Algebraic model of genetic code and biospin.

S.Y. Kotkovsky

Based on the algebra of biquaternions in isotropic basis, we have built a model of the DNA genetic code that describes nucleotides, doublets and triplets. Each nucleotide in this model is represented by its own biquaternion. Together, these four nucleotide biquaternions form the basis of the entire biquaternion space. The model justifies the grouping of triplets which are encoding the same amino acids. It is possible to trace direct correspondences between the algebraic structures of our model and the spin wave functions studied in quantum relativistic field theory. This suggests a special quantum-like nature of the structures of the genetic code. A new biquaternion representation of the Dirac equation is obtained, the establishment of connections with which allows one to see the chiral states in the DNA structure. The mathematical nature that characterizes the genetic code specifies a particular skew-symmetric type of noise immunity, which is based on the operation of parallel complementary channels of code implementation.

Keywords: DNA, genetic code, biquaternions, isotropic basis, algebraic model, biospin, Dirac equation, degeneracy, symmetry, skew symmetry, skew-symmetric noise immunity, chirality.

Introduction .

Studies of the structures of the genetic code of DNA have firmly revealed their mathematical nature, which provides the necessary properties for continuous recreation of living things, the transmission of heredity and ensuring appropriate noise immunity [6][7][8]. At the same time, the question of creating a complete mathematical model of the genetic code and finding out the reality behind it remains ongoing discovery.

The central point in the operation of the genetic code is its *degenerate* nature. The degeneracy of a fault-resistant code is generally an indispensable attribute of the latter, ensuring the detection and correction of errors in both the code itself and its execution [18][20]. In the genetic code, the same amino acid is encoded by different triplets. This fact obviously increases the reliability of the transmission of genetic information, since a change in the last letter in a triplet often does not affect the final result – the amino acid produced. However this is the simplest of the scenarios that make up a larger picture. Its description is only possible in terms of skew symmetry – a certain combination of symmetry and antisymmetry. Significantly that degeneracy turns out to be a more universal property than the genetic code itself: the latter has many different variants, while the properties of degeneracy are the same for all variants of the code [18].

To date, many attempts have been made to describe the symmetric nature of the genetic code using various mathematical models [18]. These include models based on Lie groups with partially broken symmetry, models using quantum groups, and models based on the quaternion apparatus. In [27], the genetic code model operates with the apparatus of integer quaternions to simulate the mechanisms of amino acid formation and spatial protein folding. Our model of hereditary DNA is also built on quaternions, or strictly speaking on their complex extension called biquaternions. However, we use fundamentally different approaches and methods than those used

in the mentioned study. What remains common is that each nitrogenous base is mathematically formalized using its own quaternion (in [27]) or biquaternion (in our work).

Nucleotide doublets[1], also known as roots, have a modality – they can be *strong* or *weak* . The modality of a root-doublet is determined by whether its triplets encode one amino acid or two different amino acids. Guided by the same principle, we introduce into consideration two "ideal" groups of nucleotide triplets, or codons – strong and weak. In reality, there is a certain violation of the symmetry of these groups, which must be taken into account in the next steps of model development.

Our algebraic model of gene nucleotide structures is based on biquaternions. The proposed representation of biquaternion algebra and new methods of their multiplication and conjugation provide opportunities for an adequate description of the basic amino acid coding scheme. At the same time, it turns out that the algebraic objects characterizing nucleotides and their multiplets have a form similar to the spin wave functions of quantum field theory. We present a new biquaternion representation of the Dirac equation, establishing connections with which allows us to see the chiral states in the DNA structures. Thus, our model provides grounds for creating a quantum-like theory of DNA.

The article is divided into two main parts. The first part is mathematical – it is devoted to new methods of biquaternion algebra, in particular the use of isotropic basis of biquaternion space constructed from nullquaternions. In this part, previously unknown methods of biquaternion multiplication and conjugation are introduced and biquaternions with special properties of projectivity and algebraic degeneracy are defined. In the second part, the obtained mathematical methods are applied to modeling the genetic code, namely to the algebraic representation of nucleotides, doublets, triplets and the amino acids.

[1]For brevity, we refer to the nitrogenous bases of DNA nucleotides as "nucleotides."

Part 1. Algebra of biquaternions.

Biquaternions were discovered by W. Hamilton following his discovery of quaternions, as a complex-valued extension of the latter [28]. L. Zilberstein clarified the central role played by biquaternions in the relativistic theory, or the theory of a unified space-time [29]. He also introduced the most convenient and intuitive scalar-vector representation of biquaternions [30]. In scalar-vector representation, biquaternions have the form [1][4]:

$$\mathcal{B} = (s, \mathbf{u}), \qquad s \in \mathbb{C},\ \mathbf{u} \in \mathbb{C}^{\mathbf{3}} \tag{1}$$

As a rule, we will denote biquaternions in capital letters, while scalars and vectors are in lowercase letters. As follows from definition (1), a biquaternion is a pair consisting of a complex number s and a complex-valued three-dimensional vector $\mathbf{u}$. s and $\mathbf{u}$ are the scalar and vector parts of the biquaternion $\mathcal{B}$ respectively. The sum of two biquaternions is calculated component by component, separately for the scalar and vector parts. Ordinary, or *external*, product of two biquaternions $\mathcal{B}_1 = (s_1, \mathbf{u}_1)$and $\mathcal{B}_2 = (s_2, \mathbf{u}_2)$ is calculated according to the formula:

$$\mathcal{B}_1\mathcal{B}_2 = \mathcal{B}_1 \odot \mathcal{B}_2 = (s_1 s_2 + \mathbf{u}_1 \cdot \mathbf{u_2},\ s_1\mathbf{u}_2 + s_2\mathbf{u}_1 + i\,\mathbf{u}_1 \times \mathbf{u}_2), \tag{2}$$

where $\mathbf{u}_1 \cdot \mathbf{u}_2, \mathbf{u}_1 \times \mathbf{u}_2$is the scalar and vector product $\mathbf{u}_1$and $\mathbf{u}_2$, accordingly, i is the imaginary unit. Unlike other types of biquaternion products, which will be discussed below, for the ordinary (external) product we will use both equivalent notations $\mathcal{B}_1\mathcal{B}_2$and $\mathcal{B}_1 \odot \mathcal{B}_2$. The product of biquaternions is non-commutative – it depends on the order of the multipliers.

An arbitrary complex vector $\mathbf{u} \in \mathbb{C}^{\mathbf{3}}$ is a special case of a biquaternion – in which the scalar part is equal to zero:

$$\mathbf{u} = \mathbf{A} + i\mathbf{B}, \quad \mathbf{A}, \mathbf{B} \in \mathbb{R}^3 \tag{3}$$

Complex conjugate of a biquaternion $\mathcal{B} = (s, \mathbf{u})$ has the form:

$$\mathcal{B}^* = (s^*, \mathbf{u}^*) \tag{4}$$

The complex conjugation of biquaternions corresponds to the Hermitian conjugation of matrix algebra (Appendix 1).

Vector conjugation[2] of a biquaternion $\mathcal{B} = (s, \mathbf{u})$ has the form:

$$\overline{\mathcal{B}} = (s, -\mathbf{u}) \tag{5}$$

[2]The conjugation referred to here as "vector conjugation " is often called simply conjugation or "biquaternion conjugation ". We use the name “vector conjugation” in order to clearly distinguish this type from other types of conjugations.

The simultaneous use of complex and vector conjugations gives *a double conjugation* of the biquaternion *:*

$$\overline{\mathcal{B}}^{*} = (s^{*}, -\mathbf{u}^{*}) \tag{6}$$

Two biquaternions are *equivalent* if they are equal to each other up to a scalar (complex number) factor:

$$\mathcal{B}_1 \approx \mathcal{B}_2 \colon\ \mathcal{B}_1 = \lambda\, \mathcal{B}_2\ , \lambda \in \mathbb{C}, \lambda \neq 0 \tag{7}$$

Square modulus of a biquaternion $\mathcal{B} = (s, \mathbf{u})$ is a complex number defined by the formula:

$$|\mathcal{B}|^2 = \mathcal{B}\overline{\mathcal{B}} = s^2 - \mathbf{u}^2\ , \quad |\mathcal{B}|^2 \in \mathbb{C} \tag{8}$$

Isotropic basis.

Isotropic basis of the biquaternion space introduced in this section is of exceptional importance in algebras describing the spin of elementary particles in physics. According to our assumption, this same basis serves as a powerful interdisciplinary tool which can be used to derive genetic code algebras in mathematical biology. This is a basis built on biquaternions with a zero square modulus. In physics, such quantities usually describe light and are called isotropic, which determines the name of the basis.

Let us take a closer look at biquaternions Q that have a zero square modulus (8): $|Q| = 0$. In our terminology, such biquaternions are called nullquaternions [1]. The first type of nullquaternions are nullvectors[3], i.e. three-dimensional complex vectors whose square is zero. Each null vector **q**is decomposed into a complex sum of two mutually orthogonal vectors **A** and i**B** (Fig.1):

$$\begin{aligned} &\mathbf{q} = \mathbf{A} + i\mathbf{B}, \quad \mathbf{A}, \mathbf{B} \in \mathbb{R}^3, \ \ \mathbf{A} \perp \mathbf{B} \\ &\mathbf{q} \in \mathbb{C}^3, \ \ \mathbf{q}^2 = 0 \end{aligned} \tag{9}$$

The vector $\mathbf{q}^{*}$which is complex conjugate to a given nullvector **q** is also a nullvector. A vector equivalent to a given nullvector is also a nullvector.

The second type of nullquaternions consists of uniform nullquaternions N, each of which can be obtained from a corresponding unit-length real vector **n**:

$$N = \lambda(1, \mathbf{n}),\ \mathbf{n} \in \mathbb{R}^3\ ,\ \mathbf{n^2} = 1\ ,\ \lambda \in \mathbb{C} \qquad\qquad N\overline{N} = 0 \tag{10}$$

Vector conjugation of a uniform nullquaternion N again produces a uniform nullquaternion $\overline{N} = \lambda(1, -\mathbf{n})$.

[3]Nullvectors are also called isotropic vectors.

Isotropic basis of a biquaternion space consists of the following four fixed elements, each of which is a nullquaternion:

$$\begin{cases} \mathbf{q} &= \frac{1}{2}(\mathbf{A} + i\,\mathbf{B}) \\ \mathbf{q}^* &= \frac{1}{2}(\mathbf{A} - i\,\mathbf{B}) \\ N &= \frac{1}{2}(1,\ \mathbf{n}) \\ \bar{N} &= \frac{1}{2}(1, -\mathbf{n}) \end{cases} \qquad \begin{matrix} \mathbf{q}, \mathbf{q}^*, N, \bar{N} = const \\ \mathbf{A}, \mathbf{B}, \mathbf{n} \in \mathbb{R}^3 \\ \mathbf{A^2} = \mathbf{B^2} = \mathbf{n^2} = 1 \end{matrix} \qquad (11)$$

The first two of these elements are nullvectors, and the remaining two are uniform nullquaternions. Nullvectors $\mathbf{q}$ And $\mathbf{q}^*$ lie in the same plane Π (*transverse plane*). Real vectors **A** and **B** also lie in the transverse plane. The unit *longitudinal* real vector **n** is normal to this plane. Isotropic basis is thus given by some constant direction in space (vector **n**) and a fixed angle of rotation in the plane Π (a pair of related vectors **A** and **B**). Nullvectors $\mathbf{q}$ and $\mathbf{q}^*$and are uniform nullquaternions $N$and $\bar{N}$are related to each other by the following relations:

$$\mathbf{q}\mathbf{q}^* = N, \quad \mathbf{q}^*\mathbf{q} = \bar{N} \qquad (12)$$

$\mathbf{q}\mathbf{q}^*$ and $\mathbf{q}^*\mathbf{q}$ – ordinary, or external, biquaternion products (2). At the same time, a vector connection takes place: $\mathbf{A} \times \mathbf{B} = \mathbf{n}$, Where $\mathbf{A} \times \mathbf{B}$ denotes the vector product of the vectors **A** and **B**. Various possible pairwise products of elements of isotropic basis are given in Appendix 2. Fig.2 offers a schematic representation of this basis.

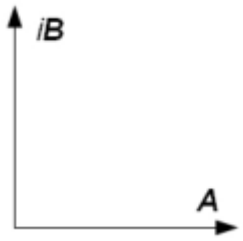

Fig.1. Nullvector $\mathbf{q}$ (plane P).

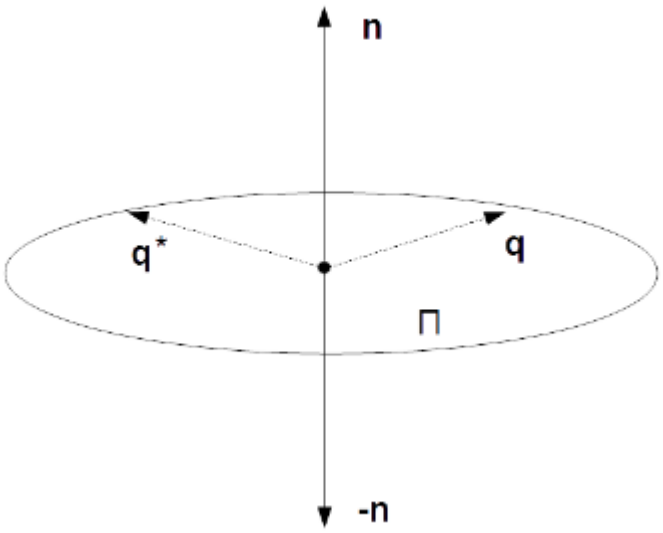

Fig.2. Isotropic basis.

In the usual orthonormal basis built on real vectors $\mathbf{A}, \mathbf{B}, \mathbf{n}$, the vectors $\mathbf{n}, \mathbf{q}, \mathbf{q}^*$have the following complex Cartesian coordinates:

$$\mathbf{n} = \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix}, \quad \mathbf{q} = \frac{1}{2}\begin{pmatrix} 1 \\ i \\ 0 \end{pmatrix}, \quad \mathbf{q}^* = \frac{1}{2}\begin{pmatrix} 1 \\ -i \\ 0 \end{pmatrix} \tag{13}$$

An arbitrary biquaternion $\mathcal{B}$ is expanded into isotropic basis using complex number coordinates α, β, ξ, η:

$$\mathcal{B} = \alpha\mathbf{q} + \beta\mathbf{q}^* + \xi N + \eta\bar{N}, \quad \alpha, \beta, \xi, \eta \in \mathbb{C} \tag{14}$$

The uniqueness of this decomposition is easily shown.

Let's expand the biquaternion$\mathcal{B}$ (14) into two components:

$$\mathcal{B} = \mathbf{u} + \mathcal{P}\,, \qquad \begin{cases} \mathrm{u} = \alpha\mathbf{q} + \beta\mathbf{q}^* \\ \mathcal{P} = \xi N + \eta\bar{N} \end{cases} \tag{15}$$

The first component **u**, let's call it *transverse* component, is a complex vector, lying in the plane Π. The second component $\mathcal{P}$, let's call it *longitudinal* component, is a biquaternion, the vector part of which is parallel to the normal **n** to the plane Π. Expansion (15) thus gives *a longitudinal-transverse* representation of the biquaternion $\mathcal{B}$.

Signed biquaternions and projectors.

Let us group the terms of expansion (14) so as to present it as follows:

$$\mathcal{B} = \mathcal{B}_+ + \mathcal{B}_-\,, \qquad \begin{cases} \mathcal{B}_+ = \alpha\mathbf{q} + \eta\bar{N} \\ \mathcal{B}_- = \beta\mathbf{q}^* + \xi N \end{cases} \tag{16}$$

Biquaternions of the form $\mathcal{B}_+$and $\mathcal{B}_-$will be called *signed* – positive and negative, respectively. We will denote the fact that a certain biquaternion $\mathcal{B}$is positive signed in symbolic form as $\mathcal{B} = B_+$, and negative signed , respectively, as $\mathcal{B} = B_-$.

Let us now expand the same biquaternion $\mathcal{B}$ (14) in another way:

$$\mathcal{B} = P^+ + P^-\,, \qquad \begin{cases} P^- = \alpha\mathbf{q} + \xi N \\ P^+ = \beta\mathbf{q}^* + \eta\bar{N} \end{cases} \tag{17}$$

Biquaternions of the form $P^-$and P^+will be called *projectors* – negative and positive, respectively. From the uniqueness of the expansion over isotropic basis it follows that each biquaternion can be uniquely decomposed both into a sum of signed biquaternions and into a sum of projectors.

Signed biquaternions and projectors are interconnected by the vector conjugation operation (5):

$$\begin{cases} \overline{B_+} = P^- \\ \overline{B_-} = P^+ \end{cases} \qquad \begin{cases} \overline{P^-} = B_+ \\ \overline{P^+} = B_- \end{cases} \tag{18}$$

From correspondence (18) it follows that there is an isomorphism between signed biquaternions and projectors by external multiplication, taking into account that the product of two projectors should be taken in the reverse order of the product of signed biquaternions. It should be noted that although both these types of biquaternions – projectors and signed biquaternions - have a signed characteristic, we apply the terms "signed" and "signedness" only to the first. As shown in Appendix 4, the sign nature of biquaternions means their chiral[4] (right- or left-handed) nature.

Biquaternion multiplication.

In addition to the ordinary, or external, method of multiplying biquaternions (2), we introduce other methods of multiplying them. In the current study, four different methods for multiplying biquaternions are used. Below you can see products of these types for two biquaternions $\mathcal{B}_1$and $\mathcal{B}_2$, presented in the longitudinal-transverse representation and in isotropic basis as:

$$\begin{cases}\mathcal{B}_1 = \mathbf{u_1} + \mathcal{P}_1 = \alpha_1\mathbf{q} + \beta_1\mathbf{q}^* + \xi_1 N + \eta_1\overline{N} \\ \mathcal{B}_2 = \mathbf{u_2} + \mathcal{P}_2 = \alpha_2\mathbf{q} + \beta_2\mathbf{q}^* + \xi_2 N + \eta_2\overline{N}\end{cases} \tag{19}$$

In accordance with (16), each of these biquaternions can be decomposed into signed parts:

$$\begin{cases}\mathcal{B}_1 = \mathcal{B}_{1+} + \mathcal{B}_{1-} \\ \mathcal{B}_2 = \mathcal{B}_{2+} + \mathcal{B}_{2-}\end{cases} \tag{20}$$

The first two of the types of biquaternion multiplication given below, external and internal, correspond to two possible ways of multiplying square matrices of the second order – by adding or subtracting the products of the elements of the rows of the first matrix by the elements of the columns of the second matrix (see Appendix 1).

1) External product $\odot$

External[5], or ordinary, product of biquaternions was defined above in formula (2). In isotropic basis the external product of two biquaternions $\mathcal{B}_1$is $\mathcal{B}_2$ is expressed as

$$\mathcal{B}_1 \odot \mathcal{B}_2 = (\xi_1\alpha_2 + \alpha_1\eta_2)\mathbf{q} + (\eta_1\beta_2 + \beta_1\xi_2)\mathbf{q}^* + (\alpha_1\beta_2 + \xi_1\xi_2)N + (\beta_1\alpha_2 + \eta_1\eta_2)\overline{N} \tag{21}$$

2) Internal product $\otimes$

In isotropic basis, internal product of two biquaternions $\mathcal{B}_1$is $\mathcal{B}_2$ is expressed as

$$\mathcal{B}_1 \otimes \mathcal{B}_2 = (\alpha_1\alpha_2 + \xi_1\eta_2)\mathbf{q} + (\beta_1\beta_2 + \eta_1\xi_2)\mathbf{q}^* + (\beta_1\xi_2 + \alpha_2\xi_1)N + (\alpha_1\eta_2 + \beta_2\eta_1)\overline{N} \tag{22}$$

[4]*Chirality* is understood here in the sense of symmetry studied in spin theory, and not as a type of spatial twisting of biological molecules. We denote the latter by the term *biomolecular chirality* .

[5]*External* and *internal products* used in this work have different meanings than outer and inner products in Grassmann algebras.

As the matrix representation shows (see Appendix 1), external and internal multiplications complement each other in a skew-symmetric manner. Parallel and crossing multiplications defined below combine external and internal products in a certain way.

3) Parallel product □

$$\mathcal{B}_1 \square \mathcal{B}_2 = \mathbf{u_1} \otimes \mathbf{u_2} + \mathcal{P}_1 \odot \mathcal{P}_2 \tag{23}$$

$$\mathcal{B}_1 \square \mathcal{B}_2 = \alpha_1\alpha_2\mathbf{q} + \beta_1\beta_2\mathbf{q}^* + \xi_1\xi_2 N + \eta_1\eta_2\overline{N} \tag{24}$$

As we see, in the case of parallel multiplication there is a complete separation of variables.

4) Crossing product ✧

$$\mathcal{B}_1 \diamondsuit \mathcal{B}_2 = \mathbf{u_1} \odot \mathbf{u_2} + \mathcal{P}_1 \otimes \mathcal{P}_2 \tag{25}$$

$$\mathcal{B}_1 \diamondsuit \mathcal{B}_2 = \eta_1\xi_2\mathbf{q} + \xi_1\eta_2\mathbf{q}^* + \alpha_1\beta_2 N + \beta_1\alpha_2\overline{N} \tag{26}$$

The operations of parallel and crossing multiplication also complement each other: the first separates the variables, and the second mixes them.

The crossing product of a positive projector (on the left) with any biquaternion (on the right) always produces a positive signed biquaternion, and the crossing product (on the left) of a negative projector with any biquaternion (on the right) always produces a negative signed biquaternion. The products of projectors on the right and biquaternions on the left have similar properties. Let us write down all four possible variants of products of projectors of different signs $P^{\pm}$ onto an arbitrary biquaternion $\mathcal{B}$ on the left and right:

$$\forall \mathcal{B}: \begin{cases} P^+ \diamondsuit \mathcal{B} = B_+ \\ P^- \diamondsuit \mathcal{B} = B_- \\ \mathcal{B} \diamondsuit P^+ = B_- \\ \mathcal{B} \diamondsuit P^- = B_+ \end{cases} \tag{27}$$

These formulas determine their very name of projectors: biquaternions of this type project an arbitrary biquaternion onto a positive or negative signed biquaternion. So, projectors and signed biquaternions are closely related to each other – firstly, through vector conjugation (18), and secondly, through projection relations (27).

Biquaternion conjugates.

The classical types of conjugations of biquaternions were considered above: complex $\mathcal{B}^*$ (4) and vector $\overline{\mathcal{B}}$ (5). An important feature of both of these operations is that when applied to a product of biquaternions, they reverse the order of the factors: $(\mathcal{AB})^* = \mathcal{B}^*\mathcal{A}^*$, $\overline{\mathcal{AB}} = \overline{\mathcal{B}}\overline{\mathcal{A}}$. For a particular type of conjugation, the behavior with respect to the reversal of multipliers in products will be considered a characteristic property of this conjugation. In addition to the conjugations mentioned above, we introduce other types.

1) Symbolic conjugation $\mathcal{B}^\star$.
Let's define symbolic conjugation first for signed biquaternions:

$$\begin{aligned} \mathcal{B}_+ &= \alpha\mathbf{q} + \eta\overline{N} \quad \rightarrow \quad \mathcal{B}_+^\star = \alpha\,\mathbf{q}^* + \eta N = B_- \\ \mathcal{B}_- &= \beta\mathbf{q}^* + \xi N \quad \rightarrow \quad \mathcal{B}_-^\star = \beta\mathbf{q} + \xi\overline{N} \;= B_+ \end{aligned} \tag{28}$$

As follows from (28), the operation of symbolic conjugation is reduced to mutual replacement $\mathbf{q}$ by $\mathbf{q}^*$ and mutual replacement $N$with $\overline{N}$ in this expression. As can be seen from (28), in symbolic conjugation, positive signed biquaternions turn into negative ones and vice versa. According to (16), each biquaternion is decomposed into the sum of positive and negative biquaternions, from which it is easy to obtain a symbolic conjugation formula for an arbitrary biquaternion $\mathcal{B}$:

$$\mathcal{B} = \alpha\mathbf{q} + \eta\overline{N} + \beta\mathbf{q}^* + \xi N \quad \rightarrow \quad \mathcal{B}^\star = \alpha\mathbf{q}^* + \eta N + \beta\mathbf{q} + \xi\overline{N} \tag{29}$$

The symbolic conjugation operation is symmetrical: $\mathcal{B}_2 = \mathcal{B}_1^\star \Leftrightarrow \mathcal{B}_1 = \mathcal{B}_2^\star$. When applying symbolic conjugation to the internal product of longitudinal biquaternions, the factors are reversed: $(\mathcal{P}_1 \otimes \mathcal{P}_2)^\star = \mathcal{P}_2 \otimes \mathcal{P}_1$. The last relationship serves as a characteristic feature of this conjugation.

2) Swap conjugation $\widetilde{\mathcal{B}}$.
Let's introduce *swap conjugation* operation first for signed biquaternions:

$$\begin{aligned} \mathcal{B}_+ &= \alpha\mathbf{q} + \eta\overline{N} \quad \rightarrow \quad \widetilde{\mathcal{B}}_+ = \eta\mathbf{q}^* + \alpha N = B_- \\ \mathcal{B}_- &= \beta\mathbf{q}^* + \xi N \quad \rightarrow \quad \widetilde{\mathcal{B}}_- = \xi\mathbf{q} + \beta\overline{N} \;= B_+ \end{aligned} \tag{30}$$

From (30) it follows that swap conjugation transforms positive signed biquaternions into negative ones and vice versa. Based on formulas (30) and (16), it is not difficult to write out the swap conjugation formula for an arbitrary biquaternion:

$$\mathcal{B} = \alpha\mathbf{q} + \eta\overline{N} + \beta\mathbf{q}^* + \xi N \quad \rightarrow \quad \widetilde{\mathcal{B}} = \xi\mathbf{q} + \beta\overline{N} + \eta\mathbf{q}^* + \alpha N \tag{31}$$

The swap conjugation operation is also symmetrical: $\mathcal{B}_2 = \widetilde{\mathcal{B}}_1 \Leftrightarrow \mathcal{B}_1 = \widetilde{\mathcal{B}}_2$.

In relation to the external and internal products, signed biquaternions have special ideal-like properties of degeneracy, which are of particular importance for the gene code modeling. For arbitrary signed biquaternions $\mathcal{A}_+, \mathcal{A}_-, \mathcal{B}_+, \mathcal{B}_-$the following easily verifiable relations involving

external multiplication take place:

$$\begin{cases} \mathcal{A}_+ \odot \mathcal{B}_+ \approx \mathcal{A}_+ \\ \mathcal{A}_- \odot \mathcal{B}_- \approx \mathcal{A}_- \\ \mathcal{A}_- \odot \mathcal{B}_+ \approx \widetilde{\mathcal{A}_-} \\ \mathcal{A}_+ \odot \mathcal{B}_- \approx \widetilde{\mathcal{A}_+} \end{cases} \quad (32)$$

These relations use the definition of biquaternion equivalence given above in (7). Using the symmetry property of swap conjugation, the last two identities from (32) can be rewritten as:

$$\begin{cases} \widetilde{\mathcal{A}_-} \odot \mathcal{B}_+ \approx \mathcal{A}_- \\ \widetilde{\mathcal{A}_+} \odot \mathcal{B}_- \approx \mathcal{A}_+ \end{cases} \quad (33)$$

For internal multiplication, similar relations hold.
In addition to the types of biquaternion conjugations discussed above, in Appendix 4 we also introduce another type of biquaternion conjugation – cyclic conjugation (52), which plays a key role in the formulation of the Dirac biquaternion equation.

Part 2. Algebraic model of the genetic code.

In our algebraic model of the genetic code, all its three base levels (nucleotides, doublets, triplets) are represented by the same mathematical object – a biquaternion. Initially, we define a nucleotide biquaternions. Then special products are used to construct biquaternions of doublets and triplets-codons. The main requirement for the created mathematical model is that the codons provide the necessary variety of amino acids and at the same time have the properties of convergence to the same amino acid (algebraic degeneracy).

Representation of nucleotides.

Recall that by nucleotides we refer to the nitrogenous bases of DNA nucleotides: adenine (A), cytosine (C), thymine (T), and guanine (G). In our model, each of the four nucleotides is represented by its own biquaternion:

$$\begin{cases} \mathrm{A} = \alpha_2 \mathbf{q} + \xi_2 N \\ \mathrm{G} = \alpha_1 \mathbf{q} + \xi_1 N \end{cases} \qquad \begin{cases} \mathrm{C} = \beta_1 \mathbf{q}^* + \eta_1 \overline{N} \\ \mathrm{T} = \beta_2 \mathbf{q}^* + \eta_2 \overline{N} \end{cases} \tag{34}$$

Coordinates of each of the nucleotide biquaternions in isotropic basis (34) are fixed complex numbers: $\alpha_{1,2}, \beta_{1,2}, \xi_{1,2}, \eta_{1,2}$, which can be considered as model parameters. By definition, each of these biquaternions is a positive or negative projector:

$$\begin{cases} \mathrm{A} = P_2^- \\ \mathrm{G} = P_1^- \end{cases} \qquad \begin{cases} \mathrm{C} = P_1^+ \\ \mathrm{T} = P_2^+ \end{cases} \tag{35}$$

As we shall see, it is the projective nature of nucleotide biquaternions that endows them with the required characteristics to generate the variety of multiplets and provide the corresponding levels of algebraic degeneracy. Recalling the properties of projectors (18), we write out the vector conjugations of biquaternions of nucleotides (34):

$$\begin{cases} \overline{\mathrm{A}} = \overline{P_2^-} = \mathcal{B}_{2+} \\ \overline{\mathrm{G}} = \overline{P_1^-} = \mathcal{B}_{1+} \end{cases} \qquad \begin{cases} \overline{\mathrm{C}} = \overline{P_1^+} = \mathcal{B}_{1-} \\ \overline{\mathrm{T}} = \overline{P_2^+} = \mathcal{B}_{2-} \end{cases} \tag{36}$$

As follows from (36), nucleotides are divided into two pairs. The first pair in conjugate form $\overline{\mathrm{A}}, \overline{\mathrm{G}}$ are positive signed biquaternions, and the second pair $\overline{\mathrm{C}}, \overline{\mathrm{T}}$ are negative signed biquaternions.

The quartet of nucleotide biquaternions (34) and the quartet of isotropic basis biquaternions (11) are linearly related to each other. From this connection it follows that the quartet of nucleotide biquaternions represents the basis of biquaternion space, provided the exclusion of special conditions for the parameters $\alpha_{1,2}, \beta_{1,2}, \xi_{1,2}, \eta_{1,2}$.

In the presented model, pyramidins (nucleotides consisting of one aromatic ring) are represented by positive projectors, while purines (consisting of two rings) are represented by negative projectors (35). In the conjugate form, each of the nucleotides is represented by a signed biquaternion (36).

Representation of doublets.

By doublet we do not mean an arbitrary pair of consecutive nucleotides of a single DNA chain, but precisely the one that starts a codon – triplet encoding amino acid. Such doublets are also called roots. By the term *modality* of a doublet we mean whether it is strong (f) or weak (p). A strong doublet uniquely identifies the amino acid produced by its triplets. A weak doublet produces two different amino acids. This binary division into strong and weak roots was called Rumer's in honor of Yu.B. Rumer, the author of the first work [11], in which this principle was discovered and applied to study the symmetries of the gene code [19][22][23]. The Rumer's division was independently discovered by S.V. Petoukhov and became the basis of his theory of fundamental matrices of genetic inheritance, or genetic matrices [5][6][7]. Petoukhov genetic matrices clearly show a hierarchical fractal-like system of genetic code based on interconnected symmetric ensembles of multiplets of nitrogenous bases of various levels.

In Table 1 all available nucleotide doublets are divided into two groups (degeneracy classes) according to their modality.

Table 1. Strong and weak doublets.

Strong roots (f)	Weak roots (p)
AC	CA
GT	TG
CC, GG	AA, TT
TC, CT	GA, AG
CG, GC	AT, TA

Let us express a doublet as a biquaternion $\mathcal{D}$, resulting from the crossing product of the biquaternion-nucleotides $\mathcal{N}_1$and $\mathcal{N}_2$:

$$\mathcal{D} = \mathcal{N}_1 \diamond \mathcal{N}_2 \qquad (37)$$

The product (37) is *contextual* : a given nucleotide can be represented by both its biquaternion (35) $P_{1,2}^{\pm}$ and its symbolical conjugate $P_{1,2}^{\pm\,\star}$. The appropriate choice is determined by the requirement that the result of the product be non-zero: $\mathcal{N}_1 \diamond \mathcal{N}_2 \neq 0$. Thus, the product of biquaternions-nucleotides AA is $P_2^- \diamond P_2^{-\star}$, because $P_2^- \diamond P_2^- = 0$. To have an example, let's calculate the indicated product using formula (25):

$$\text{AA} = P_2^- \diamond P_2^{-\star} = (\alpha_2 \mathbf{q} + \xi_2 N) \diamond (\alpha_2 \mathbf{q}^* + \xi_2 \overline{N}) = \xi_2^2 \mathbf{q}^* + \alpha_2^2 N$$

Doublet biquaternions obtained according to formula (37) are presented in Table 2. For the last four doublets, this table shows signedness of their biquaternions $\mathcal{D}_{\pm}$ (explanations below in the article).

Table 2. Biquaternion representation of doublets ($\mathcal{D}$).

$$\begin{cases} \mathrm{AA} = P_2^- \diamond P_2^{-\star} = \xi_2^2 \mathbf{q}^* + \alpha_2^2 N = p \\ \mathrm{TT} = P_2^+ \diamond P_2^{+\star} = \eta_2^2 \mathbf{q} \ + \beta_2^2 \overline{N} = p \\ \mathrm{CC} = P_1^+ \diamond P_1^{+\star} = \eta_1^2 \mathbf{q} \ + \beta_1^2 \overline{N} = f \\ \mathrm{GG} = P_1^- \diamond P_1^{-\star} = \xi_1^2 \mathbf{q}^* + \alpha_1^2 N = f \end{cases}$$

$$\begin{cases} \mathrm{AT} = P_2^- \diamond P_2^+ = \xi_2 \eta_2 \mathbf{q}^* + \alpha_2 \beta_2 N = p \\ \mathrm{TA} = P_2^+ \diamond P_2^- = \xi_2 \eta_2 \mathbf{q} \ + \alpha_2 \beta_2 \overline{N} = p \end{cases} \qquad \begin{cases} \mathrm{CG} = P_1^+ \diamond P_1^- = \xi_1 \eta_1 \mathbf{q} \ + \alpha_1 \beta_1 \overline{N} = f \\ \mathrm{GC} = P_1^- \diamond P_2^+ = \xi_1 \eta_1 \mathbf{q}^* + \alpha_1 \beta_1 N = f \end{cases}$$

$$\begin{cases} \mathrm{AG} = P_2^- \diamond P_1^- \ = \xi_1 \xi_2 \mathbf{q} \ + \alpha_1 \alpha_2 \overline{N} \ = p \\ \mathrm{GA} = P_1^- \diamond P_2^{-\star} = \xi_1 \xi_2 \mathbf{q}^* + \alpha_1 \alpha_2 N = p \end{cases} \qquad \begin{cases} \mathrm{TC} = P_2^{+\star} \diamond P_1^+ = \eta_1 \eta_2 \mathbf{q}^* + \beta_1 \beta_2 N = f \\ \mathrm{CT} = P_1^+ \diamond P_2^{+\star} = \eta_1 \eta_2 \mathbf{q} \ + \beta_1 \beta_2 \overline{N} = f \end{cases}$$

$$\begin{cases} \mathrm{AC} = P_2^- \diamond P_1^+ = \eta_1 \xi_2 \mathbf{q}^* + \ \beta_1 \alpha_2 N = \mathcal{D}_- = f \\ \mathrm{CA} = P_1^+ \diamond P_2^- = \eta_1 \xi_2 \mathbf{q} \ + \ \beta_1 \alpha_2 \overline{N} = \mathcal{D}_+ = p \end{cases} \qquad \begin{cases} \mathrm{GT} = P_1^- \diamond P_2^+ = \xi_1 \eta_2 \mathbf{q}^* + \alpha_1 \beta_2 N = \mathcal{D}_- = f \\ \mathrm{TG} = P_2^+ \diamond P_1^- = \xi_1 \eta_2 \mathbf{q} \ + \alpha_1 \beta_2 \overline{N} = \mathcal{D}_+ = p \end{cases}$$

With model parameters of a fairly general form, taking into account certain restrictions, none of the various biquaternion doublets presented in Table 2 coincide with each other. This is a necessary condition for the non-degeneracy (non-coincidence) of biquaternion triplets encoding different amino acids. This issue is discussed in more detail in Appendix 3.

In Table 2 the first four doublets are homogeneous – formed by the same nucleotide. The remaining doublets are grouped into pairs. Each pair consists of two doublets obtained from each other by swapping the nucleotides. The doublets within each of the permutation pairs in Table 2 are interconnected by symbolic conjugation:

$$\mathcal{N}_1 \, \mathcal{N}_2 = (\mathcal{N}_2 \, \mathcal{N}_1)^\star \tag{38}$$

So, for *paired* doublets {AG,GA} :

$$\mathrm{AG} = (\mathrm{GA})^\star \quad \Leftrightarrow \quad \xi_1 \xi_2 \mathbf{q} + \alpha_1 \alpha_2 \overline{N} = (\xi_1 \xi_2 \mathbf{q}^* + \alpha_1 \alpha_2 N)^\star$$

Doublets are built on nucleotide biquaternions which are projectors. Therefore according to the projection property (27) all biquaternion doublets turn out to be signed. Let us introduce special notation for them $\mathcal{D}_\pm$.

$$\forall \mathcal{D}: \mathcal{D} = \mathcal{D}_\pm \tag{39}$$

$\mathcal{D}_+, \mathcal{D}_-$ are positive and negative signed biquaternions, respectively. For further purposes, we will write out in a Table 3 signed biquaternions for each of the doublets.

Table 3. Signedness of doublet biquaternions.

$$\begin{cases} AA = \mathcal{D}_+ \\ TT = \mathcal{D}_- \\ CC = \mathcal{D}_+ \\ GG = \mathcal{D}_- \end{cases} \quad \begin{cases} AT = \mathcal{D}_- \\ TA = \mathcal{D}_+ \end{cases} \quad \begin{cases} CG = \mathcal{D}_- \\ GC = \mathcal{D}_+ \end{cases} \quad \begin{cases} AG = \mathcal{D}_+ \\ GA = \mathcal{D}_- \end{cases} \quad \begin{cases} TC = \mathcal{D}_- \\ CT = \mathcal{D}_+ \end{cases} \quad \begin{cases} AC = \mathcal{D}_- \\ CA = \mathcal{D}_+ \end{cases} \quad \begin{cases} GT = \mathcal{D}_- \\ TG = \mathcal{D}_+ \end{cases}$$

Modality of doublets.

From the analysis of biquaternion doublets included in the first four pairs counting from the top in Table 2 (after homogeneous doublets), at least two possible ways to algebraically determine their modality follow: by the real or imaginary part of the coefficient standing in front of the longitudinal element (Nor $\overline{N}$). In our model, for this definition we will use the imaginary part: the modality $Mod(\mathcal{D})$ of the doublet $\mathcal{D}$ will be determined according to the formula:

$$\begin{bmatrix} \mathcal{D} = \mathbf{u} + \lambda\, N \\ \mathcal{D} = \mathbf{u} + \lambda\, \overline{N} \end{bmatrix} \quad \Rightarrow \quad Mod(\mathcal{D}) = Sgn(Im(\lambda)), \tag{40}$$

where the function $Sgn(x)$ expresses the sign of a real number x, $Im(\lambda)$ is the imaginary part of a complex number λ. A square bracket indicates an alternative choice (either/or). Positive values $Mod(\mathcal{D})$ correspond to a strong modality, and negative values correspond to a weak one. Thus, for a pair of weak doublets {AT,TA} it is required $Im(\lambda) = Im(\alpha_2\beta_2) < 0$. For a pair of strong doublets {CG,GC} the opposite condition is required $Im(\lambda) = Im(\alpha_1\beta_1) < 0$.

However, the rule for determining modality (40) turns out to be insufficient for different modalities of doublets within pairs {AC,CA} and {GT,TG}. So, in the pair {GT,TG}, each of the biquaternions of the doublets has the same value λ, but nevertheless GT is a strong doublet, and TG is a weak doublet. This means that the condition must be met for this pair $Im(\lambda) = 0 \Rightarrow Im(\alpha_1\beta_2) = 0$. A similar condition $Im(\lambda) = 0$ for the pair {AC,CA} results in an identity $Im(\beta_1\alpha_2) = 0$. {AC,CA} and {GT, TG} pairs must have one additional rule added to (40). As the second rule, it is natural to accept the definition of modality based on the signedness of the biquaternion: $\mathcal{D}_- = f, \mathcal{D}_+ = p$ (see Table 2, pairs {AC,CA}, {GT,TG}). So, in order to determine the modality of doublets, two conditions must be met:

$$\begin{cases} Im(\alpha_1\beta_2) = 0 \\ Im(\beta_1\alpha_2) = 0 \end{cases} \tag{41}$$

Let us impose the following skew-symmetric conditions on the complex coordinates of the biquaternion-nucleotides $\alpha_{1,2}, \beta_{1,2}, \xi_{1,2}, \eta_{1,2}$, which will be sufficient for (41) to hold:

$$\begin{cases} \beta_1 = -\alpha_2^* \\ \beta_2 = -\alpha_1^* \\ \eta_1 = \xi_2^* \\ \eta_2 = \xi_1^* \end{cases} \tag{42}$$

Then, as follows from (34), biquaternions of nucleotides take the following form:

$$\begin{cases} \mathrm{G} = \alpha_1 \mathbf{q} + \xi_1 N \\ \mathrm{A} = \alpha_2 \mathbf{q} + \xi_2 N \\ \mathrm{C} = -\alpha_2^* \mathbf{q}^* + \xi_2^* \overline{N} \\ \mathrm{T} = -\alpha_1^* \mathbf{q}^* + \xi_1^* \overline{N} \end{cases} \tag{43}$$

So, the conditions for differentiating doublets by modality led us to a certain, albeit incomplete, specification of the initial parameters of the model $\alpha_{1,2}, \beta_{1,2}, \xi_{1,2}, \eta_{1,2}$. According to (43), the model is now parameterized by four complex parameters $\alpha_{1,2}, \xi_{1,2}$ or eight real numbers.

From (43) it follows that the Rumer's transformation (amino ↔keto) [17][22] in biquaternions has the form of double conjugation (6):

$$\begin{cases} \mathrm{A} \leftrightarrow \mathrm{C} \\ \mathrm{T} \leftrightarrow \mathrm{G} \end{cases} \quad \Leftrightarrow \quad \begin{cases} \mathrm{C} = \overline{\mathrm{A}}^* \\ \mathrm{T} = \overline{\mathrm{G}}^* \end{cases}$$

As is known, nucleotides that have the same number of hydrogen bonds (two or three bonds) form Watson-Crick complementary pairs : C - G , A - T. From (43) it follows that the transformation converting complementary nucleotides into each other has the following form:

$$\begin{cases} \mathrm{A} \leftrightarrow \mathrm{T} \\ \mathrm{C} \leftrightarrow \mathrm{G} \end{cases} \quad \Leftrightarrow \quad \begin{cases} \mathbf{q} \leftrightarrow \mathbf{q}^* \\ N \leftrightarrow \overline{N} \\ \alpha_2 \leftrightarrow -\alpha_1^* \\ \xi_2 \leftrightarrow \xi_1^* \end{cases} \tag{44}$$

Ideal codon groups.

As above in the case of defining a doublet, by triplet we mean not arbitrary consecutive triplet of nucleotides, but only the one that encodes an amino acid. A triplet understood in this way is also called a codon.

In the works of S.V. Petoukhov [6][7] there were introduced two conditional groups of codons, defined by strong and weak doublets; each of these groups contains 32 triplets. Let's call these two groups *ideal* codon groups. Between these two groups in their matrix-tensor alphabetic representation, a certain symmetry in the arrangement of elements was discovered, which inherits the symmetry of the corresponding groups of doublets and nucleotides. In this property we see an indication of the presence of internal symmetry of nucleotides, which are inherited in the multiplets they form. Table 4 shows two ideal groups of codons, grouped into series according to the amino acids they encode[6].

Table 4. Ideal groups of codons.

I. Strong codons (f)	II. Weak codons (p)
TCC, TCA, TCT, TCG } *Ser* CTC, CTA, CTT, CTG } *Leu* GCC, GCA, GCT, GCG } *Ala* GGC, GGA, GGT, GGG } *Gly* CCC, CCA, CCT, CCG } *Pro* CGC, CGA, CGT, CGG } *Arg* GTC, GTA, GTT, GTG } *Val* ACC, ACA, ACT, ACG } *Thr*	AGC, AGT } *Ser* AGA, AGG } *stop* TTC, TTT } *Phe* TTA, TTG } *Leu* TAC, TAT } *Tyr* TAA, TAG } *stop* TGC, TGT } *Cys* TGA, TGG } *Trp* ATC, ATT } *Ile* ATA, ATG } *Met* AAC, AAT } *Asn* AAA, AAG } *Lys* GAC, GAT } *Asp* GAA, GAG } *Glu* CAC, CAT } *His* CAA, CAG } *Gln*

The mitochondrial code has three degeneracy groups 1, 2 and 3, corresponding to the number of codon pairs encoding the same amino acid. In particular, the amino acids *Ser* and *Leu* are encoded by three pairs of triplets, and therefore have degeneracy 3. By resorting to ideal groups of codons, we can temporarily "get rid" of the degeneracy 3 inherent in the codons of amino acids *Ser* and *Leu* , and reduce the problem to two to degeneracy groups, skew-symmetrical to each other.

[6]The amino acid coding scheme presented here is based on considered the most ancient and symmetrical vertebrate mitochondrial code [7][25].

Group I consists of "strong" codon triplets formed from strong roots, and group II consists of "weak" codon triplets formed from weak roots. Each of the group II amino acids or stop codons is encoded by a pair of codons that ends with a third nucleotide C and T (eg *Phe*) or a third nucleotide A and G (eg *Lys*). Note that the pair C,T is described by positive projectors, and the pair A,G – by negative projectors (35). In group II, two pairs of codons do not code amino acids, but stop codons. The amino acid codon pair *Met* contains the start codon ATG. The exclusive amino acids *Ser* and *Leu* , each encoded by six codons, have their codons in both ideal groups.

Let us write down the model formula to calculate the biquaternion $\mathcal{T}$ of a triplet consisting of a doublet $\mathcal{D}$ and a third nucleotide $\mathcal{N}_3$:

$$\mathcal{T} = \mathcal{D} * \bar{\mathcal{N}}_3 \tag{45}$$

The sign $*$ in this formula denotes an external $\odot$, but contextual product: depending on the modality of the doublet and the sign types of cofactors, the first factor can be either the biquaternion of the doublet itself $\mathcal{D}$ (calculated according to Table 2), or its swap conjugate $\widetilde{\mathcal{D}}$. Recall that the biquaternion doublet itself is always a signed biquaternion ((39), Table 3), i.e. can only exist in one of two forms $\mathcal{D}_{\pm}$. Also, the third nucleotide of the triplet in its swap-conjugated form is a signed biquaternion: $\bar{\mathcal{N}}_3 = \mathcal{B}_{\pm}$. Thus, both cofactors in (45) are signed biquaternions. As we saw above in (32), (33), the latter have ideal-like properties.

Table 5. Rules for calculating biquaternion triplets
$\mathcal{T} = \mathcal{D} * \bar{\mathcal{N}}_3$,$\mathcal{D} = \mathcal{D}_{\pm}$, $\bar{\mathcal{N}}_3 = \mathcal{B}_{\pm}$

$\mathcal{D}$	$\bar{\mathcal{N}}_3$	$\mathcal{D} * \bar{\mathcal{N}}_3$	Strong roots $\mathcal{D}(f)$	Weak roots $\mathcal{D}(p)$
$\mathcal{D}_+$	$\mathcal{B}_+$	$\mathcal{D}_+ * \mathcal{B}_+$	$\mathcal{D}_+ \odot \mathcal{B}_+ \approx \mathcal{D}_+$	$\mathcal{D}_+ \odot \mathcal{B}_+ \approx \mathcal{D}_+$
$\mathcal{D}_+$	$\mathcal{B}_-$	$\mathcal{D}_+ * \mathcal{B}_-$	$\widetilde{\mathcal{D}}_+ \odot \mathcal{B}_- \approx \mathcal{D}_+$	$\mathcal{D}_+ \odot \mathcal{B}_- \approx \widetilde{\mathcal{D}}_+$
$\mathcal{D}_-$	$\mathcal{B}_-$	$\mathcal{D}_- * \mathcal{B}_-$	$\mathcal{D}_- \odot \mathcal{B}_- \approx \mathcal{D}_-$	$\mathcal{D}_- \odot \mathcal{B}_- \approx \mathcal{D}_-$
$\mathcal{D}_-$	$\mathcal{B}_+$	$\mathcal{D}_- * \mathcal{B}_+$	$\widetilde{\mathcal{D}}_- \odot \mathcal{B}_+ \approx \mathcal{D}_-$	$\mathcal{D}_- \odot \mathcal{B}_+ \approx \widetilde{\mathcal{D}}_-$

According to the rules of Table 5, if the doublet is strong, then the first multiplier in the product (45) is determined by interrelation between "signs" of both multipliers. If the doublet is weak, then the first factor in (45) is always taken $\mathcal{D}$. The same table shows, up to equivalence class (7), the results of the corresponding products. From these rules it follows that weak doublets give two different biquaternions as codon-triplet, while strong doublets give only one. In other words, weak doublets produce two amino acids, while strong doublets produce only one. Now we write in general form the results of codon products for strong ($\mathcal{D}_f$) and weak ($\mathcal{D}_p$) roots:

$$\mathcal{D}_f * \bar{\mathcal{N}}_3 \approx \mathcal{D}_f \qquad \mathcal{D}_p * \bar{\mathcal{N}}_3 \approx \begin{bmatrix} \mathcal{D}_p \\ \widetilde{\mathcal{D}}_p \end{bmatrix} \tag{46}$$

It is important to emphasize that the Table 5 demonstrates the skew-symmetric nature of the relationship between strong and weak doublets. For example, the rule $\widetilde{\mathcal{D}}_+ \odot \mathcal{B}_- \approx \mathcal{D}_+$ for strong

doublets is replaced with a rule $\mathcal{D}_+ \odot \mathcal{B}_- \approx \widetilde{\mathcal{D}}_+$ for weak ones. This algebraic rule serves as the ground of the division of doublets by modality within our model.

Using the rules for calculating triplets ((45), Table 5) one can obtain specific values of biquaternion codons and the amino acids they encode in each of the ideal groups. Let us write down, as an example, a biquaternion expression for a strong codon GTC. From Table 2 doublet-biquaternion GT $= \xi_1\eta_2\mathbf{q}^* + \alpha_1\beta_2 N = \mathcal{D}_-$. For the third nucleotide C : $\bar{\mathcal{N}}_3 = \overline{P_1^+} = \mathcal{B}_-$. From formula (45) and Table 5 the biquaternion of one of the triplets formed by this doublet: GTC $= \mathcal{D}_- * \mathcal{B}_- = \mathcal{D}_- \odot \mathcal{B}_- \approx \mathcal{D}_-$. The biquaternion of the codon GTCturns out to be equivalent to the biquaternion of the doublet itself GT $= \xi_1\eta_2\mathbf{q}^* + \alpha_1\beta_2 N$. The amino acid biquaternions corresponding to the ideal group codons calculated in this way are shown in Table 6. The amino acid *Ser* is conventionally divided into two amino acids Ser_1 and Ser_2, each belonging to its own ideal group. The amino acid *Leu* is similarly divided into Leu_1 and Leu_2.

Table 6. Biquaternion representation of amino acids in ideal groups.

Group I (f)	Group II (p)
$Ser_1 \approx \mathrm{TC} = \xi_1^*\xi_2^*\,\mathbf{q}^* + \alpha_1^*\,\alpha_2^* N$	$Ser_2 = \mathrm{AGC, AGT} \approx \widetilde{\mathrm{AG}} = \alpha_1\alpha_2\mathbf{q}^* + \xi_1\xi_2 N$
$Leu_1 \approx \mathrm{CT} = \xi_1^*\xi_2^*\mathbf{q} + \alpha_1^*\,\alpha_2^*\overline{N}$	$stop_1 = \mathrm{AGA, AGG} \approx \mathrm{AG} = \xi_1\xi_2\mathbf{q} + \alpha_1\alpha_2\overline{N}$
$Ala \approx \mathrm{GC} = \xi_1\xi_2^*\mathbf{q}^* - \alpha_1\alpha_2^* N$	$Leu_2 = \mathrm{TTA, TTG} \approx \mathrm{TT} = \xi_2^{*\mathbf{2}}\mathbf{q} + \alpha_1^{*\mathbf{2}}\overline{N}$
$Gly \approx \mathrm{GG} = \xi_1^2\mathbf{q}^* + \alpha_1^2 N$	$Phe = \mathrm{TTC, TTT} \approx \widetilde{\mathrm{TT}} = \alpha_2^{*\mathbf{2}}\mathbf{q}^* + \xi_1^{*\mathbf{2}} N$
$Pro \approx \mathrm{CC} = \xi_2^{*\mathbf{2}}\mathbf{q} + \alpha_2^{*^2}\,\overline{N}$	$Tyr = \mathrm{TAC, TAT} \approx \widetilde{\mathrm{TA}} = -\alpha_1^*\alpha_2\mathbf{q}^* + \xi_1^*\xi_2 N$
$Arg \approx \mathrm{CG} = \xi_1\xi_2^*\mathbf{q} - \alpha_1\alpha_2^*\overline{N}$	$stop_2 = \mathrm{TAA, TAG} \approx \mathrm{TA} = \xi_1^*\xi_2\mathbf{q} - \alpha_1^*\alpha_2\overline{N}$
$Val \approx \mathrm{GT} = \lvert\xi_1\rvert^2\mathbf{q}^* - \lvert\alpha_1\rvert^2 N$	$Cys = \mathrm{TGC, TGT} \approx \widetilde{\mathrm{TG}} = -\lvert\alpha_1\rvert^2\mathbf{q}^* + \lvert\xi_1\rvert^2 N$
$Thr \approx \mathrm{AC} = \lvert\xi_2\rvert^2\mathbf{q}^* - \lvert\alpha_2\rvert^2 N$	$Trp = \mathrm{TGA, TGG} \approx \mathrm{TG} = \lvert\xi_1\rvert^2\mathbf{q} - \lvert\alpha_1\rvert^2\overline{N}$
	$Ile = \mathrm{ATC, ATT} \approx \mathrm{AT} = \xi_1^*\xi_2\mathbf{q}^* - \alpha_1^*\alpha_2 N$
	$Met/start = \mathrm{ATA, ATG} \approx \widetilde{\mathrm{AT}} = -\alpha_1^*\alpha_2\mathbf{q} + \xi_1^*\xi_2\overline{N}$
	$Asn = \mathrm{AAC, AAT} \approx \mathrm{AA} = \xi_2^2\mathbf{q}^* + \alpha_2^2 N$
	$Lys = \mathrm{AAA, AAG} \approx \widetilde{\mathrm{AA}} = \alpha_2^2\mathbf{q} + \xi_2^2\overline{N}$
	$Asp = \mathrm{GAC, GAT} \approx \mathrm{GA} = \xi_1\xi_2\mathbf{q}^* + \alpha_1\alpha_2 N$
	$Glu = \mathrm{GAA, GAG} \approx \widetilde{\mathrm{GA}} = \alpha_1\alpha_2\mathbf{q} + \xi_1\xi_2\overline{N}$
	$His = \mathrm{CAC, CAT} \approx \mathrm{CA} = \lvert\xi_2\rvert^2\mathbf{q} - \lvert\alpha_2\rvert^2\overline{N}$
	$Gln = \mathrm{CAA, CAG} \approx \widetilde{\mathrm{CA}} = -\lvert\alpha_2\rvert^2\mathbf{q}^* + \lvert\xi_2\rvert^2 N$

In our scheme, each amino acid in its ideal group is described by a single biquaternion (Appendix 3). To clarify, an amino acid biquaternion equals to the biquaternion of its any codon, accounting for the amino acids *Ser* and *Leu* conventional division described above. Specific amino acid biquaternion is determined mainly by its root-doublet, while only its sign is taken from the third conjugate biquaternion-nucleotide. Recall that vector conjugate biquaternions-nucleotides $\overline{\mathrm{C}}, \overline{\mathrm{T}}$ are sign-positive, and $\overline{\mathrm{G}}, \overline{\mathrm{A}}$ are sign-negative (36).

By virtue of its construction, Table 6 reflects in algebraic language the known symmetries of codons associated with complementarity, Rumer's transformation and the number of hydrogen bonds of nucleotides. Moreover, in this table one can trace other symmetries identified by V. Shcherbak in [17] and called him *cooperative symmetries*. An example of such symmetry is provided by a pair of stop codons $stop_2 = \{\mathrm{TAA, TAG}\}$ and a pair of codons {ATA, ATG}. The latter encode the amino acid *Met* ; ATG is also a start codon. In a remarkable way, these two pairs are described in the model by symmetric biquaternions $Met/start \approx -\alpha_1^*\alpha_2\mathbf{q} + \xi_1^*\xi_2\overline{N}$ and $stop_2 \approx$

$\xi_1^*\xi_2\mathbf{q} - \alpha_1^*\alpha_2\overline{N}$. Note that it is still an open question what mechanisms are behind the assignment of *start* and *stop* roles to individual triplets and their pairs .

Summarizing the above, let's write out the general formula for calculating the biquaternion of a codon from the biquaternions of its constituent nucleotides $\mathcal{N}_1, \mathcal{N}_2, \mathcal{N}_3$. To do this, we combine (37) and (45) into one formula:

$$\mathcal{T} = (\mathcal{N}_1 \diamond \mathcal{N}_2) \odot \overline{\mathcal{N}_3} \qquad (47)$$

Let us recall that both products $\diamond$ in $\odot$ formula (47) are contextual – the choice of their specific type depends on the multipliers. Formula (47) gives a summary of our model.

Violation of ideal symmetry.

In this section, we will only outline some directions for the future development of the presented model in terms of the transition from the ideal groups of codons and amino acids discussed above to real ones. Two codon pairs from ideal weak group II (Table 4) { AGC, AGT } and { TTA, TTG } break perfect symmetry: they encode the amino acids *Ser* and *Leu* , the remaining codons of which lie in strong group II . Note that in the strong group these two amino acids are defined by paired (swapped) doublets, algebraically related to each other through symbolic conjugation (38): $\mathrm{TC} = \mathrm{CT}^{\star}$.

As shown in Appendix 3, the biquaternions of codons Ser_1 and Ser_2 from groups I and II (Table 6) cannot be made equal to each other. The same applies to biquaternions of codons Leu_1 and Leu_2 from these two groups. Therefore, some additional transformation is needed to violate the ideal symmetry of codons, which would change the biquaternions of the indicated codons of groups I or II , so as to make them equal to each other: $Leu_1 := Leu_2, Ser_1 := Ser_2$.

Likely, the violation of the symmetry of ideal groups also affects the spatial twist (chirality) of the resulting amino acids and is responsible for the fact that one of the 20 amino acids glycine has a molecule of right chirality (R-configuration), while all the others have left-handed (L-configuration). Once again we emphasize the difference between the concepts of chirality of biological molecules and the chirality of spin wave functions, which are of primary focus in this article.

We limited our study to mitochondrial code of vertebrates, which are considered to be the most symmetrical and ancient genetic code. The transition from the mitochondrial to the nuclear gene code suggests another symmetry breaking, which probably arose evolutionarily [23].

The concept of biospin.

A number of studies have suggested the quantum-like nature of the genetic code and DNA [9][34][35][36]. The article [34] consider the gene code as a transmitter, and the produced protein as a recipient of quantum information expressed by the Hamiltonian matrix. Quantum-likeness is forms the basis for the construction of a new biological field theory [35][36]. Based on the proposed

model of the gene code, we come to a close idea: DNA possesses a quantum-like biological nature, rooted in some analogue of the physical spin, referred here as *biospin.*

Our genetic code model is based on the representation of nucleotides and their multiplets in the form of biquaternions. As shown in [24], there is an isomorphism between biquaternions and Dirac bispinors. In the theory of field bispinors describe the quantum wave functions of fermions (electron, positron, neutrino, etc.). In Appendix 4 we offer our own version of the biquaternion representation of the Dirac equation, which is different from that proposed in [24]. Applying this representation, an isomorphism between bispinors and biquaternions (56)- (58) is also established. Thereafter the various operations of biquaternion algebra acquire a "physical" meaning, or a meaning with respect to internal symmetries.

Above we introduced the biquaternion expression of nucleotides, doublets and triplets. On the other hand, according to "physical" logic, these biquaternion quantities correspond to some quasi-spinor wave functions, which, in turn, must have their own dynamic invariants. This means that for each of the nucleotides, doublets and triplets there may be found analogues of charge, mass, spin and other physical characteristics. In formula (47) one can see the expression of a quantum-like relationship between the implicit "wave functions" of nucleotides $\mathcal{N}_1, \mathcal{N}_2, \mathcal{N}_3$and the "observable quantity" (*sense*) $\mathcal{T}$ that the final amino acid represents.

In fermion physics, two cases are possible: massive Dirac spinors describing an electron and massless Majorana spinors describing a neutrino. Our model requires precisely the first case, when singular objects with "charge" and "mass" occur. The algebra corresponding to Majorana spinors cannot be applied to the genetic code, since it cannot provide the entire variety of doublets and codons.

The relation of the genetic code to spin also follows from the rules for multiplying genetic matrices proposed by S.V. Petoukhov in [8]. These rules are the same as the rules for multiplying split quaternions. On the other hand, as shown in [26], split-quaternion pairs provide another alternative to Dirac bispinors description of relativistic spin. In this correlation we see additional indications of the presence of spin-like structures underlying DNA. Moreover, split quaternions are a special case of biquaternions, on which our model is based.

In our model, we limited ourselves to third-order nucleotide structures, i.e. triplets-codons. However, this model can be extended further to longer sequences of nucleotides, including genes. Biquaternion algebra and the idea of biospin can help the development of such areas as comma-free codes [20], circular codes [21], and cyclic Gray codes in inherited biostructures [7]. In relation to the last two, cyclic conjugation (Appendix 4) can play a special role. Recall that cyclic conjugation produces a cyclic inverse permutation of isotropic coordinates of the biquaternion (53).

The work of M. Rempel et al. [33] upraises the hypothesis that DNA resonances serve as the sources of morphogenetic (biological) field [16]. The biospin concept provides certain theoretical foundations for these hypotheses. Indeed, like physical spin and magnetic moment, the biospin structure must carry on some rotation and be a source and receiver of some field. The latter can naturally be identified with the biological field, which is responsible for the holistic plan of building the organism and for its locomotive movements.

The foundations of the theory of the biological (morphogenetic) field were laid by A.G. Gurvich [15]. This theory received its maximum conceptual development, in our opinion, in the books of R. Sheldrake [16]. This researcher connects the past of a given individual with its present. This connection is carried out through *morphic resonance*. Thus, a living organism acts as an integral spatiotemporal formation. Sheldrake's concept also explains the phenomenon of differentiation of the work of the same DNA in cells of different types. This key phenomenon for the development of each organism can be explained by the idea that the morphogenetic field of the organism has a reverse effect on its DNA. Our assumption about biospin nature of DNA and its physics-like properties, such as quasi-charges and quasi-magnetic moments, points to more specific ways to describe the interactions between the morphogenetic field and DNA.

Skew-symmetric noise immunity.

In the figurative expression of S.V. Petoukhov, the genetic code of the DNA molecule chain is written simultaneously in three alphabets: it can be represented as three binary sequences: the sequence of hydrogen bonds of nucleotides (2 or 3), the sequence of purines (A. G) and pyramidins (C,T), the sequence of keto molecules (G,T) and amino molecules (A,C) [5]. Study of the algebraic relationships between these three types of equivalence (or conjugation) of nucleotides indicates the skew-symmetric nature of the connections between the corresponding channels of genetic code implementation.

Skew symmetry as a fundamental physical principle was deeply studied in the works of V.V. Shchennikov [12][13]. In the most general way, skew symmetry can be defined as a particular combination of symmetry and antisymmetry. Thus, skew symmetry is a higher level of organizational complexity in relation to simple symmetry. Skew symmetry is symmetry in a broader sense. As an expression of complementarity and interaction, skew symmetry underlies the fundamental equations of physics and mathematics, including the Cauchy-Riemann conditions and the Dirac equation [3]. In our opinion, the last equation in its integral mosaic complexity is the most beautiful of all existing expressions of skew-symmetric relations.

The concrete form of skew symmetry as a relation of symmetry and antisymmetry depends on the nature of the mathematical objects we are dealing with and the representation used. Common to all skew-symmetric structures and relations is the factor of internal torsion or cyclicity [12][13], which is especially clearly manifested in the nature of the spin – the particle's own moment of rotation. The genetic code is also based on its own internal skew symmetry.

An antisymmetry transformation can be a sign reversal, a change from a left operator to a right one, a switch from clockwise direction to counterwise, etc. The various types of conjugations of biquaternions, which we discussed above, give one or another form of skew-symmetric transformations, thereby being *skew conjugates*. The most famous and significant type of mathematical conjugation is complex conjugation. Our mirror image offers an example of skew conjugation from ordinary life. Two types of multiplication, external and internal, are also connected by skew conjugation. In the matrix representation (Appendix 1) skew conjugation is expressed in the mutual replacement of the addition of products of matrix elements by their subtraction. The antisymmetric transformation here is the reversal of the sign of the second term. The symmetric transformation in this case obviously means preserving the sign of the first term.

Together, these two transformations make a skew-symmetric transition from the external multiplication of matrices (or biquaternions) to their internal multiplication.

The mathematical nature of the genetic code defines a special skew-symmetric type of noise immunity, which is based on the work of several parallel complementary channels of code implementation. A diagram of this type of noise immunity is shown in Figure 3. Horizontal lines with arrows depict four channels of code execution. Each channel executes its own code (which itself can change over time). All four channels are interconnected by skew-symmetric links, as shown by the vertical dotted lines. If errors or failures occur in one of the channels, the code and the program it executes are restored based on the other channels using skew-symmetric addition operations.

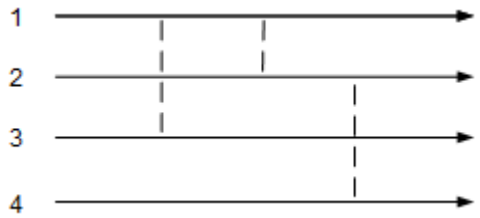

Fig. 3. Skew-symmetric noise immunity.

As the author discovered from personal experience, skew-symmetric noise immunity effectively helps in working with calculations. Four different representations of the Dirac equation (Appendix 4) can serve as four channels of code execution. When searching for solutions to one of these equations, for example, in the form of plane or spherical waves, possible errors are detected and corrected by comparing this solution with similar solutions in the other three "channels". Similar noise immunity mechanisms also operate in the genetic code, which is characterized by its multi-level skew symmetry. At the most basic level, skew-symmetric noise immunity of the gene code is implemented via two complementary DNA strands. Unlike duplicating systems based on simple symmetry, skew-symmetric complementation is much more reliable. The same mutation is more likely to occur in identical elements, but less likely in different, although related, elements.

Noise immunity is a mechanism for maintaining the integrity of a complex system, an example of which is the system of an organism. For the overall organization of such systems, their scalability is a key feature. And here the skew-symmetric nature of the basic processes of organization and continuous recreation of living things plays a fundamental role. As shown in the book [5], genomatrices have symmetries of a special scalable nature. As one of our future projects and goals, we see the establishment of a correspondence between Petoukhov genomatrices and the biquaternions of the genetic code of the present model.

S.V. Petoukhov in [9] develops a quantum information approach to the study of the genetic code, based on the application of wave functions to the gene code. Such wave functions determine the probability of certain nucleotide sequences to occur in a given DNA chain. It is noteworthy that 2-qubit nucleotide systems serve as the computational basis of this model, which in turn indicates a certain spin-like nature of nitrogenous bases and their multiplets. We also hope to connect the concept of biospin with Petoukhov's quantum information approach.

Appendices.

1. Matrix representation of biquaternions.

There is an isomorphism between biquaternions and second-order square matrices [32]. Let us choose some isotropic basis in the space of biquaternions (11). Then for each biquaternion $\mathcal{B}$ represented in this basis according to (14), we can be put a second-order square matrix M into one-to-one correspondence with it:

$$\mathcal{B} = \alpha\mathbf{q} + \beta\mathbf{q}^* + \xi N + \eta\bar{N} \quad \leftrightarrow \quad M = \begin{pmatrix} \xi & \alpha \\ \beta & \eta \end{pmatrix} \tag{48}$$

According to this correspondence rule, there is an isomorphism between biquaternions and second-order square matrices in addition and ordinary multiplication. The usual rule for matrix multiplication, let us denote it as for biquaternions by the symbol $\odot$, has the well-known form:

$$M_1 \odot M_2 = \begin{pmatrix} a_{11} & a_{21} \\ a_{12} & a_{22} \end{pmatrix} \odot \begin{pmatrix} b_{11} & b_{21} \\ b_{12} & b_{22} \end{pmatrix} = \begin{pmatrix} a_{11}b_{11} + a_{21}b_{12} & a_{11}b_{21} + a_{21}b_{22} \\ a_{12}b_{11} + a_{22}b_{12} & a_{12}b_{12} + a_{22}b_{22} \end{pmatrix}$$

If for biquaternions the ordinary (external) multiplication $\odot$ is replaced by internal one $\otimes$, then an isomorphism can also be established between them and the matrices:

$$\mathcal{B} = \alpha\mathbf{q} + \beta\mathbf{q}^* + \xi N + \eta\bar{N} \quad \leftrightarrow \quad M = \begin{pmatrix} \xi & \alpha \\ -\beta & -\eta \end{pmatrix} \tag{49}$$

However, this requires changing the multiplication rule for matrices to the following:

$$M_1 \otimes M_2 = \begin{pmatrix} a_{11} & a_{21} \\ a_{12} & a_{22} \end{pmatrix} \otimes \begin{pmatrix} b_{11} & b_{21} \\ b_{12} & b_{22} \end{pmatrix} = \begin{pmatrix} a_{11}b_{11} - a_{21}b_{12} & a_{11}b_{21} - a_{21}b_{22} \\ a_{12}b_{11} - a_{22}b_{12} & a_{12}b_{12} - a_{22}b_{22} \end{pmatrix}$$

It follows that the external multiplication of biquaternions corresponds to the usual matrix multiplication, and the internal multiplication corresponds to matrix multiplication, in which the products of the elements of the rows of the first matrix by the elements of the columns of the second matrix are not added, but subtracted. In this study, we use a representation of biquaternions based on isomorphism of the first type. Because of that, the external product of biquaternions has the usual properties of matrix multiplication, including associativity. The internal product of biquaternions, unlike the external one, is not associative. It also turns out that the external product of biquaternions does not depend on the chosen basis, while their internal product is basis-dependent. Although, one can use an alternative representation of biquaternions, in which the internal product will be associative and basis-independent, and the external product will be non-associative and basis-dependent.

2. Products of elements of isotropic basis.

Table 7 shows various possible combinations of products of elements of a biquaternion isotropic basis for two basic types of multiplication: external ⊙ and internal ⊗.

Table 7. Products of elements of isotropic basis.

External (ordinary) product ⊙		Internal product ⊗	
$\mathbf{q}\odot\mathbf{q}=0$	$\mathbf{q}^*\odot\mathbf{q}^*=0$	$\mathbf{q}\otimes\mathbf{q}^*=0$	$\mathbf{q}^*\otimes\mathbf{q}=0$
$N\odot\bar{N}=0$	$\bar{N}\odot N=0$	$N\otimes N=0$	$\bar{N}\otimes\bar{N}=0$
$\mathbf{q}\odot\mathbf{q}^*=N$	$\mathbf{q}^*\odot\mathbf{q}=\bar{N}$	$\mathbf{q}\otimes\mathbf{q}=\mathbf{q}$	$\mathbf{q}^*\otimes\mathbf{q}^*=\mathbf{q}^*$
$N\odot N=N$	$\bar{N}\odot\bar{N}=\bar{N}$	$N\otimes\bar{N}=\mathbf{q}^*$	$\bar{N}\otimes N=\mathbf{q}$
$\mathbf{q}\odot N=0$	$\mathbf{q}^*\odot\bar{N}=0$	$\mathbf{q}\otimes N=0$	$\mathbf{q}^*\otimes\bar{N}=0$
$N\odot\mathbf{q}=0$	$\bar{N}\odot\mathbf{q}^*=0$	$\bar{N}\otimes\mathbf{q}=0$	$N\otimes\mathbf{q}^*=0$
$\mathbf{q}\odot\bar{N}=\mathbf{q}$	$\mathbf{q}^*\odot N=\mathbf{q}^*$	$\mathbf{q}\otimes\bar{N}=\bar{N}$	$\mathbf{q}^*\otimes N=N$
$N\odot\mathbf{q}=\mathbf{q}$	$\bar{N}\odot\mathbf{q}^*=\mathbf{q}^*$	$N\otimes\mathbf{q}=N$	$\bar{N}\otimes\mathbf{q}^*=\bar{N}$

In particular, it follows from this table that the elements $N, \bar{N}$ are idempotent with respect to external multiplication ⊙ and nilpotent with respect to internal multiplication, and the elements $\mathbf{q}, \mathbf{q}^*$ visa versa are nilpotent with respect to internal multiplication ⊗ and idempotent with respect to external multiplication. Switching from one type of multiplication to another transforms idempotents and nilpotents into each other.

3. Model parameters.

1) *The uniqueness of amino acid biquaternions.* We shall show in general terms that, with the exception of special conditions, the biquaternions of various amino acids (Table 6) do not intersect with each other, i.e. each amino acid is described by its own biquaternion. This obviously requires that all parameters $\alpha_{1,2}, \beta_{1,2}, \xi_{1,2}, \eta_{1,2}$ be different, i.e. no two of them are identical. Further, if we take the first biquaternion of an amino acid in the list $Ser_1 \approx \mathrm{TC} = \xi_1^*\xi_2^*\,\mathbf{q}^* + \alpha_1^*\,\alpha_2^* N$ and demand that it differ from all the others, then we obtain a series of inequalities: $\xi_1^*\xi_2^* \neq \xi_1^2, \alpha_1^*\alpha_2 \neq -\alpha_1^2, \xi_1^*\xi_2^* \neq \alpha_1^*$ etc. All these inequalities are satisfied almost always, with the exception of special conditions determined by their inverse equalities. The comparison of other amino acid biquaternions is similar. Thus, in the most general case, the biquaternions of all amino acids are different.

2) *The need to break ideal symmetry.* As we saw above, the two amino acids *Ser* and *Leu* are represented by their codons simultaneously in each of the ideal groups I and II . As a consequence of the above requirements for model parameters, biquaternions describing the same amino acid *Leu* in groups I and II (Leu_1 and Leu_2) cannot be equal to each other. A similar situation occurs for

the second exceptional amino acid *Ser.* Therefore, an additional transformation of the violation of ideal symmetry is required – the corresponding paragraph of the article is devoted to its discussion.

4. Biquaternionic Dirac equation.

The Dirac equation occupies a central position in quantum field theory. This equation describes the wave functions of elementary particles of half-integer spin. In the context of this work, it is important that the Dirac equation and our model of genetic code operate with the same algebraic means and have common types of skew symmetry.

Above we pointed out the representation of the Dirac equation in biquaternion form, given in [24]. Here we give an alternative biquaternion representation of the Dirac equation that we derived[7]:

$$\widehat{D} \odot F_{+} + F_{-} \otimes \widehat{\overline{D}} = im\overset{\curvearrowleft}{F}, \tag{50}$$

In equation (50) F there is a biquaternion fermion wave function, expanded according to (16) as the sum of its signed components: $F = F_{+} + F_{-}$, m – particle mass, $\widehat{D}$ is a biquaternion gradient operator, and the operator $\widehat{\overline{D}}$ is vector conjugate to $\widehat{D}$:

$$\begin{cases} \widehat{D} = \mathbf{q}\partial_{\beta} + \mathbf{q}^{*}\partial_{\alpha} + N\partial_{\xi} + \overline{N}\partial_{\eta} \\ \widehat{\overline{D}} = -\mathbf{q}\partial_{\beta} - \mathbf{q}^{*}\partial_{\alpha} + N\partial_{\eta} + \overline{N}\partial_{\eta} \end{cases} \tag{51}$$

$\overset{\curvearrowleft}{F}$ in equation (50) denotes *cyclic conjugation of the first type* taken from biquaternion F, defined according to the formula:

$$F = \mathbf{q}f_{\alpha} + \mathbf{q}^{*}f_{\beta} + Nf_{\xi} + \overline{N}f_{\eta} \quad \Rightarrow \quad \overset{\curvearrowleft}{F} = -\mathbf{q}f_{\beta} - \mathbf{q}^{*}f_{\eta} - Nf_{\alpha} + \overline{N}f_{\eta} \tag{52}$$

Cyclic conjugation (52) can be expressed using the following diagram, which shows a cyclic permutation of coordinates with inversions for a biquaternion F, which gives the output $\overset{\curvearrowleft}{F}$:

$$F = \overset{+}{\overbrace{\mathbf{q}f_{\alpha} + \mathbf{q}^{*}f_{\beta} + Nf_{\xi} + \overline{N}f_{\eta}}} \quad \rightarrow \quad \overset{\curvearrowleft}{F} \tag{53}$$

$$\underset{-}{\phantom{\mathbf{q}f_{\alpha}}} \quad \underset{-}{\phantom{\mathbf{q}^{*}f_{\beta}}} \quad \underset{-}{\phantom{Nf_{\xi} + \overline{N}f_{\eta}}}$$

As a result of four cyclic conjugations, each coordinate returns to its place, but at the same time the sign of the entire biquaternion changes to the opposite. It takes another cycle of four conversions (53) to completely return the original biquaternion. In other words, two full turns (cycles) are required for the wave function of the particle to completely return to itself. And this just means that the particle described by the equation is a fermion and has a spin of ½.

[7]The form of the Dirac equation (50) is published for the first time.

In addition to (50), there are three more other analogous representations of the Dirac equation, using their own three types of cyclic conjugations. A detailed consideration of all types of these equations and its cyclic conjugates is beyond the scope of this article. Cyclic conjugations are closely related to swap conjugation (31). In particular, the cyclic conjugation of the first type (52) for positive signed biquaternions coincides up to sign with the swap conjugation:

$$\overset{\curvearrowleft}{B_+} = -\widetilde{B_+} \tag{54}$$

As we can see, the Dirac equation in the biquaternion formulation uses the same operations of internal and external multiplication and swap conjugation which form the basis of our model.

Let us show that equation (50) is equivalent to the usual Dirac equation in the representation of Weyl spinors. The latter is written as [31]:

$$\begin{cases} \dfrac{\partial \psi_L}{\partial t} = -(\boldsymbol{\sigma} \cdot \boldsymbol{\nabla})\psi_L - im\psi_R \\ \dfrac{\partial \psi_R}{\partial t} = +(\boldsymbol{\sigma} \cdot \boldsymbol{\nabla})\psi_R - im\psi_R \end{cases} \tag{55}$$

Here $\boldsymbol{\sigma}$ – a three-dimensional vector consisting of Pauli matrices; $\boldsymbol{\nabla}$ – three-dimensional nabla operator; $\psi_L$and ψ_R – Weyl three-dimensional spinors, which are right-handed and left-handed chiral states:

$$\begin{cases} \psi_L = \begin{pmatrix} u \\ v \end{pmatrix} \\ \psi_R = \begin{pmatrix} u' \\ v' \end{pmatrix} \end{cases} \qquad u, v, u', v' \in \mathbb{C} \tag{56}$$

The correspondence between Weyl spinors ψ_L and ψ_R (56) and the biquaternion wave function expanded in isotropic basis (14) $F = \mathbf{q}f_\alpha + \mathbf{q}^* f_\beta + Nf_\xi + \bar{N}f_\eta$is given by the following formula:

$$\begin{cases} u = f_\beta \\ v = f_\eta \end{cases} \qquad \begin{cases} u' = f_\alpha \\ v' = f_\xi \end{cases} \tag{57}$$

or

$$F = \mathbf{q}u' + \mathbf{q}^* u + Nv' + \bar{N}v \tag{58}$$

From the above we can conclude that signed biquaternions represent chiral states. The signed positive biquaternion F_+ describes a right-handed chiral state, and the signed negative biquaternion F_- describes a left-handed chiral state:

$$\begin{cases} F_- \sim \psi_L \\ F_+ \sim \psi_R \end{cases} \tag{59}$$

Thus, arbitrary signed biquaternions $B_\pm$ can also be called *chiral biquaternions* of the corresponding direction (right- or left-handed).

Discussion and conclusions.

Let us outline the main features of the genetic code model we have presented. This model is constructed utilizing new methods of biquaternion algebra including isotropic basis and internal, external and other types of biquaternionic multiplication, as well as various types of conjugation. In the model, each nucleotide is represented by its own biquaternion. Together, these four nucleotide biquaternions form the basis of the entire biquaternion space. Using products of various types, their doublets and triplets are constructed from biquaternions of nucleotides. Moving along this path, we can algebraically divide all nucleotide doublets, and then triplets (in idealization), into two modality groups – strong and weak. Well-known codon symmetries associated with complementarity, Rumer's transformation and the number of hydrogen bonds of nucleotides acquire algebraic embodiment.

In biquaternion form, each codon is written as a special triple product of nucleotide biquaternions. The model put the ground under phenomena of code degeneracy, i.e. specific grouping of triplets that code the same amino acids. The degeneracy of multiplets results from ideal-like properties of the biquaternions that model nucleotides and their multiplets. Nucleotides (in conjugate form), doublets, triplets and amino-acids all occur to be right-chiral or left-chiral states (in spin sense). Thus, chirality plays a key role in the operation of genes.

Historically spin formalism has been applied to areas other than the original spin theory. Thus, in theoretical physics, the theory of isotopic spin was proposed and successfully applied to describe the internal symmetries of baryons, which led to the creation of the quark model [37]. The proposed algebraic model of the genetic code indicates the quantum-like nature of nucleotides and the DNA molecule as a whole. Indeed, biquaternions provide an alternative representation of fermion spin wave functions in relativistic quantum theory. Biquaternions representing nucleotides can be considered as their wave functions, from which the complete wave functions of the genes and whole DNA are assembled. In future development biquaternion formalism may also be applied to the description of the non-coding part of DNA as well.

The properties of DNA nucleotides obtained in biquaternion algebra are similar to the physical properties of elementary particles and fields, such as spin, charge, and mass. However, it would be rash to attempt to directly identify these characteristics for biological objects. When describing the genetic code, nucleotides and their multiplets, we should be talking not about the physical spin, charge, mass, etc., but about the spin-, charge-, mass-like properties of the corresponding structures and their elements. The quantum-like biological nature of DNA is based on an analogue of physical spin, which we called biospin. It will probably be appropriate for genetic structures and a living organism as a whole to talk about its own biological space-time in which these properties are realized. Physical space-time and the proposed biological space-time must be connected in some way.

It can be assumed that the skew symmetry in the distribution of amino acid codons in ideal groups established within the framework of our model has its origin in the well-known asymmetry in living nature [14]. This assumption is based on the quasi-spin nature of the obtained algebraic structures. The “strength” or “weakness” of doublets and codons in ideal groups is largely determined by the chirality (in spin sense) of their constituent nucleotides. Moreover, between strong and weak roots we observe breaking of chiral symmetry, similar to one occurring in the

physics of weak interactions. Indeed, the distribution of chiral (signed) biquaternions is uneven between these two groups: there are three positive $D_+$and five negative D_-strong roots, and, conversely, five positive and three negative weak roots (see Tables 1 and 3). The internal chirality of nucleotides is assumingly responsible for the right-handed nature of the spatial twist of the DNA helix.

In our previous work [1][2] we identified an algebraic property that indicates the similarity of mathematical and biological objects: nullvectors and genes. This is indicated by the so-called nullvector factorization: when multiplied by each other, nullquaternions each give the product its structural half. In sexual crossing, half of the parent's genetic information is passed on to the offspring. In the case of nullquaternions, either the left or right structural half acts as such a half, depending on the order of the two nullquaternions in their product There is a remarkable likeness between nullvector algebra and genetics: the product of nullvectors is similar to the combination of allelic genes in a chromosome. The model constructed in this work is also based on nullquaternions, which provides additional evidence that nullquaternions should play a key role in the mathematics of life.

The proposed model in its own way answers many questions that have always faced researchers of the genetic code. Why there are four types of DNA nucleotides? Where did the division between strong and weak doublet roots come from? Why are triplets-codons grouped in a certain way when coding amino acids? The works [5][10] showed the manifestation of the ancient Eastern principle of Yin-Yang in its mathematical expression in the structures of the genetic code. In line with this, the main conclusion that we can draw here about the nature of DNA and the organism as a whole is that their work is based on the principle of complementarity, expressed in mathematical language of skew symmetry.

Biquaternion algebra in isotropic basis provides a new mathematical language for describing skew-symmetric structures. The model proposed above is likely not the only possible, other models could be built using this language. However, any model is just a step towards creating a theory. Such a theory describing the biological and informational nature of DNA, as we believe, should be field and quantum-like in nature.

The author sincerely thanks Sergey Valentinovich Petoukhov, without acquaintance with whose works and joint discussion of many deep issues of mathematical biology, writing this article would not have been possible.

Bibliography.

1. S.Ya. Kotkovskiy. "Nullvector algebra". Hypercomplex numbers in geometry and physics. 2(23) 12, pp.159-172. 2015

2. S.Ya. Kotkovskiy. "Quaternions, nullvectors and vector cycles in physics and biology". Report at the seminar “Algebraic biology and systems theory.” 2020. https://www.youtube.com/watch?v=LtxxrNWG6hs

3. S.Ya. Kotkovskiy. “Gold complex section. Skew symmetry. Dual fields". Report at the Congress “Systems Theory, Algebraic Biology, Artificial Intelligence.” 2023. https://www.youtube.com/watch?v=uI5ioOFHuok

4. S.Ya. Kotkovskiy. "Bivector algebra". Preprint. https://vixra.org/abs/2108.0015 , 2021.

5. S.V. Petoukhov. “Matrix genetics, genetic code algebras, noise immunity.” M., publishing house Regular and Chaotic Dynamics, 2008.

6. S.V. Petoukhov. " Vibrational genetic biomechanics and inherited systems of biological resonances." Medicine And high technology , 2015, N2, pp . 16-28.

7. Petoukhov, S. “Cyclic Gray Codes in Modeling Inherited Cyclic Biostructures and Analysis of Statistical Rules of Genomic DNAs.” Preprints 2024, 2024020713.

8. S.V. Petoukhov. “Hypercomplex numbers and the algebraic system of genetic alphabets. Elements of algebraic biology". Hypercomplex numbers in geometry and physics, volume 8, no. 2(16), p. 122, 2011.

9. Sergey Petoukhov. "The rules of long DNA-sequences and tetra-groups of oligonucleotides". arXiv :1709.04943[q - bio . OT]. 2017.

10. S.V. Petoukhov . "Biperiodic table of the genetic code and the number of protons". M., Nauka, 2001.

11. Yu.B. Rumer "Systematization of codons in the genetic code." Dokl . Academy of Sciences of the USSR. April 21, 1966; 167(6):1393-4.

12. O.M. Belotserkovsky, V.V. Shchennikov. "Kinematics of the operating space." 2006. http://integralsd.com/otp

13. V.V. Shchennikov. “The phenomenon of “nonlinear” time within the framework of the General Theory of Representations.” 2006. http://integralsd.com/otp

14. H. Weyl. "Symmetry".

15. A.G. Gurvich. "Theory of biological field". M. Sovetskaya nauka. 1944.

16. R. Sheldrake. "A New Science of Life: The Hypothesis of Morphic Resonance." Park Street Press. 1995.

17. Shcherbak, Vladimir I.. “Rumer's rule and transformation in the context of the co-operative symmetry of the genetic code.” Journal of theoretical biology 139 2 (1989): 271-6 .

18. Jestin, J.L.; Kempf, A. "Degeneracy in the genetic code: How and why?" Genes Genomes Genom. 2007, 1, 100–103.

19. Fimmel E, Strüngmann L. "Yury Borisovich Rumer and his 'biological papers' on the genetic code". Philos Trans A Math Phys Eng Sci. 2016 Mar 13.

20. Fimmel E, Strüngmann L. "Codon Distribution in Error-Detecting Circular Codes". Life (Basel). 2016 Mar 15;6(1):14.

21. Arquès, D.G.; Michel, C.J. "A complementary circular code in the protein coding genes". J. Theor. Biol. 1996, 182, 45–58.

22. Gonzalez DL, Giannerini S, Rosa R. Rumer's transformation: A symmetry puzzle standing for half a century. Biosystems. 2020 Jan.

23. Gonzalez, Diego & Giannerini, Simone & Rosa, Roco. (2012). On the origin of the mitochondrial genetic code: Towards a unified mathematical framework for the management of genetic information. Nature Precedings. 10.1038/npre.2012.7136.

24. A. Nofech. "Biquaternionic Dirac Equation Predicts Zero Mass for Majorana Fermions". Symmetry, 2020, 12. 1144. 10.3390/sym12071144.

25. M. Frank-Kamenetsky. "The most important molecule". M: Nauka. 1988

26. F. Antonuccio, "Split-Quaternions and the Dirac Equation", arXiv:1405.0187 [physics.gen-ph]. 2014

27. C. Manuel Carlevaro, Ramiro M. Irastorza, Fernando Vericat. "Quaternionic representation of the genetic code". arXiv:1505.04656 [q-bio.OT]. 2015

28. W.R. Hamilton. "On the geometrical interpretation of some results obtained (by calculation with biquaternions)", Proc. Roy. Irish Acad., Vol. 5, pp. 388 – 390, 1853.

29. L. Silberstein. "Quaternionic Form of Relativity", Philos. Mag. S., 6, Vol. 23, №137, pp. 790–809, 1912.

30. A.A. Alekseeva. “Differential algebra of biquaternions. Lorentz transformations of biwave equations.” Mathematical Journal, Almaty, Vol . 10, No. 35, 2010, pp . 33 – 41.

31. I. Bialynicki - Birula , " Photon " Wave Function ", Progress in Optics , 36 (1996). p . 15.

32. L. Dickson. «Equivalence of the complex quaternion and matric algebras". Linear Algebras, 1914, p. 13.

33. Savelev, I.V., Miller, R.A., Myakishev-Rempel, M. (2022). How the Biofield is Created by DNA Resonance. In: Bandyopadhyay, A., Ray, K. (eds) Rhythmic Advantages in Big Data and Machine Learning . Studies in Rhythm Engineering. Springer, Singapore.

34. Karafyllidis, Ioannis. (2008). Quantum Mechanical Model for Information Transfer from DNA to Protein. Bio Systems. 93. 191-8. 10.1016/j.biosystems.2008.04.002.

35. Kafatos MC, Chevalier G, Chopra D, Hubacher J, Kak S, Theise ND. Biofield Science: Current Physics Perspectives. Glob Adv Health Med. 2015 Nov;4(Suppl):25-34. doi: 10.7453/gahmj.2015.011.suppl. Epub 2015 Nov 1.

36. Grandpierre, Attila & Chopra, Deepak & Kafatos, Menas. (2014). The Universal Principle of Biology: Determinism, Quantum Physics and Spontaneity. NeuroQuantology. 12. 364-373. 10.14704/nq.2014.12.3.747.

37. https://en.wikipedia.org/wiki/Isospin

June 30th, 2024

s_kotkovsky@mail.ru