His** 001010 (12)	AAT **Asn** 001110 (11)	AAG **Lys** 001111 (10)	ACG **Thr** 001101 (9)	ACT **Thr** 001100 (8)
011 (2)	CTT **Leu** 011000 (16)	CTG **Leu** 011001 (17)	CGG **Arg** 011011 (18)	CGT **Arg** 011010 (19)	AGT **Ser** 011110 (20)	AGG **Stop** 011111 (21)	ATG **Met** 011101 (22)	ATT **Ile** 011100 (23)
010 (3)	CTC **Leu** 010000 (31)	CTA **Leu** 010001 (30)	CGA **Arg** 010011 (29)	CGC **Arg** 010010 (28)	AGC **Ser** 010110 (27)	AGA **Stop** 010111 (26)	ATA **Met** 010101 (25)	ATC **Ile** 010100 (24)
110 (4)	TTC **Phe** 110000 (32)	TTA **Leu** 110001 (33)	TGA **Trp** 110011 (34)	TGC **Cys** 110010 (35)	GGC **Gly** 110110 (36)	GGA **Gly** 110111 (37)	GTA **Val** 110101 (38)	GTC **Val** 110100 (39)
111 (5)	TTT **Phe** 111000 (47)	TTG **Leu** 111001 (46)	TGG **Trp** 111011 (45)	TGT **Cys** 111010 (44)	GGT **Gly** 111110 (43)	GGG **Gly** 111111 (42)	GTG **Val** 111101 (41)	GTT **Val** 111100 (40)
101 (6)	TCT **Ser** 101000 (48)	TCG **Ser** 101001 (49)	TAG **Stop** 101011 (50)	TAT **Tyr** 101010 (51)	GAT **Asp** 101110 (52)	GAG **Glu** 101111 (53)	GCG **Ala** 101101 (54)	GCT **Ala** 101100 (55)
100 (7)	TCC **Ser** 100000 (63)	TCA **Ser** 100001 (62)	TAA **Stop** 100011 (61)	TAC **Tyr** 100010 (60)	GAC **Asp** 100110 (59)	GAA **Glu** 100111 (58)	GCA **Ala** 100101 (57)	GCC **Ala** 100100 (56)

Fig. 2. The symmetrical arrangement of amino acids and stop-codons in the Karnaugh matrix of 64 triplets. The case of the Vertebrate Mitochondrial Genetic Code is shown

Cells in Karnaugh maps are known as minterms, while each cell value represents the corresponding output value of the Boolean function. The presented genetic facts show one of examples of a deep connection of the DNA n-plets alphabets with systems of Boolean functions. This connection is important taking into account the following well-known academic statement significant to understand and simulate biological and artificial intelligence: "*without mathematical logic, discussions about whether a machine can think lose all ground... and the urgent problem of creating artificial intelligence becomes meaningless*" [Yaglom, 1980].

It is characteristic that the physiology of active tissues is based on the fundamental binary law "all-or-none": a nerve cell and a muscle unit give only "yes" or "no" answers to the actions of various stimuli. They do not respond to subthreshold stimuli, but to suprathreshold stimuli they respond with full amplitude. This is similar to the operation of computer triggers [Kalat, 2016]. Briefly note the following. If in the genetic Karnaugh matrix of 64 triplets (Fig. 1), the cells of which are numbered with members of the 6-bit Gray code, we replace the numerical members of the Gray code with the corresponding decimal numbers, then the entire numerated sequence of cells turns out to be a sequence of even and odd numbers from 0 to 63. Designating the cells with even numbers, for example, in black, and the cells with odd numbers in white, we obtain a black-and-white mosaic of a chessboard with diagonal dispositions of families of cells of each color; this chessboard mosaic is represented as an important

element in provisions of ancient Indian philosophy, as will be described at the end of the article when considering the structural parallelisms between these ancient philosophical provisions and the molecular genetic system.

Mutual replacement of binary symbols 0↔1 in the Gray code (complementarity operation) generates a complementary cyclic sequence with a shifted order of terms and a unit Hamming distance between neighboring terms. The application of this operation of complementarity to a new sequence generates the original Gray code, associated with the property of self-duplication and multiplication of DNA (Table 2).

Table 2. Mutual replacement of binary symbols 0↔1 in the Gray code.

Example of initial Gray code:	**000-001-011-010-110-111-101-100**
Its complementary Gray code:	**111-110-100-101-001-000-010-011**

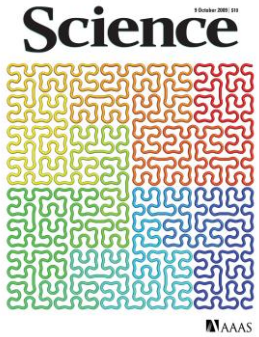

Fig. 3. The Hilbert curve reproduces the spatial packaging of chromatin in the genome (from the cover of the journal Science, vol. 326, 5950, 2009).

Based on analogies between the structural properties of the genetic coding system and Gray codes, I am developing a family of models of cyclic genetic biomechanics, using symmetry principles and my model postulate: living organisms are cyclically coded cyclic entities [Petoukhov, 2024a,b]. In particular, in these models, the well-known fact is used that Gray codes are closely related to the fractal Hilbert curve, which allows you to "discretize" any space, creating a convenient coordinate system in it. This relates to the problem of how genetic information recorded on one-dimensional DNA strands determines the three-dimensional morphology of living bodies. It is important that the spatial packaging of chromatin in the genome turns out to correspond to the Hilbert curve, which is its polymer fractal 3D globule, free of nodes and featured on the cover of the journal "Science" (Fig. 4). It should be added that Gray codes are closely related to the following tools and scientific fields [Petoukhov, He, 2023]: complete orthogonal systems of Walsh functions; Harmuth sequency analysis; spectral logic, which are widely used in communication technology, aerospace image analysis, logical holography on Walsh functions [Morita, Sakurai, 1973]; Walsh antennas with unique properties; dyadic clocks and many other technologies and concepts (see a review [Soroko, 1979]). This relationship is useful for developing new approaches to modeling hereditary phenomena and artificial intelligence problems [Petoukhov, 2024a].

For example, these connections are used in the author's doctrine of energy-information evolution based on bio-antenna arrays [Petoukhov, 2022; Petoukhov, He, 2023]. This doctrine gives new approaches to many inherited biological phenomena and functional abilities of living organisms, including intellectual abilities of echolocation of dolphins and bats (Fig. 4), harmony behavior of many separate parts of the whole body, etc. It also connects biological phenomena with theory and engineering practices of digital antenna arrays (frequently named in literature as Smart Antennas), which are used in millions of units worldwide. Modern science sees great prospects with such nanoantenna arrays, which are expected to lead to revolutionary changes in computer technology (photonics) and energy (efficient use of solar energy) and which are needed to create quantum computers and wireless networks on chips. Study of genetically inherited bioantenna array systems and their wave functioning, taking into account cyclic Gray codes and facts of cyclic physiology, is leading to discovery of living nature patents for use in technology.

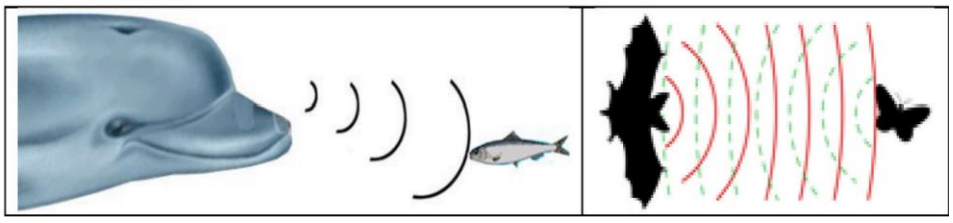

Fig. 4. Illustration of innate echolocation abilities in dolphins and bats associated with inherited bio antenna array systems (from [Petoukhov, He, 2023, Chapter 6])

Some results of my study indicate that DNA nucleotide sequences encode not only amino acid sequences in proteins, but also inherited logical connections. They indicate that the genetic coding system has two different types of code: 1) the long-known 3-plet code of amino acid sequences; 2) the n-plet code of Boolean functions. Taking into account the genetic Boolean code allows us to better understand, for example, the innate ability of a butterfly to emerge from its chrysalis and begin to fly, which is impossible without the logical coordination of millions of its neurons and muscle units.

Taking into account the claimed genetic Boolean n-plet code provides an explanation for a number of difficult questions in genetic informatics, such as:

1. why the overwhelming majority of genomic DNA sequences do not encode any proteins;
2. why the degeneracy of the genetic code of amino acid sequences is needed, in which 20 amino acids are encoded by 64 triplets;
3. what causes the existence of "jumping" genes;
4. why DNA and RNA alphabets are structurally related to dyadic groups of binary numbers and Walsh functions, etc. (for explanations, see the preprint [Petoukhov, 2024a].

The presented identification of structural links between the genetic coding system and the algebra of logic brings to mind the founder of mathematical logic, Jeorge Boole, and his book "An Investigation of the Laws of Thought on Which the Mathematical Theories of Logic and Probability Are Based" (1854). The mathematical logic proposed by Boole was considered useless for practice for decades, but now computer technologies, the Internet, variants of artificial intelligence, etc., are based on it. The future of algebraic biology, in our opinion, is also connected with Boole's creation.

2. Universal Statistical Rules of Genomic DNAs and Quantum Bioinformatics

One of the founders of quantum mechanics and the author of the first article on quantum biology, P. Jordan, asserted that the laws of living organisms missed by science are the laws of probabilities [McFadden J., Al-Khalili, 2018]. In our researches, using the author's method of hierarchy of binary statistics, a holistic system of universal rules of statistical organization of DNA-informatics in genomes of higher and lower organisms [Petoukhov, 2024a,b; Petoukhov, he, 2023]. These rules speak of the fractal-dichotomous organization of the probabilities system in genomes and lead to ideas of fractal quantum bioinformatics. They were confirmed in the author's laboratory on a representative set of single-stranded genomic DNAs of higher and lower organisms, the initial data for which were taken from the publicly available Genbank.

The obtained results draw attention to the fact that the harmonic organization of living matter with its genetic inheritance is based on an algebraic harmony of probabilities of a special stochastic-deterministic type and is connected with a family of dichotomous fractals of probabilities. These dichotomous fractals of probabilities can be represented as multilayer fractal quantum-information networks of n-qubits $|\Psi_n>$, dichotomously interconnected by the probabilities of their computational basis states (represented by code words of cyclic Gray codes) (Fig. 5). A change in the probability amplitudes in one n-qubit layer causes a restructuring of all n-qubit layers of this holistic quantum-information network. Accounting for this harmony of genomic probabilities enables the development of: quantum bioinformatics of multilevel poly-qubit systems; approaches to artificial intelligence of the genomorphic type and new genetic algorithms; new methods and tools for the analysis of genes and other bioinformatic objects.

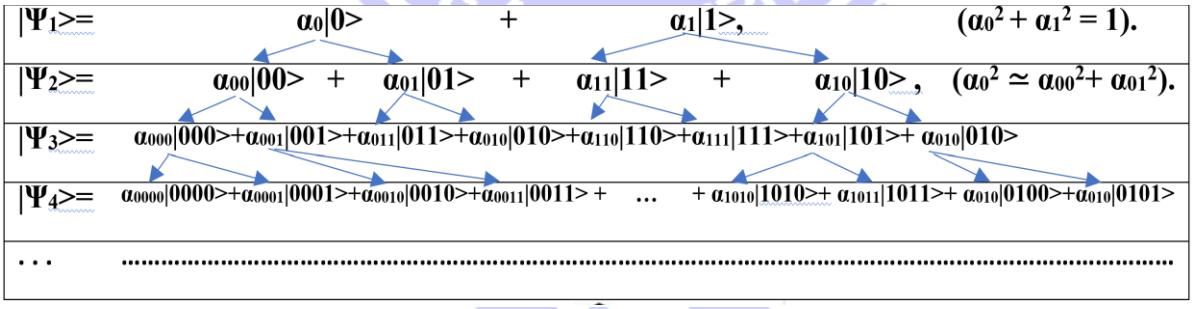

Fig. 5: A model of multi-level poly-qubit states, which are interconnected each with others and corresponds to rules of dichotomous fractals of probabilities in genomic DNAs [Petoukhov, 2025]

We see the world through the probability streams of great number of neurons from the retina (having about 126 million receptor cells on it) and other genetically inherited sensory organs. That is why it is so important to study universal rules of probability segregation in genomic DNAs and to develop quantum bioinformatics of multi-level poly-qubit systems.

3. Collective Algebra-Logical Consciousness

Biology is saturated with phenomena of purposeful logical interaction between parts of a whole biosystem. The discovery of the connection between the genetic coding system and Boolean functions (Boolean genetic code, etc.) provides new approaches to understanding these fundamental phenomena inherited from generation to generation. Let us consider some examples. The single-celled organism *Mixotricha Paradoxa* moves due to 250

thousand spiral bacteria *Treponema spirochetes* located on its surface, the spiral flagella of which twist in a coordinated manner as a single whole, ensuring the appropriate movement in the required directions and speeds due to logical interactions and logical control.

Volvox algae are colonial mobile organisms consisting of many flagellated unicellular organisms and purposefully moving due to the logically coordinated beating of the flagella of all cells. In biology, it is believed that multicellular organisms evolved from unicellular organisms through such colonial forms. It can be assumed that the foundations of logical relationships between the components of colonial organisms passed to multicellular organisms, including humans.

Holistic organisms, when solving collective problems, also interact with each other on the basis of innate logical mechanisms without the need for complex individual learning. Examples:

- the dance of bees with the transfer of information through the logic of movements;
- collectivism in an ant colony, where each ant has its own specialization, but acts in the interests of the colony, on whose survival its life depends. At the same time, a complex system of communication between individuals operates for common purposeful actions (we can conventionally say that the anthill has a "collective logical consciousness");
- multimillion termite communities are endowed with a collective logical consciousness ("mega-brain" - https://dzen.ru/a/ZppBuZwBUHb4aYU3), creating the unthinkable for an individual insect. They build termite mounds up to 13 meters high with a huge system of air ducts and living chambers in order to maintain a certain humidity and temperature necessary for their life. They conduct agriculture, growing mushrooms in termite mounds to feed the colony, etc.

It seems that biological self-organization as a whole is based on the inherited logic of interrelations, connected with the Boolean algebra of logic, with which the system of genetic coding and the fundamental law of "all-or-none" of active bio-tissues are related. In the general philosophical and difficult to define concept of "consciousness", I propose to single out - as its subdivision - "collective algebraic-logical consciousness". To model its manifestations, one can use the formalisms of Boolean algebra of logic associated with genetic coding, the fundamental law of "all-or-none" of active bio-tissues, etc. On this path, mutual enrichment of biology and engineering is seen, since on the basis of Boolean operators (functions) in technology, multi-cycle circuits with finite-automaton mappings are built, having memory and containing cycles, unlike single-cycle circuits that do not have memory. Much work should be done else. A comparison between topics of the genetic archetypes and the human archetypes of the collective unconscious by C. Jung is presented in [Petoukhov, 2025].

4. Ancient Indian Philosophy, Genetic Informatics, and Chess

The author notes the existence of structural parallelisms between the molecular system of genetic coding and the provisions of ancient Indian philosophy. Important provisions on the connection between ancient Indian philosophy and mathematical logic and algebraic constructions are contained in the book [Rajan, 2024]. These parallelisms allow us to think that at least some of the schemes of ancient Indian philosophy did not arise out of nowhere, but are a reflection of the algebraic organization of the genetic coding system. Let us present some of these parallelisms, partially using data on ancient Indian ideas from [AcCalam786, 2019].

According to the Vedic cosmology, the universe is mathematical. The Lord of the manifested world, Brahma, created the Universe in foursomes, consisting of two complementary - complementary and, at the same time, opposite - pairs-binaries. Sculptural images of Brahma convey the idea of foursomes in the symbolic form: Brahma always has four heads with four faces turned in four cardinal directions, and four hands. The mythology, religion and philosophy of the Indians were based on the foursomes: chatur-veda (4 Vedas), chatur-yuga (4 Yuga-eras), chatur-varna (4 castes), etc. India is considered the birthplace of chess, and the early chess - chaturanga - consisted of four parts, and was played by four players, the set of pieces for each contained four pawns and four role pieces. Its figures were placed in the north, south, east and west.

One of the arguments in favor of the fact that the birthplace of chess is India is the mention in the Vedas (Agni-Purana) of a plan of 64 cells as a mystical diagram of the Vedas, a model of the world. The chessboard, which carries a cross-like mosaic of 64 white and black cells, represents the harmony of fractal-like constructions since it contains four cross-shaped quadrants, each of which also contains four cross-shaped sub-quadrants. The Brahmin priestly caste used a similar (8x8)-diagram of 64 cells, which is called Vastu Mandala, as such a fractal; it was taken as a basis for the construction of settlements and temples. Ancient India adored squares, so even their astrologers' star charts were square. In the fractal-like layout of the 64-cell square, each cell was assigned its own deity, that is, such a set of 64 cells corresponded to a whole pantheon of deities. Significant attention in the Vedas and ancient Indian concepts is given to cyclic processes in natural systems.

In the genetics, the basic DNA-alphabet of DNA nucleotides consists of 4 nucleotides A, C, G, and T. This molecular alphabet is the carrier of a system of binary-oppositional traits, the consideration of which leads to the algorithmic construction of a family of genetic (2^n*2^n)-Karnaugh matrices from the Boolean algebra of logic (Fig. 1). In each of these genetic Karnaugh matrices, all cells are numbered by members of the corresponding cyclic n-bit Gray code. As noted above, by marking cells with even (odd) numbers in black (white), we obtain black-and-white cross-shaped mosaics similar to chessboard mosaics. In particular, from the genetic Karnaugh matrix for 64 triplets we obtain the matrix (Fig. 6) reproducing the cross-shaped mosaic of a 64-cell chessboard, but with the numbering of all 64 cells by members of the 6-bit Gray code. The author conventionally calls this genetic matrix a "genetic chessboard", which is connected with the topic of genetic archetypes.

	000	001	011	010	110	111	101	100
000	CCC 000000	CCA 000001	CAA 000011	CAC 000010	AAC 000110	AAA 000111	ACA 000101	ACC 000100
001	CCT 001000	CCG 001001	CAG 001011	CAT 001010	AAT 001110	AAG 001111	ACG 001101	ACT 001100
011	CTT 011000	CTG 011001	CGG 011011	CGT 011010	AGT 011110	AGG 011111	ATG 011101	ATT 011100
010	CTC 010000	CTA 010001	CGA 010011	CGC 010010	AGC 010110	AGA 010111	ATA 010101	ATC 010100
110	TTC 110000	TTA 110001	TGA 110011	TGC 110010	GGC 110110	GGA 110111	GTA 110101	GTC 110100
111	TTT 111000	TTG 111001	TGG 111011	TGT 111010	GGT 111110	GGG 111111	GTG 111101	GTT 111100
101	TCT 101000	TCG 101001	TAG 101011	TAT 101010	GAT 101110	GAG 101111	GCG 101101	GCT 101100
100	TCC 100000	TCA 100001	TAA 100011	TAC 100010	GAC 100110	GAA 100111	GCA 100101	GCC 100100

Fig. 6: The matrix which is called the "genetic chessboard".

The most important differences between the genetic chessboard and the regular chessboard are as follows:

1. all 64 cells of the genetic chessboard are numbered by members of the 6-bit Gray code, which introduces the Hamming distance between the cells by their code numbers and which connects it with the Boolean algebra of logic conjugated with the genetic (8*8) Karnaugh matrix;
2. each of its 64 cells corresponds to one of the 64 triplets of the genetic code.

It turns out that the known algorithmic moves of chess pieces are also connected with cyclic Gray codes in their known 1D-, 2D-, and 3D-versions, that give additional pieces of evidence about deep connections of chess with the genetic structures (see detail in the preprint [Petoukhov, 2025]. In a 2D-Gray code, the Hamming distance between adjacent terms is 2 (but not 1 as in the 1D-Gray code). Accordingly, in a 3D-Gray code, the Hamming distance between adjacent terms is 3. For example, the moves of the chess knight turn out to correspond to the 3D-Gray code, since the knight's move always takes it to a cell whose number, according to the 6-bit Gray code, differs by exactly three bits from a number of the original cell (that is, Hamming distance between them is 3). The routes of the knight on the chessboard have been the subject of the works of many mathematicians, starting at least in the 18th century. The most famous of these are the works of L. Euler and his followers on the question of whether a knight can go around all 64 cells of a chessboard without stepping on any cell twice (see detail in [Petoukhov, 2025]). The author believes that chess is linked to genetic archetypes, that serves a hidden reason of its popularity all over the world for thousands of years.

In genetic chessboard (Fig. 6), adjacent cells with a Hamming distance of 2 between them are located diagonally. Accordingly, the n-bit 2D-Gray code divides the entire set of cells of the genetic chessboard into two subsets with even and odd numberings, which is reflected in the diagonal mosaic of black and white cells representing these

numerical subsets. Note that in the case of the genetic vertebrate mitochondria code, which is considered the most ancient and symmetrical among all dialects of the genetic code, the entire natural set of amino acids and stop-codons in black-and-white genetic chessboard for triplets (Fig. 6) is structured in a very regular way: this set is divided into two subsets of absolutely identical composition, one of which occupies all the black cells, i.e. cells with even numbers according to the 6-bit Gray code, and the second of which occupies all the white cells, i.e. cells with odd numbers of the 6-bit Gray code.

The Karnaugh matrix for 64 triplets (that is, the genetic chessboard in Fig. 6) is associated not only with the algorithms of moves in checkers and chess but also with the amino acids that are encoded by these triplets. This allows us to formally match the routes of checkers and chess pieces (including the chess knight) with amino acid sequences in proteins, etc. For example, a particular route of a knight on such a genetic board corresponds to a certain sequence of n-plets and amino acids, which can be matched with real sequences of n-plets in genomes and genes, as well as amino acid sequences in proteins. In this case, each cell of the board has a certain probability of the corresponding triplet in the considered DNA of the genome. Therefore, it is possible to build selective routes of the knight based on the principle of, for example, the next move of the knight to the cell with the maximum (or minimum) probability. For different genomes, there may be various routes of the knight, since the probabilities of triplets in the DNA of different genomes are different. Stop-codon cells in this sequence of moves may not be taken into account, since they do not encode amino acids. Could there be benefits from developing such a kind of "chess genetics", in which genetic sequences are matched to the algorithmic paths of checkers and chess pieces? This is a question for future study.

5. Some Concluding Remarks

Living organisms are cyclically coded cyclic entities. Genetic informatics are connected with cyclic Gray codes, Karnaugh matrices and Boolean algebra of logic. The presented data on the existence of a genetic n-plet code of Boolean functions are important for understanding the inherited logic of interactions between body parts and for developing new approaches in fields of artificial intelligence, bioinformatics, evolutionary biology, and biotechnology. The presented universal rules of statistical peculiarities of nucleotide sequences in single-stranded DNAs of genomes of higher and lower organisms should be tested on maximal wide set of genomes for comparison analysis of genomes. Harmony of living bodies is based on laws of probabilities in information genetic sequences. Provisions of ancient Indian philosophy have deep structural parallelisms with the molecular genetic system and, as one can think, they did not arise out of nowhere, but are a reflection of the algebraic organization of the genetic coding system.

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It was indeed a great honor to receive Prof. Dr. Sergey V. Petoukhov
at the International Airport, Hyderabad on April 6, 2025
E. G. Rajan (Conference Chair)