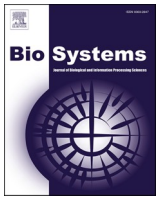
BioSystems 265 (2026) 105805

Contents lists available at ScienceDirect

BioSystems

journal homepage: www.elsevier.com/locate/biosystems



Full Length Article

Quantum-logical modeling of bioinformatics of inheritance of algorithmic biostructures based on unitary operators and their cyclic groups

S.V. Petoukhov

Mechanical Engineering Research Institute By Name A.A. Blagonravov, Russian Academy of Sciences, Maly Kharitonievsky Pereulok, 4, Moscow, 101990, Russia

ARTICLE INFO

Keywords:
Genetic biomechanics
Genetic automata
Quantum bioinformatics
Biological inheritance
Alphabets
Unitary matrices
Cycles
Biorhythms
Biological time
Quantum logic

ABSTRACT

The article is devoted to topical issues of genetic biomechanics, which studies structural connections between molecular-genetic informatics and inherited physiological complexes. It is known that amino acid sequences of proteins are genetically inherited using code messages in DNA and RNA molecules based on the alphabet of 4 nucleotides. But, as Nobel laureate geneticist T. Steitz emphasizes, all knowledge about these biomolecules encoded in the genome in this biochemical alphabet will not tell us about the inheritance of biomechanical algorithms and functions by genetic automata. Thus, in modern science of biological inheritance, there is no knowledge about a bioinformation system capable of ensuring the inheritance of cooperative phenomena of algorithmic behavior of body parts. These inherited logical forms of algorithmic behavior in biosystems require the search for bioinformation alphabets that could form the basis for the operation of genetic automata and the algorithmic inheritance of biological structures. The article describes the genetic algebraic-operator alphabets, identified as a result of such a search, based on unitary Hadamard matrices, as well as cyclic power groups based on them, which make it possible to model inherited cyclic and biorhythmic structures in connection with the formalisms of quantum logic. The evolutionary paradigm of algebraic-alphabetic Darwinism has been formulated. Related issues of inherited brain mechanisms, artificial intelligence, and the functioning of operators in human-machine systems are discussed.

1. Introduction

P. Jordan and E. Schrödinger, two of the founders of quantum mechanics, formulated the main difference between living and inanimate objects: inanimate objects are controlled by the average random motion of millions of particles, whose individual influence is negligible, whereas in a living organism, selected — genetic — molecules exert a dictatorial influence on the entire living organism [McFadden and Al-Khalili, 2018]. All genetically inherited physiological organs are structurally coupled with the bioinformation system of genetic texts in DNA and RNA molecules. Understanding the secrets of genetic informatics is important for the development of biotechnologies, optimization of human-machine-environment systems, artificial intelligence, etc. Information communication systems are built on the use of a particular alphabet for forming information messages. For example, all computer programs rely on corresponding programming alphabets. The science of biological inheritance today is based on knowledge of the alphabets of the 4 nucleotides of DNA and RNA, i.e., on nucleotide-alphabet bioinformatics, which has contributed much to the understanding of proteins and nucleic acids. But, as Nobel laureate in chemistry geneticist T. Steitz emphasizes, all knowledge about the biochemical structure of proteins and nucleic acids encoded in the genome will not tell us how the algorithmic actions of organisms are inherited [Steitz, 2007]. For example, it will not tell us how a butterfly flies. Or how a turtle, upon hatching, immediately begins crawling toward the water with coordinated movements of its limbs, which requires the logically coordinated activity of millions of nerve and muscle cells. Or how a newborn infant emits an identifying cry and begins to suckle the mother's breast, which also requires the logically coordinated activity of billions of his nerve and muscle cells. From knowledge of the nucleotide sequences in DNA/RNA, one cannot deduce the inheritance of the geometric beauty of biological forms, repeated in bodies of very different biochemical composition and built through the spatio-temporal ordering of trillions of different biomolecules. Also, knowledge of the biochemical alphabet of 4 types of nucleotides does not allow us to understand how, in general, one-dimensional sequences of nucleotides in genomic DNAs can code for the inherited three-dimensional forms of living bodies.

This article is part of a special issue entitled: Quantum Biology published in BioSystems.

E-mail address: spetoukhov@gmail.com.
URL: http://petoukhov.com/.

https://doi.org/10.1016/j.biosystems.2026.105805
Received 21 March 2026; Received in revised form 20 April 2026; Accepted 26 April 2026
Available online 30 April 2026

Thus, in modern science of biological inheritance, there is no knowledge about a bioinformation system capable of ensuring the inheritance of phenomena of coordinated algorithmic behavior of body parts. These inherited logical forms of collective behavior in biosystems require, for their modeling, the search for an appropriate operator bioinformation system based on a suitable alphabet. The point is that, alongside nucleotide-alphabet bioinformatics, an operator-alphabet bioinformatics, complementary to it, operates in the living world. This hidden algebraic-operator bioinformatics and its alphabet are apparently associated with quantum mechanics and quantum informatics, since genetic molecules belong to the micro-world of quantum mechanics. In this search, special attention should be paid to unitary operators, on which, as logic gates, all computations in quantum computing are built [Nielsen and Chuang, 2010] and which in quantum mechanics describe the evolution of closed quantum systems. Note that the search for effective approaches to modeling logically organized biological processes is conducted worldwide, including recourse to quantum mechanics and quantum informatics (see, for example [Abbott et al., 2008; Asano et al., 2013; Khrennikov, 2004, 2006; Patel, 2001a,b; Petoukhov, 2023; Petoukhov and Svirin, 2024],). The article is devoted primarily to the genetic alphabet of 4 unitary Hadamard operators found by the author and the development of operator quantum-logical bioinformatics based on it for advancing mathematical models of the inheritance of algorithmic structure and behavior of multicomponent body parts, including the inheritance of many time-coordinated cyclic processes.

The founder of quantum informatics, Yu.I. Manin, introduced the concept of the quantum computer in his 1980 book precisely while analyzing the features of high-speed information processing by "*genetic automata*" in chromosomal DNA, prophetically pointing out the important role of unitary operators and tensor products [Manin, 1980, p.15]: "*A quantum automaton must be abstract: its mathematical model should use only the most general quantum principles, without predetermining physical realizations. Then the model of evolution is a unitary rotation in a finite-dimensional Hilbert space, and the model of virtual separation into subsystems corresponds to the decomposition of space into a tensor product. Somewhere in this picture, interaction, traditionally described by Hermitian operators and probabilities, must find its place*." Thus, the very birth of quantum informatics, so promising for the development of artificial intelligence and quantum-logical biology, occurred due to the desire to understand the features of genetic informatics. The data in this article are consistent with the quoted prophecy of Yu.I. Manin and continue his investigation of the connection between genetic quantum automata and the formalisms of quantum mechanics.

The aim of the article is to present the results of studying the structural features and applications in the field of mathematical modeling of the named operator-unitary alphabet of genetics and the bioinformation system based on it, for the development of models of the biological inheritance system using the algebraic apparatus of quantum mechanics and quantum informatics.

2. Genetic matrices of nucleotide alphabets of DNA and the genetic alphabet of 4 unitary Hadamard operators

Amino acid sequences of proteins are inherited thanks to information messages on genetic DNA molecules, written in the alphabet of 4 nucleotides: adenine A, cytosine C, guanine G, and thymine T. This alphabet is a carrier of a system of binary-opposition indicators (molecular features) that distinguish three types of binary sub-alphabets within it:

−1) Two of these nucleotides are pyrimidines (C and T), containing one benzene ring in their molecule, while the other two are purines (A and G), having two rings in their molecule. This gives a binary representation (binary sub-alphabet) $\mathbf{C} = \mathbf{T} = +\mathbf{1}$, $\mathbf{A} = \mathbf{G} = \mathbf{-1}$; - 2) Two of these nucleotides are amino-molecules (C and A), and the other two (T and G) are keto-molecules, which gives a binary representation $\mathbf{C} = \mathbf{A} = +\mathbf{1}$, $\mathbf{T} = \mathbf{G} = \mathbf{-1}$; - 3) The pairs of complementary nucleotides C-G and A-T are connected by 3 and 2 hydrogen bonds respectively (called in genetics weak and strong hydrogen bonds), which gives a binary representation $\mathbf{C} = \mathbf{G} = +\mathbf{1}$, $\mathbf{A} = \mathbf{T} = \mathbf{-1}$.

These binary features of the nucleotide alphabet of DNA (and RNA) of all living organisms are summarized in Table 1.

In the right part of this phenomenological Table 1, a symmetric Hadamard matrix of the fourth order appeared, which is a real Hermitian matrix, whose quadrants are occupied by 4 types of Hadamard matrices of the second order. Recall that Hadamard matrices H_n of order n are square matrices composed of elements +1 and −1 satisfying the criterion $\mathbf{H_n} \times \mathbf{H_n^T} = n\mathbf{E}$, where **E** is the identity matrix of order n. Fig. 1 shows these 4 Hadamard matrices of the second order from Table 1, normalized by the factor $2^{-0.5}$, traditionally used in quantum mechanics and quantum computers to give the matrices a unitary character. Hadamard matrices have many remarkable properties and applications.

The identification of this connection between the molecular nucleotide alphabet of DNA and these 4 unitary Hadamard matrices is important due to the significance of unitary transformations (unitary operators) for quantum mechanics, quantum computing, signal processing engineering, etc. Unitary transformations preserve vector lengths and scalar products (preserve the metric), representing rotation and reflection operators. Unitary matrices by definition satisfy the criterion: the product of a unitary matrix and its transposed version equal unity matrix. Unitary transformations with real components are also called orthogonal transformations, but we will use their more general name in this article - "unitary transformations" - under which they are better known in various fields of science. In quantum mechanics, unitary transformations describe the time evolution of closed quantum systems, and in quantum mechanics observable quantities are represented not by numbers, but by operators (unlike classical mechanics). In quantum computers, all computations are performed precisely on the basis of unitary operators, acting as gates, and any unitary operator can be used as a gate in quantum computing [Nielsen and Chuang, 2010]. Hadamard matrices are fundamental building blocks of quantum computers, providing qubit superposition, and are also a key element of quantum parallelism in the quantum Fourier transform and other quantum algorithms.

The genetic coding system is highly noise-immune. According to Mendel's law of independent inheritance of traits, information from the quantum level of DNA molecules determines the macrostructure of living organisms through multiple independent channels, despite significant noise. Thus, hair, eye, and skin color are inherited independently. Accordingly, each organism is a multichannel noise-immune coding probabilistic machine and possesses certain algebraic-holographic properties [Petoukhov, 2022; Petoukhov, 2023, Chapters 2, 5]. In light of this, we note that Hadamard matrices are the basic elements of tensor networks, on which the well-known holographic quantum error-correcting codes developed at the Institute for Quantum Information Science and Matter (Caltech, USA) are built [Pastawski et al., 2015; Preskill, 2016]. Fig. 2 reproduces an explanatory illustration from the work [Preskill, 2016] by the director of this Institute, Professor Preskill. He shows a close connection between two remarkable ideas in physics - the holographic principle and quantum error correction; this connection opens, in particular, the possibility of considering space-time as a quantum code that corrects errors. This work also emphasizes the conjugation of the described holographic quantum codes

Table 1
The system of binary-opposition traits of 4 DNA nucleotides. Benzene rings are found in all of these nucleotides.

Molecular traits and their symbols	G	A	T	C
pyrimidines **+1**, purines **-1**	**−1**	**−1**	**+1**	**+1**
amino-nucleotides **+1**, keto-nucleotides **-1**	**−1**	**+1**	**−1**	**+1**
complementarity with 3 or 2 hydrogen bonds: **+1**, **-1**	**+1**	**−1**	**−1**	**+1**
the presence of benzene rings: **+1**	**+1**	**+1**	**+1**	**+1**

$$\mathbf{H_C} = 2^{-0.5}\begin{vmatrix} 1, -1 \\ 1, 1 \end{vmatrix};\quad \mathbf{H_T} = 2^{-0.5}\begin{vmatrix} 1, 1 \\ 1, -1 \end{vmatrix};\quad \mathbf{H_G} = 2^{-0.5}\begin{vmatrix} 1, 1 \\ -1, 1 \end{vmatrix};\quad \mathbf{H_A} = 2^{-0.5}\begin{vmatrix} -1, 1 \\ 1, 1 \end{vmatrix}$$

Fig. 1. Four unitary Hadamard matrices $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$.

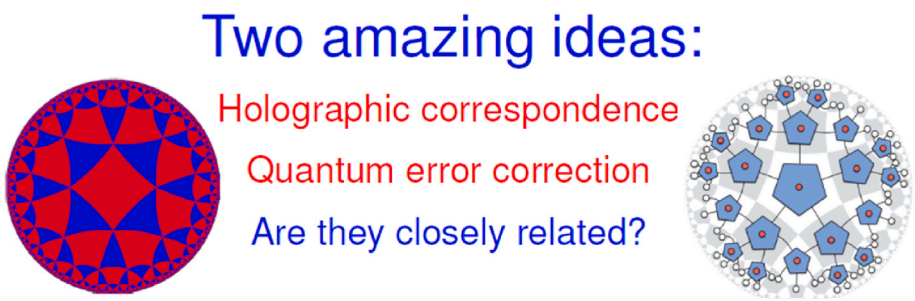


Fig. 2. The illustration of the theme of holographic quantum error-correcting codes from [Preskill, 2016]. On the left is the symbol for the Poincaré conformal disk model of hyperbolic geometry. The illustration is reproduced with the kind permission of Prof. J. Preskill.

with the Poincaré conformal-disk model of hyperbolic geometry (Fig. 2 includes a graphic symbol of this model). But the connection between the Poincaré conformal-disk model of hyperbolic geometry and the genetic coding system was independently revealed based on the analysis of the binary-opposition structure of this genetic system and the statistical rules of genomic informatics [Petoukhov, 2022; Petoukhov, 2023; Petoukhov, 2023, Chapters 2, 5]. These data testify in favor that holographic quantum error-correcting codes using unitary Hadamard matrices are appropriate algebraic tools for modeling and understanding the considered inherited properties of quantum-like organisms.

We will call the four unitary operators $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ (Fig. 1) genetic Hadamard gates and consider them as the sought quantum-operator alphabet, forming the basis of a quantum-logical bio-information system for mathematical modeling of the phenomena of inheritance of algorithmic structures in genetic biomechanics. These 4 matrices cyclically transform into each other upon repeated 90-degree rotations. This same set of 4 Hadamard matrices is revealed when analyzing molecular-genetic informatics from other approaches in matrix genetics, where genetic ensembles are analyzed in matrix forms [Petoukhov and He, 2010, 2023]. For example, placing all 4 nucleotides in a (2x2)-matrix in an arbitrary order and considering all possible variants of cyclic shifts of nucleotides within it (or its cyclic rotations by 90°), we obtain a set of 4 matrices in Fig. 3.

But in the DNA alphabet of 4 nucleotides, nature has embedded one more binary opposition: during the transition from DNA to RNA, only one nucleotide T (thymine) is replaced by nucleotide U (uracil), while the remaining nucleotides C, A, G remain unchanged. This binary opposition is expressed by the representation: C = A = G = +1, T = −1. Taking this binary representation into account transforms the 4 symbolic genetic matrices from Fig. 3 into the 4 numerical matrices in Fig. 4, which are the same Hadamard matrices considered above in connection with Fig. 1 and which become unitary matrices $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ upon the same traditional normalization by multiplying by the factor $2^{-0.5}$.

Briefly mention that analogous Hadamard (2 × 2)-matrices are also revealed in other types of analysis of structural and stochastic features of genetic informatics. For example, taking into account the well-known

C	A
T	G

A	C
G	T

G	T
A	C

T	G
C	A

Fig. 3. Example of a cyclic set of 4 matrices of nucleotides C, A, G, T, transforming into each other upon cyclic shifts of nucleotides in the initial left matrix containing an arbitrary arrangement of nucleotides.

1	1
-1	1

1	1
1	-1

1	-1
1	1

-1	1
1	1

Fig. 4. Set of 4 Hadamard matrices arising from the 4 symbolic genetic matrices in Fig. 3 when considering the described binary opposition of nucleotide T to nucleotides A, C, G, giving the binary representation: C = A = G = +1, T = −1.

second Chargaff rule [Fimmel et al., 2020] about the ratio of probabilities of the 4 nucleotides in all long single-stranded DNAs (length >100 kbit) of higher and lower organisms leads to a real Hermitian probability matrix $\mathbf{W_D} = [0.5, 0.5; 0.5, 0.5]$. This genetic Hermitian matrix $\mathbf{W_D}$ is doubly stochastic: the sum of elements in each row and each column of such a matrix equals one. Regarding doubly stochastic matrices, the following theorem is known [Prasolov, 2008]:

- If matrix $\mathbf{V} = ||\mathbf{v_{ij}}||^{n}$ is unitary, then matrix $\mathbf{W} = ||\mathbf{w_{ij}}||^{n}$, where $\mathbf{w_{ij}} = |\mathbf{v_{ij}}|^{2}$, is doubly stochastic.

According to this theorem, the specified doubly stochastic genetic probability matrix $\overset{\mathbf{W}}{\mathbf{D}}$ corresponds to 4 unitary alphabet Hadamard matrices $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ (Fig. 1): squaring all components of each of these unitary matrices generates the doubly stochastic matrix $\overset{\mathbf{W}}{\mathbf{D}}$. Note that these same 4 unitary matrices $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$, but taken with a minus sign, are treated as their trivial analog and are not considered separately. The collection of obtained results from analyzing molecular-genetic informatics allows us to speak of the fundamental bio-information significance of these alphabet unitary Hadamard matrices for the bioinformation coding of inherited algorithmic structures associated with the ideology of closed quantum-like biosystems. These should include inherited cyclic and biorhythmic phenomena, which, as will be shown below, are effectively modeled using the named unitary matrices.

One of these 4 genetic unitary Hadamard operators (gates) – $\mathbf{H_T}$ – has long been used in quantum computers for fundamental operations on qubits, being a key element in many quantum algorithms, including the Deutsch-Jozsa algorithm and Shor's algorithm. This Hadamard gate provides the superposition principle in quantum algorithms for working with quantum entanglement, thereby demonstrating quantum supremacy — their significantly more efficient operation compared to known classical algorithms [Nielsen and Chuang, 2010].

Of the 4 genetic Hadamard gates, two gates $\mathbf{H_A}$, $\mathbf{H_T}$ are reflection operators. Raising them to integer powers generates corresponding cyclic groups of unitary operators with period 2. The other two unitary matrices ($\mathbf{H_C}$, $\mathbf{H_G}$) are rotation operators ($\mathbf{H_C}$ counterclockwise, $\mathbf{H_G}$ clockwise) and matrix representations of the complex number $Z = 2^{-0.5}(1 + i)$, where i is the imaginary unit of complex numbers ($i^2 = -1$). Repeatedly raising these unitary matrices $\mathbf{H_C}$ and $\mathbf{H_G}$ to integer powers (positive and negative) generates cyclic (with period 8) groups of unitary operators, which are matrix representations of complex numbers (1).

$$H_C{}^n = H_C{}^{n+8}, H_G{}^n = H_G{}^{n+8}, H_A{}^n = H_A{}^{n+2}, H_T{}^n = H_T{}^{n+2} \quad (1)$$

Any of the unitary matrices $\mathbf{H_C}$ and $\mathbf{H_G}$ can be represented as the product of k unitary matrices that are the k-th roots of it. In other words, the action of one unitary operator, for example, operator $\mathbf{H_C}$, can be represented as the action of a sequence of k more fractional unitary operators $\mathbf{H_C}^{1/k}$. Thus, in the matrix-vector approach, any large transformation in a system from the action of such a whole operator $\mathbf{H_C}$ can be represented as consisting of a sequence of arbitrarily small transformations from the action of the corresponding sequence of unitary operators $\mathbf{H_C}^{1/k}$ for modeling quasi-continuous transformations in cyclic processes. Additionally, note that raising the genetic gates $\mathbf{H_C}$ and $\mathbf{H_G}$ to a power, representing stepwise a cyclic function of time, allows the construction of digital twins of quasi-continuous cyclic bioprocesses in the form of vector sequences of their stepwise states.

In quantum logic, projectors (projection operators) play an important role. In light of this, note that the unitary Hadamard matrices in operators $\mathbf{H_C}$ and $\mathbf{H_G}$ are sums of sparse matrices representing projectors $\mathbf{P_s}$, satisfying the projector criterion $\mathbf{P}^2 = \mathbf{P}$, and shown in expression (2) in parentheses:

$$H_C = 2^{-0.5}\cdot[1\ -1; 1\ 1] = 2^{-0.5}\cdot([1,0;1,0] + [0,-1;0,1]),$$
$$H_G = 2^{-0.5}\cdot[1\ 1; -1\ 1] = 2^{-0.5}\cdot([1,0;-1,0] + [0,1;0,1])$$

Many genetically inherited biological structures in organisms are obviously associated with unitary transformations of rotations and reflections. For example, the kinematic scheme of the human body and its locomotion is based on unitary transformations of rotations in joints (the human body has about 300 joints) and the mirror symmetry of the left and right halves of the body. Human motor activity comes down to the skillful control by the nervous system of ensembles of these unitary transformations in body kinematics, which is associated with the genetically inherited ability of the nervous system to operate with unitary transformations. Moreover, a person's very representation of their body schema is innate: people born without limbs and having no personal experience of using them nevertheless feel them as really existing, with phantom pains in them [Vetter and Weinstein, 1967; Weinstein and Sersen, 1961].

When studying human sensorimotor features, it must be considered that the genetically inherited nervous system is related in its structural organization to genetic structures. A person sees the world through probabilities in statistical signal streams from retinal neurons (containing millions of receptor cells) and other sense organs. The father of cybernetics, Norbert Wiener, asserted: "*genetic memory – the memory of our genes – is determined, essentially, by nucleic acid complexes … there are reasons to think that the memory of the nervous system has the same nature*" [Wiener, 1964; Rebrova and Rebrova, 2020].

Another example of the biological importance of unitary transformations is the construction of the complex three-dimensional shape of proteins in the organism, i.e., protein folding. These shapes are built on unitary transformations of rotation of protein molecule segments relative to each other around relatively strong carbon-carbon bonds.

The author proposes to consider and use the family of 4 genetic unitary Hadamard operators $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ (Fig. 1) as a basic quantum-logical genetic alphabet for developing, on its basis, a theory of a quantum-logical bioinformation system that allows modeling the inheritance of algorithmically organized biological structures and phenomena, primarily of a cyclic and rhythmic nature, as described in the preprint [Petoukhov, 2025a]. Due to this, this type of algebraic-operator bioinformation system is briefly termed "cyclic bioinformatics". Within its framework, unitary matrix representations of Hamilton quaternions and biquaternions, projection operators, etc., arise and are investigated [ibid.].

Here, the distinctive features of quantum logic should be explained [Cohen, 1989; Vasyukov, 2005]. Quantum logic, from a formal point of view, is an algebraic system for describing, using quantum gates, how qubits work and interact, and how to extract information from them. In quantum logic, "logic" lies not in reasoning, but in the mathematical description of states and operations. Quantum logic can be formulated as a modified version of propositional logic. For comparison, recall that classical Boolean logic is a set of logical rules (AND, OR, NOT, etc.) describing how bits (0 or 1) can be combined and transformed according to the laws of Boolean algebra with its key principle of distributivity and statements of "true" or "false". Quantum logic considers not "true/false" statements, but questions posed to a quantum system. The answer to such a question is the probability value obtained from measurement. Logical operations are replaced by quantum gates (unitary operations): NOT becomes the X gate, and completely new operations appear, having no analogues in classical logic, for example, the Hadamard gate, which creates superposition. Quantum logic works with qubits, vectors, and matrices, not with mathematical sets. Its mathematical foundation is the theory of Hilbert spaces and projective and unitary operators. The state space of a quantum system is described by vectors, and rotations of these vectors serve as logical operations. In quantum logic, distributivity is absent, which is considered its key difference from Boolean logic. Quantum logic is a branch of logic necessary for reasoning about propositions that take into account the principles of quantum theory. It was founded by the work of G. Birkhoff and J. von Neumann [Birkhoff and von Neumann, 1936], who attempted to reconcile the inconsistency of classical logic with facts concerning measurements in quantum mechanics and saw in quantum logic a possible foundation for physics.

3. Unitary Hadamard operators and modeling of inheritance of cyclic biostructures

The unitary Hadamard matrices of the quantum-operator bioinformatics alphabet $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ (Fig. 1) and many types of their combinations into higher-order unitary matrices form — upon repeated exponentiation (i.e., repeated action of these matrix operators) — cyclic groups of operators having different periods and used for modeling cyclic sequences of states of quantum-like systems. The resulting algebraic-geometric apparatus is intended, first of all, for quantum-logical modeling of the inheritance of many cyclic and hypercyclic biostructures in genetic biomechanics.

A living organism is a huge chorus of inherited cyclic processes. Examples include the cyclical functioning of the heart and lungs, as well as the functioning of proteins, which exist in continuous cycles of life and death, alternately breaking down into amino acids and reassembling them. For example, the half-life of the hormone insulin is 6-9 min. The universal source of energy for all biochemical processes of living organisms on Earth is ATP (adenosine triphosphate). The lifetime of one ATP molecule in humans is less than a minute. Within a day, one ATP molecule in humans cycles through the Krebs cycle on average 2000-3000 times. The human body synthesizes about 40 kg of ATP per day because ATP cannot be stored [Neupane et al., 2019]. In short, the inherited parts of our body constantly die and are reborn in a cyclical manner. Taking this into account, the renowned physiologist A.G. Gurvich asserted: "*The main problem in biology is maintaining form while constantly renewing the substrate*" [Gurvich, 1977]. Somatic cells of the body divide cyclically (mitosis), accompanied by a cyclic change in the stages of cell division. An important role in this is played by proteins with the characteristic name "cyclins," whose concentration in the cell

changes cyclically, and their study is important for combating oncological diseases, etc. Corresponding work on cyclins and cyclic cell division was awarded the Nobel Prize in 2001 [Bruce, 2001]. A cyclic regular change in states during the day exists, in particular, in chromatin, containing DNA and regulatory proteins, as well as in the liver, whose cyclic change in states is regulated by more than three thousand molecular switches [Vollmers et al., 2012]. These interconnected cyclic phenomena are closely intertwined with the topic of internal biological clocks, the study of the molecular cyclic foundations of which was awarded the Nobel Prize in 2017 for the discovery that biological clocks function according to the same principles in the cells of various multicellular organisms, including humans [Press release, 2017]. Cyclomeric multi-block forms of living bodies also represent a vast area for the described quantum-logical modeling using cyclic groups of operators. A series of works is devoted to the substantive topic of cyclic shifts in code genetic sequences [Fimmel, Michel, Pirot, et al., 2019; Fimmel et al., 2020; Fimmel et al., 2020, and others].

It should be noted that the artistic creativity of people at all times has been associated with the use of cyclic and hypercyclic constructions. The book "The Glass Bead Game" by Nobel literature laureate H. Hesse is dedicated to a game whose goal is to find a deep structural-mathematical connection between subjects from different fields of science and art [Hesse, 2007]. In essence, the "glass bead game" is the art of composing a metatext, a synthesis of all branches of art into one, universal art. In our opinion, the genetic texts of DNA, with their hidden patterns and conjugation with the formalisms of quantum logic, are those metatexts on which biological texts and cyclic constructions of various natures are built, including the constructions of mathematical and artistic creativity of people. Note that the quantum-logical approach developed by the author to inherited cyclic and hypercyclic biostructures based on the alphabet of genetic Hadamard gates and the mathematical apparatus of quantum-logical biology fundamentally differs from the well-known biochemical concept of catalytic cycles and hypercycles [Eigen and Schuster, 1979].

In clearing the mechanisms linking Hadamard unitary operators to real periodic and other biological processes, the author believes that the following three aspects should be used. First, the resonance theory of oscillatory systems with many degrees of freedom, whose conjugation with the structures of molecular genetic informatics is known [Petoukhov, 2016]. Second, the ancient principle of "like begets like," fundamental to biology and used in genetics [Petoukhov, 2023]. Third, as noted above, Hadamard unitary matrices are related to the holographic quantum codes and the Poincaré conformal-disk model of hyperbolic geometry (Fig. 2). It was precisely on Lobachevsky's hyperbolic geometry that Poincaré built his theory of automorphic functions, which play a key role in number theory, algebraic geometry, and mathematical physics. Automorphic functions are a generalization of periodic functions, and they can be naturally applied to modeling inherited ensembles of biorhythmic and quasi-periodic processes, whose frequencies can vary and in which the phenomenon of autosynchronization is possible, described by the Kuramoto model for ensembles of oscillators [Kuramoto, 1984].

World research in the field of genetic informatics largely relies on the basic fact of the existence in the DNA of all organisms of a bioinformation system based on the molecular alphabet of 4 nucleotides C, G, A, T and its extensions into alphabets of 16 duplets, 64 triplets, etc. In parallel with this system based on the molecular alphabet of 4 nucleotides, it is now possible and necessary in bioinformatics and genetic biomechanics to work with a system based on the operator alphabet of 4 genetic Hadamard gates, i.e., with an alphabet system of a fundamentally new type: a system of a quantum-logical operator-code alphabet of 4 unitary matrices $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ (Fig. 1) and its tensor extensions into operator alphabets of 16 unitary duplets, 64 unitary triplets, etc. On this basis, interconnected sets of higher-order unitary operators arise, as well as their cyclic power groups, providing new approaches for modeling, first of all, inherited cyclic and biorhythmic phenomena, as outlined by the author in the preprint [Petoukhov, 2025]. Let us give two examples of such modeling here, related to unitary quaternions and biquaternions.

Let us turn to the formation, based on genetic Hadamard gates $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ (Fig. 1), of multi-block unitary Hadamard matrices representing unitary forms of Hamiltonian quaternions and biquaternions, with which much in physics, robotics, artificial intelligence, etc., is associated and to which thousands of works have been devoted only in the 20th century [Gsponer and Hurni, 2008]. This attention to them is due to the fact that quaternions are closely related to Pauli matrices, the theory of the electromagnetic field, the quantum-mechanical theory of chemical valence, spin theory, rotation of bodies in three-dimensional space, etc. In particular, operators describing the vibrational-rotational states of molecules have a quaternion structure [Lobodennko, 2009].

Fig. 5 shows a block matrix $\mathbf{Q}$, whose blocks are the genetic gates $\mathbf{H_G}$ and $\mathbf{H_A}$ with a weight factor ensuring its unitarity. It is a unitary Hadamard matrix (the factor 0.5 for the usual (4x4)-Hadamard matrix ensures its unitarity). Let us show that this matrix $\mathbf{Q}$ is a matrix representation of a Hamilton quaternion.

Indeed, as shown in Fig. 6, this matrix $\mathbf{Q}$ is the sum of four sparse matrices $\mathbf{v_0}$, $\mathbf{v_1}$, $\mathbf{v_2}$, $\mathbf{v_3}$: $\mathbf{Q} = 0.5\ (\mathbf{v_0}+\mathbf{v_1}+\mathbf{v_2}+\mathbf{v_3})$, where $\mathbf{v_0}$ is the identity matrix. This set of sparse matrices is closed under multiplication and defines their multiplication table, coinciding with the known multiplication table of the basic elements of the Hamilton quaternion algebra [Kantor and Solodovnikov, 1989]. This means that matrix $\mathbf{Q}$ is a unitary matrix representation of the quaternion $\mathbf{Q} = 0.5\mathbf{v_0} + 0.5\mathbf{v_1} + 0.5\mathbf{v_2} + 0.5\mathbf{v_3}$, where $\mathbf{v_1}$, $\mathbf{v_2}$, $\mathbf{v_3}$ represent the imaginary units of the quaternion. Quaternions and biquaternions having unitary matrix representations can be conditionally called for brevity "unitary quaternions" and "unitary biquaternions".

A unitary quaternion, when raised to a power, forms cyclic unitary group with a period of 6. An example of 6 members of one period of such a group $\mathbf{Q^n}$ is given in Fig. 7.

The members of the cyclic group of the unitary quaternion $\mathbf{Q^n}$ shown in Fig. 7 are mutually consistent under the addition operation. Indeed, this cyclic group of unitary quaternions $\mathbf{Q^n}$ with period 6 has the following properties, which can be conveniently illustrated by arranging the sequence of matrix members of the group on a clock-shaped circle (Fig. 8):

- 1) Unitary quaternions opposite to each other on a circle have opposite signs ($\mathbf{Q^k} = -\mathbf{Q^{k+3}}$) and, when added together, yield zero, i. e., they are complementary;
- 2) Each unitary quaternion on a circle is the sum of two adjacent unitary quaternions on its sides, i.e., $\mathbf{Q^k} = \mathbf{Q^{k-1}} + \mathbf{Q^{k+1}}$;
- 3) The sum of the unitary quaternions at the vertices of each of the two triangles of the "Star of David" is zero, i.e., $\mathbf{Q^1} + \mathbf{Q^3} + \mathbf{Q^5} = \mathbf{Q^2} + \mathbf{Q^4} + \mathbf{Q^6} =$ the zero matrix.

These cyclic groups of unitary quaternions can be used to model biological systems as quantum-logical objects. One possible model application of this cyclic power group of unitary quaternions with period 6 concerns inherited color perception, the properties of which structurally correspond to Newton's 6-sector color circle shown in Fig. 8. This

$$\mathbf{Q} = 2^{-0.5} \begin{vmatrix} \mathbf{H_G} & \mathbf{H_A} \\ -\mathbf{H_A} & \mathbf{H_G} \end{vmatrix} = 0.5 \begin{vmatrix} 1 & 1 & -1 & 1 \\ -1 & 1 & 1 & 1 \\ 1 & -1 & 1 & 1 \\ -1 & -1 & -1 & 1 \end{vmatrix}$$

Fig. 5. Unitary matrix representation $\mathbf{Q}$ of a Hamilton quaternion.

$$0.5\begin{bmatrix} 1, 1,-1,1 \\ -1, 1, 1,1 \\ 1,-1, 1,1 \\ -1,-1,-1,1 \end{bmatrix} = 0.5\begin{bmatrix} 1,0,0,0 \\ 0,1,0,0 \\ 0,0,1,0 \\ 0,0,0,1 \end{bmatrix} + 0.5\begin{bmatrix} 0,1, 0,0 \\ -1,0, 0,0 \\ 0,0, 0,1 \\ 0,0,-1,0 \end{bmatrix} + 0.5\begin{bmatrix} 0, 0,-1,0 \\ 0, 0, 0,1 \\ 1, 0, 0,0 \\ 0,-1, 0,0 \end{bmatrix} + 0.5\begin{bmatrix} 0, 0,0,1 \\ 0, 0,1,0 \\ 0,-1,0,0 \\ -1, 0,0,0 \end{bmatrix}$$

$$= 0.5(\mathbf{v_0} + \mathbf{v_1} + \mathbf{v_2} + \mathbf{v_3}).$$

•	$\mathbf{v_0}$	$\mathbf{v_1}$	$\mathbf{v_2}$	$\mathbf{v_3}$
$\mathbf{v_0}$	$\mathbf{v_0}$	$\mathbf{v_1}$	$\mathbf{v_2}$	$\mathbf{v_3}$
$\mathbf{v_1}$	$\mathbf{v_1}$	$-\mathbf{v_0}$	$\mathbf{v_3}$	$-\mathbf{v_2}$
$\mathbf{v_2}$	$\mathbf{v_2}$	$-\mathbf{v_3}$	$-\mathbf{v_0}$	$\mathbf{v_1}$
$\mathbf{v_3}$	$\mathbf{v_3}$	$\mathbf{v_2}$	$-\mathbf{v_1}$	$-\mathbf{v_0}$

Fig. 6. Unitary Hadamard matrix $\mathbf{Q} = 0.5\ (\mathbf{v_0}+\mathbf{v_1}+\mathbf{v_2}+\mathbf{v_3})$ as a sum of 4 sparse matrices. The multiplication table of this set of sparse matrices is shown, closed under multiplication and corresponding to the multiplication table of the Hamilton quaternion algebra.

$$\mathbf{Q^1} = 0.5\begin{bmatrix} 1, 1,-1,1 \\ -1, 1, 1,1 \\ 1,-1, 1,1 \\ -1,-1,-1,1 \end{bmatrix};\quad \mathbf{Q^2} = 0.5\begin{bmatrix} -1,1,-1,1 \\ -1,-1,1,1 \\ 1,-1,-1,1 \\ -1,-1,-1,-1 \end{bmatrix};\quad \mathbf{Q^3} = 0.5\begin{bmatrix} -1,0,0,0 \\ 0,-1,0,0 \\ 0,0,-1,0 \\ 0,0,0,-1 \end{bmatrix}$$

$$\mathbf{Q^4} = 0.5\begin{bmatrix} -1,-1, 1,-1 \\ 1,-1,-1,-1 \\ -1, 1,-1,-1 \\ 1, 1, 1, -1 \end{bmatrix};\quad \mathbf{Q^5} = 0.5\begin{bmatrix} 1,-1, 1,-1 \\ 1, 1,-1,-1 \\ -1, 1, 1,-1 \\ 1, 1, 1, 1 \end{bmatrix};\quad \mathbf{Q^6} = 0.5\begin{bmatrix} 1,0,0,0 \\ 0,1,0,0 \\ 0,0,1,0 \\ 0,0,0,1 \end{bmatrix}$$

Fig. 7. Sequence of matrices $\mathbf{Q^n}$ (n = 1, 2, 3, 4, 5, 6) for the unitary quaternion **Q** from Fig. 5.

figure also depicts all 6 members of one period of the cyclic group of the unitary quaternion $\mathbf{Q^n}$ from Fig. 7 (i.e., $\mathbf{Q^1}$, $\mathbf{Q^2}$, $\mathbf{Q^3}$, $\mathbf{Q^4}$, $\mathbf{Q^5}$, $\mathbf{Q^6}$) as unitary matrix representations of these colors.

The enumerated properties of the cyclic group of the unitary Hamilton quaternion $\mathbf{Q^n}$ turn out to be identical to the phenomenological properties of inherited color perception, represented on Newton's 6-sector color circle (Fig. 8). This circle illustrates that color perception is based on three primary colors (red, blue, green) and three complementary colors (cyan, yellow, magenta), lying at the vertices of two triangles of its "Star of David". On Newton's color circle, color perception is represented by the following phenomenological properties, analogous to the just-named structural-algebraic properties of the ensemble of members of the cyclic group of unitary quaternions $\mathbf{Q^n}$:

- 1) opposite colors on the circle are complementary and cancel each other out when superimposed;
- 2) each color on the circle represents the sum of the two colors adjacent to it;
- 3) the three primary colors, as well as the three complementary colors, standing at the vertices of the two triangles of the "Star of David", cancel each other out when superimposed.

Inherited color perception is built on the interaction of visual receptors with photons (quanta of electromagnetic waves), that is, it related to quantum mechanics and quantum informatics. It is not without reason that the founder of the wave theory of quantum mechanics, E. Schrödinger, conducted fundamental research in the field of color metrics and the theory of color perception in the period from 1920 to 1926, relying on the idea of the importance of understanding the laws of human sensory perception of the world for all of physics; his key idea was that the space of color perception has a non-Euclidean nature [Niall, 2017]. It seems that further study of phenomenological properties of inherited color perception in their connections with genetic informatics are important materials to progress quantum information biology. Incidentally, one can note the existence of a certain analogy between a circle divided into arbitrarily small fragments by an ordered sequence of such unitary power quaternions and ancient ideas about the cycle of rebirth (for example, the wheel of samsara – one of the central concepts in ancient Indian philosophy).

The problem of color mixing can now formally be solved using the quantum-logical language of the cyclic group of unitary Hamilton quaternions (built on the genetic alphabet of unitary Hadamard gates), if each of the 6 colors of Newton's circle is assigned a unitary quaternion **Q** to the corresponding power, as shown in Fig. 8. For example, what color results from mixing 3 parts red, 2 parts yellow, and 5 parts blue? The answer is obtained by summing the corresponding unitary quaternions: $3\mathbf{Q^1} + 2\mathbf{Q^6} + 5\mathbf{Q^3} = 3\mathbf{Q^2}$, i.e., 3 parts magenta. In psychophysics, it is known that color is not a physical property of an object, but an inherited psychophysical reaction of a person to the light stimulus coming from the object, considering the overall light environment. In modern literature, the features of color perception, like other features of sensory experience, are denoted by the term "qualia"; the topic of qualia is one of

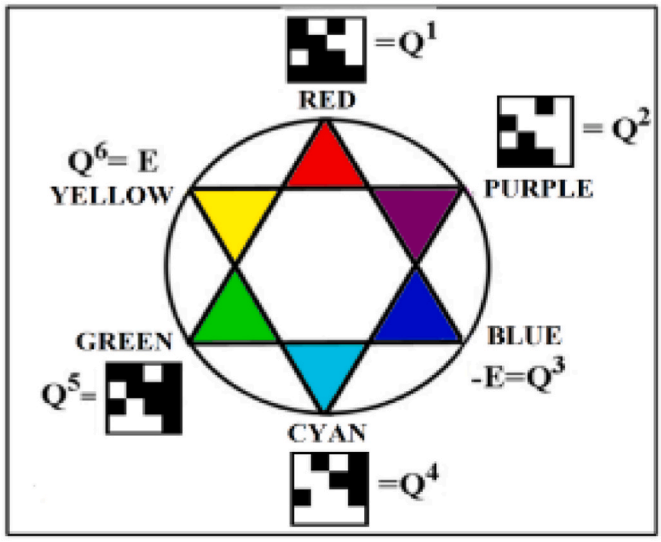


Fig. 8. Newton's color circle from the psychophysics of color perception and the correspondence to it of the matrix members of the cyclic group of the unitary Hamiltonian quaternion $\mathbf{Q^n}$, the period of which is 6. In each matrix, the black cells contain the numbers "+0.5″, and the white ones contain "-0.5". The symbol **E** denotes the identity matrix. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

the most acute and widely discussed topics in contemporary philosophy, seeing it as the key to understanding the nature of consciousness.

If we initially take a unitary quaternion to a fractional power $1/k$, where k is a positive integer, and then raise it to integer powers n, then using the resulting cyclic sequence of unitary quaternions $\mathbf{Q^{n/k}}$, by choosing the desired value of k, we can divide Newton's color circle into any desired number of parts, for example, 80, and not just 6 as in Newton's circle. In this case, each part of the circle upon such division is associated with its own unitary quaternion to the appropriate power. Based on the classical color circle in Fig. 8 and the assignment indicated there of each primary color to a unitary quaternion of the corresponding power, one can calculate, through the mathematics of unitary quaternions, which specific color shade, for example, out of 80 shades, corresponds to a unitary quaternion in a specific power. In other words, a regular sequence of unitary quaternions in fractional powers can be matched with a regular sequence of the same number of color shades, each receiving its own mathematical identification in the form of a unitary quaternion to the appropriate power. Thus, we obtain a regular "unitary-quaternion palette" of color shades, arbitrarily detailed. The considered sequence of unitary quaternions $\mathbf{Q^{n/k}}$ (where n = 1, 2, 3, …) is endowed with the following regularities (3):

$$Q^{n/k} = Q^{n/k+6}; \quad Q^{n/k} = Q^{n/k-1} + Q^{n/k+1}; \quad Q^{n/k} = -Q^{n/k+3} \tag{3}$$

The mentioned comparison of an ordered sequence of unitary quaternions with a corresponding ordered sequence of color shades is useful, for example, in connection with the widely known psychophysical Lüscher color test [Lüscher, 1971; Dragunsky, 2001]. It is applied, in particular, in ergonomics to assess the psychophysiological state of a worker, their stress resistance, activity level, communication abilities, optimal career guidance, etc. When conducting the Lüscher test, the subject is presented with a set of colored cards (there may be several dozen of cards), which the subject must arrange in a sequence starting from the most pleasant color shades to the most unpleasant. Based on the created color sequence, the specialist makes the desired conclusion about the psychophysiological state of the subject. Considering our data described above, it is now possible to represent the color sequence obtained in the test as a sequence of corresponding unitary quaternions, conducting its mathematical analysis for a deeper characterization of the psychophysiological state of the subjects, associated with their genetic quantum-logical features.

Cyclic groups of unitary quaternions can also be used for quantum-logical modeling of: innate algorithmic movements of limbs in human and animal locomotion; formation of the three-dimensional structure of proteins based on relative rotations of adjacent segments of the protein molecule (protein folding), etc. The hypothesis about the leading role of Hamilton quaternion operators (with their specific connection to rotations in three-dimensional physical space) in protein folding was already expressed earlier in the work [Carlevaro et al., 2016], together with an attempt, not related to quantum logic, quantum informatics, and unitary operators, to interpret nucleotide and amino acid sequences as sequences of quaternions. The article [Hanson and Thakur, 2012] is also devoted to applications of quaternions to inherited global protein structures.

Now consider an example of a matrix representation of unitary biquaternions in the form of a block (8×8)-matrix **B**, whose (2×2)-blocks are the alphabet genetic Hadamard gates (Fig. 9). It is a unitary Hadamard matrix, satisfying the unitarity criterion: $\mathbf{B \bullet B^T = E}$, where $\mathbf{B^T}$ is the transposed version of **B**, and **E** is the identity matrix of the eighth order.

Let us show that it serves as a matrix representation of a biquaternion. Indeed, the matrix **B** is the sum of 8 sparse matrices, the set of which is closed under multiplication and corresponds to the multiplication table known in biquaternion algebra and shown below in Fig. 10.

Thus, the unitary matrix **B** is a matrix representation of the biquaternion $2^{-1.5}(\mathbf{b_0}+\mathbf{b_1}+\mathbf{b_2}+\mathbf{b_3}+\mathbf{b_4}+\mathbf{b_5}+\mathbf{b_6}+\mathbf{b_7})$, which can be called a unitary biquaternion. Raising this unitary biquaternion **B** to integer powers generates a cyclic group of unitary transformations with a period of 24 and a number of regular relationships between its different members, including opposite-sign members of the power group separated by 12 powers (4):

$$\begin{aligned} B^n = B^{n+24}, B^n = -B^{n+12}, B^n = B^{n-4} + B^{n+4}, B^n = -\left(B^{n-8} + B^{n+8}\right), B^n \\ = 2^{-0.5}\left(B^{n-3} + B^{n+3}\right) \end{aligned} \tag{4}$$

The quantum-logical properties of this cyclic group $\mathbf{B^n}$ of the unitary biquaternion allow it to be used for modeling the features of 24-h biological rhythms (circadian rhythms), especially since biquaternions in physics are traditionally used for modeling spatio-temporal relationships. Since ancient times, it has been known that different physiological subsystems of our organism go through coordinated phases of activity and passivity during the day, which, according to ancient and modern medicine, determines humanity's division of the day into 24 h [Wright, 2003]. Time is called the "fundamental factor of life," perceived by all organisms at all times [ibid.]. The biorhythmic organization of inherited processes is distributed throughout the body of organisms of various species, including those lacking a nervous system. Biological clocks, counting minutes, months, and years, ensure the coordinated work of body parts according to a specific plan. They are responsible for the aging process and death, and their malfunctions are linked to cancer, Parkinson's disease, etc.

The cyclic group of the unitary biquaternion $\mathbf{B^n}$, obtained by raising it to integer powers and having a period of 24 (i.e., the sequence of powers 1, 2, 3, …, 24 in one period of this group of unitary operators $\mathbf{B^n}$), is, in our quantum-logical approach, analogous to the 24-h clock dial in Fig. 11 and, accordingly, a model of the circadian 24-h biorhythm (this is clearly demonstrated by placing the sequence of 24 members of one period of this cyclic group of biquaternions $\mathbf{B^n}$ on the shown clock dial, divided into 24 parts).

The unitary biquaternions $\mathbf{B^n}$ and $\mathbf{B^{n+12}}$ opposite on the dial differ only in opposite sign ($\mathbf{B^n = -B^{n+12}}$) by analogy with the opposition of daytime and nighttime hours on it. For example, in everyday life, instead of "14 o'clock", people often say "2 o'clock in the afternoon", naming the opposite number on this dial.

$$\mathbf{B} = 0.5 \begin{bmatrix} H_G & H_A & -H_G & -H_A \\ -H_A & H_G & H_A & -H_G \\ H_G & H_A & H_G & H_A \\ -H_A & H_G & -H_A & H_G \end{bmatrix} = 2^{-1.5} \begin{bmatrix} 1 & 1 & -1 & 1 & -1 & -1 & 1 & -1 \\ -1 & 1 & 1 & 1 & 1 & -1 & -1 & -1 \\ 1 & -1 & 1 & 1 & -1 & 1 & -1 & -1 \\ -1 & -1 & -1 & 1 & 1 & 1 & 1 & -1 \\ 1 & 1 & -1 & 1 & 1 & 1 & -1 & 1 \\ -1 & 1 & 1 & 1 & -1 & 1 & 1 & 1 \\ 1 & -1 & 1 & 1 & 1 & -1 & 1 & 1 \\ -1 & -1 & -1 & 1 & -1 & -1 & -1 & 1 \end{bmatrix}$$

Fig. 9. Block matrix **B** of the eighth order, which is a unitary Hadamard matrix.

$$\mathbf{B} = 2^{-1.5} \begin{bmatrix} 1,0,0,0,0,0,0,0 \\ 0,1,0,0,0,0,0,0 \\ 0,0,1,0,0,0,0,0 \\ 0,0,0,1,0,0,0,0 \\ 0,0,0,0,1,0,0,0 \\ 0,0,0,0,0,1,0,0 \\ 0,0,0,0,0,0,1,0 \\ 0,0,0,0,0,0,0,1 \end{bmatrix} + 2^{-1.5} \begin{bmatrix} 0,1,0,0,0,0,0,0 \\ -1,0,0,0,0,0,0,0 \\ 0,0,0,1,0,0,0,0 \\ 0,0,-1,0,0,0,0,0 \\ 0,0,0,0,1,0,0,0 \\ 0,0,0,0,-1,0,0,0 \\ 0,0,0,0,0,0,1,0 \\ 0,0,0,0,0,0,-1,0 \end{bmatrix} + 2^{-1.5} \begin{bmatrix} 0,0,-1,0,0,0,0,0 \\ 0,0,0,1,0,0,0,0 \\ 1,0,0,0,0,0,0,0 \\ 0,-1,0,0,0,0,0,0 \\ 0,0,0,0,0,0,-1,0 \\ 0,0,0,0,0,0,0,1 \\ 0,0,0,0,1,0,0,0 \\ 0,0,0,0,-1,0,0,0 \end{bmatrix} +$$

$$+ 2^{-1.5} \begin{bmatrix} 0,0,0,1,0,0,0,0 \\ 0,0,1,0,0,0,0,0 \\ 0,-1,0,0,0,0,0,0 \\ -1,0,0,0,0,0,0,0 \\ 0,0,0,0,0,0,0,1 \\ 0,0,0,0,0,0,1,0 \\ 0,0,0,0,0,-1,0,0 \\ 0,0,0,0,-1,0,0,0 \end{bmatrix} + 2^{-1.5} \begin{bmatrix} 0,0,0,0,-1,0,0,0 \\ 0,0,0,0,0,-1,0,0 \\ 0,0,0,0,0,0,-1,0 \\ 0,0,0,0,0,0,0,-1 \\ 1,0,0,0,0,0,0,0 \\ 0,1,0,0,0,0,0,0 \\ 0,0,1,0,0,0,0,0 \\ 0,0,0,1,0,0,0,0 \end{bmatrix} + 2^{-1.5} \begin{bmatrix} 0,0,0,0,-1,0,0,0 \\ 0,0,0,0,1,0,0,0 \\ 0,0,0,0,0,0,0,-1 \\ 0,0,0,0,0,1,0,0 \\ 0,1,0,0,0,0,0,0 \\ -1,0,0,0,0,0,0,0 \\ 0,0,0,1,0,0,0,0 \\ 0,0,-1,0,0,0,0,0 \end{bmatrix} +$$

$$+ 2^{-1.5} \begin{bmatrix} 0,0,0,0,0,0,1,0 \\ 0,0,0,0,0,0,0,-1 \\ 0,0,0,0,-1,0,0,0 \\ 0,0,0,0,0,1,0,0 \\ 0,0,-1,0,0,0,0,0 \\ 0,0,0,1,0,0,0,0 \\ 1,0,0,0,0,0,0,0 \\ 0,-1,0,0,0,0,0,0 \end{bmatrix} + 2^{-1.5} \begin{bmatrix} 0,0,0,0,0,0,-1,0 \\ 0,0,0,0,0,0,0,-1 \\ 0,0,0,0,0,1,0,0 \\ 0,0,0,0,1,0,0,0 \\ 0,0,0,1,0,0,0,0 \\ 0,0,1,0,0,0,0,0 \\ 0,-1,0,0,0,0,0,0 \\ -1,0,0,0,0,0,0,0 \end{bmatrix}$$

•	b_0	b_1	b_2	b_3	b_4	b_5	b_6	b_7
b_0	b_0	b_1	b_2	b_3	b_4	b_5	b_6	b_7
b_1	b_1	$-b_0$	b_3	$-b_2$	b_5	$-b_4$	b_7	$-b_6$
b_2	b_2	$-b_3$	$-b_0$	b_1	b_6	$-b_7$	$-b_4$	b_5
b_3	b_3	b_2	$-b_1$	$-b_0$	b_7	b_6	$-b_5$	$-b_4$
b_4	b_4	b_5	b_6	b_7	$-b_0$	$-b_1$	$-b_2$	$-b_3$
b_5	b_5	$-b_4$	b_7	$-b_6$	$-b_1$	b_0	$-b_3$	b_2
b_6	b_6	$-b_7$	$-b_4$	b_5	$-b_2$	b_3	b_0	$-b_1$
b_7	b_7	b_6	$-b_5$	$-b_4$	$-b_3$	$-b_2$	b_1	b_0

Fig. 10. Decomposition of the unitary (8*8)-matrix B from Fig. 9 into a sum of 8 sparse matrices $\mathbf{B} = 2^{-1.5}(\mathbf{b_0}+\mathbf{b_1}+\mathbf{b_2}+\mathbf{b_3}+\mathbf{b_4}+\mathbf{b_5}+\mathbf{b_6}+\mathbf{b_7})$, whose set is closed under multiplication and defines the multiplication table shown at the bottom right. Here $\mathbf{b_0}$ is the identity matrix.

Note that, by analogy with raising the unitary quaternion to fractional powers described above, raising the unitary biquaternion **B** to fractional powers allows us to obtain a division of the model 24-h dial into smaller divisions, for example, into 1440 min, as well as into larger divisions, for example, eight 3-h divisions. This transition to sequences of smaller time intervals is useful for modeling ultradian rhythms, i.e., biological cycles with a period of less than 24 h (usually from minutes to 10-12 h), repeated several times a day; they regulate vital processes, including sleep phases (about 90-100 min), heartbeat, digestion, hormonal activity, as well as fluctuations in performance levels and emotional states.

The alphabet unitary Hadamard matrices $\mathbf{H_C}$, $\mathbf{H_A}$, $\mathbf{H_T}$, and $\mathbf{H_G}$ (Fig. 1), and their tensor-extended versions are associated with corresponding complete orthogonal systems of Walsh functions. The latter are, in digital informatics, the basis of spectral analysis of signals, called Harmut's sequency analysis [Harmuth, 1977], and are associated with cyclic Gray codes, logical holography, Walsh antennas, and also the fractal Hilbert curve, which is known to correspond to spatial organization of the human genome in the cell nucleus according to the work [Lieberman-Aiden et al., 2009]. This point will not be elaborated upon here, directing the interested reader to works on the relevant topic. The next section shows the connection of Walsh-Hadamard spectral analysis with the discovered statistical universality in the organization of genomic DNAs of various organisms, which confirms the reality of the considered algebraic-alphabetic approach to bioinformatics and also indicates the existence of hidden informational structures in genetics related to the dichotomous principle of "even and odd" in relation to the number of hydrogen bonds in complementary nucleotides. The mentioned dichotomous principle is reflected in the names of even and odd Walsh functions, which will be discussed.

4. Statistical universalities of genomic DNAs, binary-genomic numbers and Walsh-Hadamard filters

The considered genetic unitary Hadamard (2x2)-matrices and their tensor powers in the form of Hadamard (2^nx2^n)-matrices contain in their

Fig. 11. 24-hour clock dial of the day with its division into daytime and nighttime 12-h halves. The numbers on the dial correspond to exponents 1, 2, 3, …, 23, 24 in the set of 24 members of one period of the cyclic group of unitary biquaternions $\mathbf{B^n}$, obtained by raising the biquaternion **B** from Figs. 9 and 10 to integer powers.

rows the Walsh functions (arranged in Hadamard order), consisting of elements +1 and −1 and forming a complete orthonormal basis for representing digital signals [Wolfram, 2002]. For the problems of spectral analysis of signals, it is most convenient to arrange the Walsh functions w (k,n) in Walsh order, that is, according to the number of sequents k, equal to the number of switching of the plus and minus signs along the function, as shown in Fig. 12 for the Hadamard matrices $\mathbf{H_2}$, $\mathbf{H_4}$, $\mathbf{H_8}$, and $\mathbf{H_{16}}$, the index of which denotes the order of the matrix. All Walsh functions w (k,n) are divided into even and odd functions, denoted respectively as cal (k,n) = w (2k,n) and sal (k,n) = w (2k-1,n). For spectral analysis problems, these functions are analogous to trigonometric sines and cosines.

Hadamard matrices $\mathbf{H_n}$ acting on n-dimensional vectors, called the Walsh-Hadamard transform, decomposes the analyzed vector into a superposition of Walsh functions, called the Hadamard spectrum $\mathbf{S_n}$ of the input vector. In this spectrum, each Walsh function from the applied Hadamard matrix receives its own spectral coefficient. Using the condition $\mathbf{H_n}\cdot\mathbf{H_n^T} = n\mathbf{E}$ (here n is the order of the Hadamard matrix, T is the transpose sign, E is the identity matrix), which Hadamard matrices $\mathbf{H_n}$ satisfy, one can — by applying the transposed matrix $\mathbf{H_n^T}$ to the spectrum vector $\mathbf{S_n}$ — obtain a vector which, when divided by n, exactly reproduces the original vector. In some cases, the Hadamard spectrum of the analyzed vector turns out to contain a number of small, and therefore insignificant, spectral coefficients of certain Walsh functions. By neglecting these small spectral coefficients (i.e., setting them to zero), we obtain a filtered Hadamard spectrum $\mathbf{S_n}$/n, from which the original vector can be reconstructed with a small error using the described procedure. This slightly approximated vector turns out to be sufficient in some cases for analyzing the system under study. This procedure in informatics is called Walsh filtering or Walsh filter. Let us describe its application to the analysis of the statistical organization of nucleotide sequences of single-stranded genomic DNAs.

Nucleotide sequences in genomic DNAs, presented in the publicly available DNAs bank of many organisms, GenBank, are very long. For example, the nucleotide sequence of single-stranded DNA of the first human chromosome contains about 250 million nucleotides of the four types A, C, G, T (data for this DNA was taken by the author from the site https://www.ncbi.nlm.nih.gov/nuccore/NC_000001.11). Nucleotide sequences can be considered as binary sequences, for example, a sequence of purines (A and G), denoted by the symbol 0, and pyrimidines (C and T), denoted by the symbol 1. In this case, we obtain a binary (purine-pyrimidine) representation of the named single-stranded DNA of the first human chromosome in the form of a super-huge binary number with about 250 million bits (the decimal analogue of such a number reaches up to $2^{250000000}$). Numbers of this origin are called "binary-genomic" (BG-numbers) [Petoukhov and Svirin, 2024]. It can be assumed that they reflect the laws and mechanisms of quantum bioinformatics, genetic memory, and algebraic biology in general.

To detect statistical patterns hidden in the BG-numbers of different types of organisms, these binary numbers were analyzed using the author's method of hierarchy of binary statistics, including the following stages of percentage composition analysis of the BG-number: first, it is represented as a sequence of single symbols 0-1-1-1-0-0- …, and the percentages %0 and %1 are counted; then it is represented as a sequence of duplets 01-11-00-10- … and the percentages of each type of binary duplets %00, %01, %10, %11 are counted; then similarly, the same binary sequence is represented as a sequence of triplets, quadruplets, quintuplets, … each time counting the percentages of the corresponding types of n-plets. Thus, each BG-number is represented as a multi-layered structure, each layer written in the alphabet of the corresponding dyadic group of n-bit numbers. As a result, for the BG-number we obtain probability values for each type of n-plet in the corresponding n-plet layer. Table 2 shows an example set of probabilities of n-plets in the corresponding n-plet layer of a binary-genomic number of the purine-pyrimidine type, corresponding to the nucleotide sequence of the aforementioned single-stranded DNA of the first human chromosome. These sets for each n-plet layer are conveniently represented as binary n-

$H_2 =$

1, 1	w(0,2)
1, -1	w(1,2)

;

$H_4 =$

1, 1, 1, 1	w(0,4)
1, 1, -1, -1	w(1,4)
1, -1, -1, 1	w(2,4)
1, -1, 1, -1	w(3,4)

;

$H_8 =$

1, 1, 1, 1, 1, 1, 1, 1	w(0,8)
1, 1, 1, 1,-1,-1,-1,-1	w(1,8)
1, 1,-1,-1,-1,-1, 1, 1	w(2,8)
1, 1,-1,-1, 1, 1,-1,-1	w(3,8)
1,-1,-1, 1, 1,-1,-1, 1	w(4,8)
1,-1,-1, 1,-1, 1, 1,-1	w(5,8)
1,-1, 1,-1,-1, 1,-1, 1	w(6,8)
1,-1, 1,-1, 1,-1, 1,-1	w(7,8)

Fig. 12. Hadamard matrices $\mathbf{H_2}$, $\mathbf{H_4}$, $\mathbf{H_8}$, and H_{16}, whose rows, containing their Walsh functions w (k,n), are arranged in ascending order of sequent (number of sign changes). To the right of the matrices, marked with bold borders, are the Walsh functions corresponding to their rows, with the value of the sequent k and the matrix order n indicated.

Table 2
Vectors $\overline{D}_n$ of probabilities of n-plets in the corresponding n-plet layers of the binary-genomic number of the purine-pyrimidine type for the considered case of single-stranded DNA of the first human chromosome (here n = 1, 2, 3, 4).

$\overline{D}_1 = [0.4997, 0.5003]$
$\overline{D}_2 = [0.2807, 0.2191, 0.2190, 0.2812]$
$\overline{D}_3 = [0.1646, 0.1161, 0.1031, 0.1160, 0.1160, 0.1031, 0.1159, 0.1652]$
$\overline{D}_4 = [0.0977, 0.0669, 0.0556, 0.0604, 0.0555, 0.0476, 0.0490, 0.0670, 0.0669, 0.0490, 0.0475, 0.0556, 0.0605, 0.0555, 0.0669, 0.0982]$

dimensional vectors $\overline{D}_n$, whose sequence of coordinates is the sequence of probabilities of the corresponding n-plets in the layer. For example, in the binary 4-dimensional vector $\overline{D}_2 = [0.2807, 0.2191, 0.2190, 0.2812]$ the sequence of its coordinates in the case of the named DNA represents the probabilities of its binary duplets in ascending order of their binary symbols: %00 = 0.2807, %01 = 0.2191, %10 = 0.2190, %11 = 0.2812. Table 2 shows the corresponding family of binary 2^n-dimensional vectors $\overline{D}_n$ of the considered probabilities for the case of the DNA of the first human chromosome.

The Hadamard spectra S_n of these probability vectors, obtained by multiplying the vectors $\overline{D}_n$ from Table 2 by the corresponding Hadamard matrices from Fig. 12, have the following form (5):

$$S_2 = \overline{D}_1 * H_2 = [1.0000, -0.0006],$$
$$S_4 = \overline{D}_2 * H_4 = [1.0000, -0.0004, 0.1238, -0.0006]$$
$$S_8 = \overline{D}_3 * H_8 = [1.0000, -0.0004, 0.1236, -0.0004, 0.1236, -0.0008, 0.0720, -0.0008]$$
$$S_{16} = \overline{D}_4 * H_{16} = [0.9998, -0.0004, 0.1236, -0.0006, 0.1234, -0.0004, 0.0720, -0.0006, 0.1238, -0.0008, 0.0200, -0.0006, 0.0722, -0.0000, 0.0324, -0.0006] \quad (5)$$

In these Hadamard spectra (5), a general pattern is visible: all their odd-numbered coordinates are close to zero and, in the filtered (by the Walsh-Hadamard filter method) Hadamard spectrum, can be zeroed out as insignificant (ordinal numbers of coordinates are considered corresponding to the ascending series of decimal numbers 0, 1, 2, 3, …). Conversely, the magnitudes of all even-numbered coordinates are relatively far from zero, and accordingly, it is precisely the even coordinates, which are the spectral coefficients of even Walsh functions of the type w (0,4), w (2,4), w (0, 8), w (2,8) and so on (Fig. 12), that have dominant importance in the statistical organization of the n-plet layers of the considered human chromosomal DNA. A similar result on the dominant importance of precisely even Walsh functions cal (k,n) = w (2k,n) is given by the analysis of the Hadamard spectrum of single-stranded DNAs from many genomes of higher and lower organisms similarly studied by the author: all 24 human chromosomes; all chromosomes of Drosophila, mouse, worm, many plants; 19 genomes of bacteria and archaea; many extremophiles living in extreme conditions, for example, with radiation levels exceeding by 1000 times the level lethal for humans [Petoukhov, 2023].

These results testify in favor of the existence of a universal rule of statistical organization of genomic DNAs in all organisms, according to which the Hadamard spectrum of binary-genomic numbers representing these DNAs is based precisely on even Walsh functions cal (k,n) = w (2k, n), which are opposed to odd Walsh functions sal (k,n) = w (2k-1,n). The identification of statistical rules in the organization of genomic DNAs is especially important because in living bodies, everything is built on stochastics, since individual molecules interact in cells in a stochastic manner. It is no wonder that P. Jordan, author of the first article on quantum biology, asserted that the laws of life missed by science are the laws of probabilities of the quantum world [McFadden and Al-Khalili, 2018]. Genetics itself as a science began with Mendel's discovery of stochastic rules of trait inheritance when crossing organisms. As it was above-mentioned, each organism is a probabilistic machine of multi-channel noise-immune coding.

This universal rule of statistical organization of genomic DNAs reveals the importance of the dichotomous principle of "even and odd" in biological organization, which has long attracted the attention of science. For example, it is known that in its origins, modern mathematics goes back to the Pythagoreans, according to whose teaching the binary opposition of even and odd determines the entire nature of the world. Pasteur noted that all living things are characterized by a special kind of asymmetry of left and right. Dichotomous division is represented in the structure of the brain consisting of two hemispheres, and is also fractally embedded in the inherited branching of blood vessels, neurons, the bronchial tree of the lungs, branches in plants, etc. The teaching about even and odd is characteristic of the ancient theory of art of the Far East with its Yin-Yang symbol and the representation of female (even) and male (odd) numbers. In particular, all ancient Chinese arithmetic was built on the female number 2 and the male number 3.

The book with the telling title "Even and Odd: Asymmetry of the Brain and Sign Systems" thoroughly demonstrates the significance of the even-odd principle in the entire history of codes of human culture [Ivanov, 1978]. The author of this book connects this principle, among other things, with the asymmetries of the two hemispheres of the brain, which participate differently in such types of activity as language and mathematics. He notes the significance of this principle in research on "human-machine" systems, the creation of algorithmic languages for artificial intelligence and automata theory, etc. He also notes that in all early human societies, the difference between the right and left hands was part of the system of basic binary oppositions that determined the structure of rituals, myths, and works of art. The problem of left-handedness and right-handedness is important for ergonomics, since tools and workplaces are created predominantly for right-handed people. And this right-handed world has to be specially adapted for left-handed people to relieve their muscle tension, fatigue, and increase productivity. For this, a mirror arrangement of elements in work tools (scissors, knives), workstation settings (mouse, documents, phone – under the left hand, keyboard with numeric keypad (num pad) on the left, etc.) is used. Additionally, it is considered that a person's right hand is controlled by the left hemisphere of the brain, and the left hand by the right. The left hemisphere is responsible for logic, analysis, and calculation, while the right is responsible for emotions and intuition. Accordingly, it is believed that right-handers are more logical and rational, while left-handers are emotional and sensitive. There are many left-handers among designers (12%), procurement specialists (11%), and programmers (10%). People who were retrained to use their right hand instead of their left are often found among security guards (11%)

and logisticians (9%). Those who are equally adept with both right and left hands work as PR specialists and doctors [https://snob.ru/news/eksperty-vyyasnili-chastye-professii-pravshei-levshey/].

According to the author of this article, the 64-triplet matrix acts as a "genetic chessboard" endowed with the dichotomy of black and white cells when using even and odd numbering of its rows and columns. Moreover, on this genetic board, the families of 32 black cells and 32 white cells contain identical sets of amino acids and stop codons; these facts indicate a connection between chess and genetic archetypes, which may serve as a hidden reason for the popularity of chess and checkers for thousands of years worldwide. Let us add that in the ancient Indian Vedas (Agni Purana), the 64-square plan is interpreted as a mystical diagram of the Vedas, a model of the world [Petoukhov, 2025a]. The next section of the article continues the theme of even and odd in connection with the two hemispheres of the brain and its inherited mechanisms of perceiving events in the surrounding world.

5. On inherited systems of mirror neurons and unitary Hadamard operators

Let us return to the alphabet of unitary Hadamard operators of algebraic-operator bioinformatics, containing the unitary matrices of reflection transformations $\mathbf{H_A}$ and $\mathbf{H_T}$, which are mirror copies of each other with respect to the second diagonal of the matrix (Fig. 1). The presence of these Hadamard reflection operators in the alphabetical foundations of algebraic bioinformatics is associated with the important topic of mirror neuron systems in the brain, inherited from generation to generation. These are neurons that fire both when an organism performs a specific action and when observing the performance of that action by another [Rizzolatti et al., 2001]. They underlie empathy, imitation, learning, and understanding intentions, essentially building a mirror image of the observed in the brain. These neurons allow one to "try on" the feelings of another person, mirroring the observed action (reminiscent of the ancient principle "like begets like," realized, in particular, in the double helix of DNA and in a number of other phenomenological structures of matrix genetics [Petoukhov, 2023]). Such neurons were discovered in the early 1990s by G. Rizzolatti and have now been reliably found in primates, particularly in humans, as well as in some birds and insects. It can be assumed that the inheritance of mirror neurons is structurally linked to a certain extent with the genetic unitary reflection operators $\mathbf{H_A}$ and $\mathbf{H_T}$ (Fig. 1). There is a popular view that the activation of mirror neurons occurs not due to any single neuron, but as a coordinated result of the work of a neural network.

Some scientists call their discovery the most important event in neuroscience in recent decades. Thus, V.S. Ramachandran (Director of the Center for Brain and Cognition, University of California, USA) believes that "*mirror neurons will do for psychology what DNA did for biology: they will provide a unified conceptual framework and help explain many mental abilities that have until now remained mysterious and inaccessible to experiments*" [Ramachandran, 2022]. Expenditures on research in the field of mirror neurons, according to The Economist, are growing almost exponentially every year, as the field itself is predicted to be one of the main trends in the development of science in the coming years [Makarov, 2006]. The mirror neuron system (MNS) is distributed in both hemispheres of the brain, but the left and right hemispheres process information differently in a mutually complementary way: the left hemisphere is responsible for the symbolic content of the action (what exactly is being done and why), and the right for its emotional coloring and spatial characteristics [Aziz-Zadeh et al., 2006]. Knowledge about the importance of mirror neurons is used in applied contexts, for example, there are works showing that visualization can significantly improve the game of every football player and that visualization of lifting weights can even increase muscle strength [Makarov, 2006]. The potential technological applications of this knowledge are currently far from exhausted. Let us emphasize once again that mirror neuron systems not only exist but are also inherited down the generations. Therefore, they are associated in some degree with algebraic-operator bioinformatics and its operator alphabets, including the reflection operators $\mathbf{H_A}$ and $\mathbf{H_T}$, as well as with the above-described rule of asymmetric significance of even and odd Walsh functions in the Hadamard spectra of genomic DNAs.

An important research tool for mirror neurons, widely used worldwide, is the spectral analysis of the mu rhythm (μ-rhythm) of the brain, recorded using EEG and being markers of the activation of these neurons: the mu rhythm is suppressed during motor activity or its imagination. The mu rhythm represents periodic oscillations of biopotentials in the sensorimotor area of the cerebral cortex at a frequency of 8-13 Hz. In particular, this tool is used in studies of the activity of the mirror neuron system during human perception of short time intervals and the role of these neurons in cognitive impairment [TSU, 2018]. The mu rhythm is widely used in constructing brain-computer interfaces, with the help of which scientists hope to give people with severe disabilities new ways of communication and computer control, means for manipulation and movement in space, control of wheelchair movement and neuroprostheses [Pfurtscheller, Christa, 2010]. The mu rhythms and mirror neuron systems are an integral part of genetically inherited physiology. One of the useful methods for analyzing brain mu-rhythms and the activity of mirror neuron systems could be the method of EEG spectral analysis, based on the structural connection of the genetic system with Walsh functions and developed in our laboratory [Stepanyan and Lednev, 2025].

Note also that Walsh functions are associated with cyclic Gray codes, consideration of which made it possible to link the inheritance of cyclic biological structures with the cyclic nature of molecular-genetic coding itself [Petoukhov and Svirin, 2024]. Models based on Gray codes are already used to describe how the brain learns and updates its "maps" [Monteiro et al., 2022].

6. Some concluding remarks

In the quantum-logical approach to bioinformatics, considering the cyclic (or pulsation) features of living bodies, the author relies on a model representation of biomechanical media consisting of interconnected pulsating structures that change coherently over time. The theory of such model program environments can be used in the development of artificial intelligence, including in connection with the pulsating information arrays (pulsars) known in computer architectures [Guzik et al., 2014]. The name "pulsating" reflects the essence of this architecture's operation, traditionally compared to the beating of a heart or a pulse. Here, pulsation appears as a wave of data, and the computation process looks like the propagation of activity waves. Data entering the array inputs begin to "pulsate" through it, transforming at each step. The array can be configured so that different data streams collide and interact in specific cells at strictly defined cycles, generating a new "pulse" of results. This architecture is fundamentally different from the von Neumann architecture of conventional processors because it lacks a central control unit; all cells operate simultaneously and synchronously; data is not written in the classical sense, but continuously "pulsates" through the processor structure, like blood flow through capillaries. The operation of such a pulsating information array is compared to the work of the heart: the array is compared to the muscle tissue of the myocardium; the processor elements to individual heart muscle cells (cardiomyocytes); the heartbeat to the electrical impulse from the sinoatrial node; computations are compared to the coordinated contraction of the heart, pumping blood; information data to the pumped blood. Here, "computation" (pumping blood) is an emergent property of the entire organ, pulsating in a coordinated rhythm; no single cell is responsible for it, but all cells follow a common rhythm and local interactions. Although huge problems in programming and hardware have so far prevented pulsating information arrays from becoming widespread. The most famous example of the implementation of the pulsar concept is the Connection Machine, developed by Thinking Machines Corporation in

the 1980s. It had up to 65,536 simple one-bit processors connected in a hypercube network. The pulsar concept is also closely related to a number of modern architectural concepts, for example, the concept of systolic arrays, whose name originated by analogy of their pulse-like operation with cardiac systoles [Abramavicius et al., 2025]. Systolic arrays are extremely efficient in artificial intelligence tasks, image processing, pattern recognition, computer vision, and other tasks that animal brains handle particularly well. An example is the Google Tensor Processing Unit (TPU), which uses a large two-dimensional systolic array as its core to perform massive matrix multiplications necessary for neural networks with high efficiency.

The existence of a multitude of inherited and mutually coordinated cyclic processes in the body raises the question of the mechanisms of their synchronization. For a model study of this issue, it is proposed to use the fundamental Kuramoto model of autosynchronization in sets of oscillators of different nature [Kuramoto, 1984; https://en.wikipedia.org/wiki/Kuramoto_model]. Given the huge distribution of inherited helical configurations in many types of biomolecules and supramolecular biosystems [Petoukhov et al., 2015; Petoukhov, 2025a], which are participants of the inherited cyclic processes of the body, the author believes it is useful to combine in the future the topics of inherited cyclic and helical structures based on the model notion of “cycle-screws”: each cycle-screw is an oscillating helical (or screw) structure (e.g., molecular), the cyclic motion of which is screw in nature, corresponding to the transformations of the screw calculus (rotations and translations). Based on this concept of cycle-screws and their ensembles in living bodies, it is possible to extend of the Kuramoto model for simulating of autosynchronization in ensembles of cycle-screws and deeper understanding the principles of inherited biological self-organization.

The algebraic-alphabetic bioinformatics presented in this article explains the rapid evolution of organisms: complex tissues are formed not so much by the emergence of new genes, but by changing the ways of using existing genes through the action of operators of this algebraic bioinformatics, associated with electromagnetic and resonance mechanisms. In light of this, the author proposes the evolutionary paradigm of “code algebraic-alphabetic Darwinism,” according to which natural selection and inheritance of the most useful for survival combinations of alphabet operators of algebraic bioinformatics play an important role in evolution. One confirming example of the proposed paradigm of algebra-alphabetic Darwinism is the “iron” snail *Chrysomallon squamiferum*, whose shell is made of iron and sticks to a magnet. In its genome, only 11% of genes are unique. The remaining 89% are reused ancient genes that existed in the common ancestors of mollusks more than 540 million years ago [Yao et al., 2010].

The role of alphabets in human culture and science is exceptionally significant. For example, in the English language, a vast array of works of various types and purposes—novels, poems, scientific treatises, and so on—are created using its alphabet and combinations of alphabetic elements. Within the framework of the proposed evolutionary paradigm of code algebraic-alphabetic Darwinism, algebraic alphabets of bioinformatics can be used to similarly create numerous models of inherited biological structures using appropriate combinations of alphabetic elements.

Currently, almost all human organs (heart, lungs, liver, kidneys, limbs, organs of vision and hearing, etc.) are provided by prosthetics and chips, sensors and electrodes are implanted into the body and brain to monitor and control their states, and modern humans are becoming “human-machines” (cyborgs) in increasing degree. This, in particular, increases the reliability and efficiency of operators; connects the human body with exoskeletons and swarms of robots; allows disabled people to become fully functional operators; with the help of artificial intelligence connected to the human-cyborg, it is possible to monitor and correct functional impairments of the operator, and much more. To provide high-quality of these solutions, the biological and technical parts of the human-cyborg must be informationally consistent and “understand” each other; to achieve this, it is important to study the genetic foundations of bioinformatics and biomechanical algorithms, inherited from generation to generation, as is done in this article.

Briefly note that the formalisms of algebraic bioinformatics also allow for comparative analysis of relatively short genetic sequences (for example, DNA sequences encoding proteins), as well as consideration of time-dependent genetic matrix operators. These issues are beyond the scope of this article and deserve a separate publication. The described algebraic-alphabetic bioinformatics is associated with the actively developing topic of code biology [Barbieri, 2015]. An important component of the formalisms of algebraic-alphabetic bioinformatics are tensor-unitary transformations, which ensure the tensor increase in dimension of configuration vector Hilbert spaces in quantum-logical models of growing biosystems [Petoukhov, 2025a].

The work was carried out within the framework of the state assignment, scientific topic code FFGU-2024-0019.

Declaration of competing interest

The author, Petoukhov S.V., declares that he has no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

The author thanks S. Ya. Kotkovsky, Yu.I. Manin, V.I. Svirin, I.V. Stepanyan, G.K. Tolokonnikov, E. Fimmel, M. He, V.I. Chernoivanov for collaboration.

Data availability

No data was used for the research described in the article.

References

Abbott, D., Davies, P.C.W., Pati, A.K. (Eds.), 2008. Quantum Aspects of Life (Foreword by Sir Roger Penrose). - World Scientific.

Abramavicius, V., Mathé, M., Velikova, G.V., et al., 2025. PulserDiff: a Pulse Differentiable Extension for Pulser. https://doi.org/10.48550/arXiv.2505.16744 arXiv:2505.16744v1 from 22.05.

Asano, M., Basieva, I., Khrennikov, A., et al., 2013. A model of epigenetic evolution based on theory of open quantum systems. Syst. Synth. Biol. 7, 161–173. https://doi.org/10.1007/s11693-013-9123-2.

Aziz-Zadeh, L., Koski, L., Zaidel, E., Mazziotta, J., Iacoboni, M., 2006. Lateralization of the human mirror neuron system. J. Neurosci. 26 (11), 2964–2970. https://doi.org/10.1523/JNEUROSCI.2921-05.2006. PMID: 16540574; PMCID: PMC6673981.

Barbieri, M., 2015. Code Biology. A New Science of Life. Springer-Verlag, ISBN 978-3-319-14534-1. https://doi.org/10.1007/978-3-319-14535-8.

Birkhoff, G., von Neumann, J., 1936. The Logic of Quantum Mechanics, vol. 37, pp. 823–843.

Bruce, D., 2001. The nobel prize for physiology or medicine 2001. Genome Biol. 2. https://doi.org/10.1186/gb-spotlight-20011008-02spotlight-20011008-02.

Carlevaro, C.M., Irastorza, R.M., Vericat, F., 2016. Quaternionic representation of the genetic code. Biosystems 141, 10–19. https://doi.org/10.1016/j.biosystems.2015.12.009. ISSN 0303-2647.

Cohen, D., 1989. An Introduction to Hilbert Space and Quantum Logic. Springer-Verlag.

Dragunsky, V.V., 2001. Color Personality Test: a Practical Guide. Minsk: Harvest, p. 448.

Eigen, M., Schuster, P., 1979. The hypercycle. A Principle of Natural Self-Organization. Springer-Verlag Berlin Heidelberg, New York.

Fimmel, E., Gumbel, M., Karpuzoglu, A., Petoukhov, S., 2019a. On comparing composition principles of long DNA sequences with those of random ones. Biosystems 180, 101–108.

Fimmel, E., Michel, C.J., Pirot, F., Sereni, J.-S., Starman, M., Strüngmann, L., 2020a. The relation between k-Circularity and circularity of codes. Bull. Math. Biol. 82 (105). https://doi.org/10.1007/s11538-020-00770-7.

Fimmel, E., Michel, Ch J., Pirot, F., Sereni, J.-S., Strüngmann, L., 2019b. Mixed circular codes. Math. Biosci. 317, 108231. https://doi.org/10.1016/j.mbs.2019.108231.

Fimmel, E., Starman, M., Strüngmann, L., 2020b. Circular Tessera codes in the evolution of the genetic code. Bull. Math. Biol. 82 (48). https://doi.org/10.1007/s11538-020-00724-z.

Gsponer A., Hurni J.-P. Quaternions in mathematical physics (2): analytical bibliography. - arXiv:math-ph/0511092v3, 124 pages, from 6 July 2008, https://doi.org/10.48550/arXiv.math-ph/0511092.

Gurvich, A.G., 1977. Selected Works. M. Meditsina.

Guzik, V.F., Shmoilov, V.I., Kirichenko, G.A., 2014. Pulsating information grids with matrix switching. - news of universities. North Caucasian region. Series: Tech. Sci. (6), 3–12. https://doi.org/10.17213/0321-2653-2014-6-3-11, 181. https://cyberlen

inka.ru/article/n/pulsiruyuschie-informatsionnye-reshyotki-s-matrichnoy-kommutatsiey.
Hanson, A.J., Thakur, S., 2012. Quaternion maps of global protein structure. J. Mol. Graph. Model. 38, 256–278. https://doi.org/10.1016/j.jmgm.2012.06.004.
Harmuth, H.F., 1977. Sequency Theory: Foundations and Applications. Academic Press.
Hesse, H., 2007. The Glass Bead Game. M.: Meshcheryakov Publishing House, p. 592. ISBN: 978-5-91045-035-0.
Ivanov, Vyach, 1978. Vs. Even and Odd: Asymmetry of the Brain and Sign Systems. - M., Sov. Radio (in Russian).
Kantor, I.L., Solodovnikov, A.S., 1989. Hypercomplex Numbers. Springer-Verlag.
Khrennikov, A., 2004. On quantum-like probabilistic structure of mental information. Open Syst. Inf. Dynam. 11 (3), 267–275.
Khrennikov, A., 2006. Quantum-like brain: interference of minds. Biosystems 84, 225–241.
Kuramoto, Y., 1984. Chemical Oscillations, Waves, and Turbulence. Springer-Verlag, New York, NY.
Lieberman-Aiden, E., van Berkum, N.L., Williams, L., Imakaev, M., Ragoczy, T., Telling, A., Amit, I., Lajoie, B.R., Sabo, P.J., Dorschner, M.O., et al., 2009. Comprehensive mapping of longrange interactions reveals folding principles of the human genome. Science 326, 289.
Lobodennko, E.I., 2009. Quaternion structure of operators describing vibrational-rotational states of molecules. Bull. Tyumen State Univ. (6), 203–209.
Lüscher, M., 1971. In: Scott, Ian A. (Ed.), The Lüscher Color Test/Transl. Pocket Books, New York, p. 187. Original ed. Random House, 1969. — ISBN 0671-78073-5.
Makarov, I., 2006. When they understand you. – expert North-West. No.24(277). https://web.archive.org/web/20070622104643/http://www.expert.ru/printissues/northwest/2006/24/interview_rizzolatti/.
Manin, Yu.I., 1980. Computable and non-computable. Sovetskoye Radio 128 (in Russian).
McFadden, J., Al-Khalili, J., 2018. The origins of quantum biology. Proceed. Royal Society A 474 (2220), 1–13. https://doi.org/10.1098/rspa.2018.0674.
Monteiro, J., Pedro, A., Silva, A.J., 2022. A gray code model for the encoding of grid cells in the entorhinal cortex. Neural Comput. Appl. 34, 2287–2306. https://doi.org/10.1007/s00521-021-06482-w.
Neupane, P., Bhuju, S., Thapa, N., Bhattari, H.K., 2019. ATP synthase: structure, function and inhibition. Biomol. Concepts 10, 1–10. https://doi.org/10.1515/bmc-2019-0001.
Niall, K.K. (Ed.), 2017. Erwin Schrödinger's Color Theory: Translated with Modern Commentary. Springer, Cham, p. 193. https://doi.org/10.1007/978-3-319-64621-3 (Contains Schrödinger's "Grundlinien einer Theorie der Farbenmetrik im Tagessehen" in translation).
Nielsen, M.A., Chuang, I.L., 2010. Quantum Computation and Quantum Information. Cambridge Univ. Press. 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. 2015, 149. https://doi.org/10.1007/JHEP06(2015)149.
Patel, A., 2001a. Quantum algorithms and the genetic code. J. Phys. 56 (2–3), 367–381 (arXiv:quant-ph/0002037).
Patel, A., 2001b. Why genetic information processing could have a quantum basis. J. Biosci. 26 (2), 145–151.
Petoukhov, S.V., 2016. The system-resonance approach in modeling genetic structures. Biosystems 139, 1–11. http://petoukhov.com/PETOUKHOV_ARTICLE_IN_BIOSYSTEMS.pdf.
Petoukhov, S.V., 2022. Binary oppositions, algebraic holography, and stochastic rules in genetic informatics. Biosystems 221, 104760. https://doi.org/10.1016/j.biosystems.2022.104760.
Petoukhov, S.V., 2023. The principle "like begets like" in algebra-matrix genetics and code biology. Biosystems 233, 105019.
Petoukhov, S.V., Svirin, V.I., Khazina, L.V., 2015. Bionics of spiral structures. J. Mach. Manuf. Reliab. 44 (3), 249–253. © Allerton Press, Inc., 2015.
Petoukhov, S.V., 2025a. Quantum logical bioinformatics: genetic alphabet of four hadamard unitary operators, and cyclic groups. Preprints 34. https://doi.org/10.20944/preprints202512.0208.v2, 2025120208. 2025a.
Petoukhov, S., He, M., 2010. Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications. IGI Global, Hershey, USA.
Petoukhov, S.V., He, M., 2023. Algebraic Biology, Matrix Genetics, and Genetic Intelligence. World Scientific, Singapore, p. 616. https://doi.org/10.1142/13468.
Petoukhov, S.V., Svirin, V.I., 2024. Binary-genomic numbers and symmetrical regularities in the statistical organization of genomic DNAs. Symmetry: Cult. Sci. (4), 469–492.
Petoukhov, S.V., 2024b. Genetic code, the problem of coding biological cycles, and cyclic gray codes. Biosystems 246, 105349. https://doi.org/10.1016/j.biosystems.2024.105349.
Petoukhov, S.V., 2025b. Cyclic physiology, cyclic codes and algebraic-logical features of the genetic coding system. Quantum bioinformatics and ancient Indian philosophy. Proceedings of "The International Conference on Science and Spirituality for Global Peace and Harmony (IAPIC-2025)", Hyderabad, Telangana State, India (April 9-12, 2025), Tutorial, pp. 1–10. https://www.iapic.net/IAPIC2025-S01.pdf.
Petoukhov, S.V., 2025c. Genetic intelligence and tensor-unitary transformations. Sys. Inform. 27, 1–14. https://doi.org/10.31144/si.2307-6410.2025.n27.p1-14. https://system-informatics.ru/article/372. https://system-informatics.ru/en/article/372.
Pfurtscheller, G., Christa, N., 2010. Electroencephalography: Basic Principles, Clinical Applications, and Related Fields. — 6th. Lippincott Williams & Wilkins, Philadelphia, PA, pp. 1227–1236, 668 pp. — ISBN 978-0-7817-8942-4.
Prasolov, V.V., 2008. Problems and theorems in linear algebra. M., R&C Dynamics, second ed., p. 536
Preskill, J., 2016. Stability, Topology, Holography: the Many Facets of Quantum Error Correction. http://theory.caltech.edu/~preskill/talks/APS-March-2016-preskill.pdf.
Press release, 2017. The Nobel Prize in Physiology or Medicine. https://www.nobelprize.org/prizes/medicine/2017/press-release/.
Ramachandran, V., 2022. Mirror neurons and imitation learning as the driving force behind the great leap forward in human evolution. https://www.edge.org/conversation/vilayanur_ramachandran-mirror-neurons-and-imitation-learning-as-the-driving-force.
Rebrova, I.M., Yu, Rebrova O., 2020. Storage devices based on artificial DNA: the birth of the idea and first publications. Voprosy Istorii Estestvoznaniya i Tekhniki 41 (4), 666–676. https://doi.org/10.31857/S020596060013006-8.
Rizzolatti, G., Fogassi, L., Gallese, V., 2001. Neurophysiological mechanisms underlying the understanding and imitation of action. Nat. Rev. Neurosci.: journal. — 2 (9), 661–670. https://doi.org/10.1038/35090060. ISSN 1471-003X.
Steitz, T.A., 2007. Collecting butterflies and the protein structure initiative: the right questions? Structure 15 (12), 1523–1524. https://doi.org/10.1016/j.str.2007.11.005.
Stepanyan, I.V., Lednev, M.Y., 2025. Investigation of wave processes and rhythmic activity of the human brain using the walsh orthogonal function system//izvestiya VUZ. Appl. Nonlinear Dynam. 33 (4), 545–556. https://doi.org/10.18500/0869-6632-003175.
TSU, 2018. Tomsk scientists helped uncover new facts about the "switching on" of mirror neurons. Tomsky Obzor. https://obzor.city/news/583192—tomskie-uchenye-pomogli-vyjasnit-novye-fakty-o-vkljucheniі-zerkalnyh-nejronov.
Vasyukov, V.L., 2005. Quantum Logic. — M.: per SE, p. 191. ISBN 5-9292-0142-0 (in Rissian).
Vetter, R.J., Weinstein, S., 1967. The history of the phantom in congenitally absent limbs. Neuropsychologia (5), 335–338.
Vollmers, C., Schmitz, R.J., Nathanson, J., Yeo, G., Ecker, J.R., Panda, S., 2012. Circadian oscillations of protein-coding and regulatory RNAs in a highly dynamic mammalian liver epigenome. Cell Metab. 16 (6), 833–845. https://doi.org/10.1016/j.cmet.2012.11.004. PMID: 23217262; PMCID: PMC3541940.
Weinstein, S., Sersen, E.A., 1961. Phantoms in cases of congenital absence of limbs. - Neurology 11, 905–911.
Wiener, N., 1964. Men and machines. The last interview of the "father of cybernetics" Norbert Wiener //Izvestia (newspaper). Supplement "Nedelya" 13 (213), 12–13, 20–21.
Wolfram, S., 2002. A New Kind of Science, 573. Wolfram Media, Champaign, IL, pp. 1072–1073.
Wright, K., The Times of Our Lives. - V Mire Nauki, No.1, 2003. Original English publication: Wright K. Times of our lives. Scientific Am. Sept. 45–51, 2002, 58-65.
Yao, H., Dao, M., Imholt, T., Huang, J., Wheeler, K., Bonilla, A., Suresh, S., Ortiz, C., 2010. Protection mechanisms of the iron-plated armor of a deep-sea hydrothermal vent gastropod. Proc. Natl. Acad. Sci. USA 107 (3), 987–992. https://doi.org/10.1073/pnas.0912988107.