Rules of stochastics of genomic DNAs, biological dualism "stochastics-determinism", and tensor-unitary transformations

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Abstract. The article is devoted to algebraic modeling of universal rules of stochastic organization of genomic DNA of higher and lower organisms, previously published by the author. The proposed algebraic apparatus, which uses formalisms of quantum mechanics and quantum informatics and which is based on the so-called tensor-unitary transformations of vectors that generate families of interrelated stochastic-deterministic vectors of increased dimensions. The features of the vectors' interconnections in these families model the stochastic-deterministic properties of the named phenomenological rules. There are new approaches to modeling of developing multi-parameter biosystems, whose number of parameters increases in the course of step-by-step development. In the light of the presented materials, the issues of fractal-like organization in genetically inherited biosystems are considered. The development of the theory of stochastic determinism as an antipode of deterministic chaos is discussed.

Keywords: genomic DNAs, stochastics, tensor-unitary transformation, quantum informatics, fractal, projection operators, gestalt phenomena, stochastic determinism

Content

1. Introduction

This article presents algebraic tools for modeling the universal rules and symmetries in structures of long single-stranded DNA sequences in eukaryotic and prokaryotic genomes. These rules and symmetries were described in previous publications [Petoukhov, 2021a,b]. They were identified by taking into account that there are many DNA alphabets: an alphabet of 4 nucleotides, an alphabet of 16 duplets, an alphabet of 64 triplets, an alphabet of 256 tetraplets, etc. Correspondingly, each DNA sequence can be considered as a set (or a bunch) of many parallel

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DNA texts, each of which is written in one of these n-plets alphabets. For example, the DNA sequence ACCTGTAACG... is a bunch of the following texts, which we briefly term as n-texts of the DNA:

- a 1-text of nucleotides (A-C-C-C-T-G- ...);
- a 2-text of doublets (AC-CT-GT-AA-CG- ...);
- a 3-text of triplets (ACC-TGT-AAC- ..); etc.

In each of such different n-texts of the same genomic DNA sequence, the author calculated the percentages of each of its n-plets and then compared sets of calculated percentages from different n-texts. Such comparative analysis of DNAs in a wide set of eukaryotic and prokaryotic genomes revealed hidden algebraic interrelations among percentage compositions of these genomic n-texts and allowed the formulation of fundamental rules of stochastic organizations of the genomes [Petoukhov, 2021a, 2022a,b]. The revealed rules give pieces of evidence of the existence of global-genomic algebraic invariants, which remain unchanged over millions of years of biological evolution, during which millions of species of organisms die and new ones arise (although locally genomic sequences are modified under the action of mutations, the pressing of natural selection, etc.).

These rules testify to the coexistence of stochastic and deterministic traits in genomes. The stochastic-deterministic properties of genomic DNAs exist in parallel with the long-known facts of the coexistence of stochastic and deterministic features in inherited biological macrostructures. For example, genetics as a science began with Mendel's discovery of the stochastic rules of inheritance of traits in experiments on the crossing of organisms. Many processes in living bodies are a stochastic nature. The well-known expressions "gene noise" or "cell noise" reflect the fact that even genetically identical cells within the same tissue exhibit different levels of protein expression, different sizes, and structures due to the stochastic nature of interactions of individual molecules in cells.

The stochastic nature of genetic processes in the "small" does not interfere with the inheritance of the traits determined in the "big" (so-called Gestalt phenomena). For example, fingerprints are different for all people, although fingers in the whole have a typical shape and composition (3 phalanges, etc.). According to Mendel's law of independent inheritance of traits, information from the level of DNA molecules dictates the macrostructure of living bodies through many independent channels, despite strong noises. Thus, hair, eye and skin colors are inherited independently of each other. Accordingly, each organism is a machine of multichannel noise-immunity encoding.

All physiological systems are genetically inherited through their genetic coding. Therefore, the origins of the phenomena “stochastics-and-determinism” in inherited macrostructures, one should look for in the genetic system of DNA informatics. The author believes that the mentioned rules of stochastic-deterministic features of genomic DNAs are useful for modeling and understanding such inherited phenomena.

But for a deep understanding of the noted phenomena and the development of algebraic biology, it is not enough just to note the existence of many such facts. It is necessary to find an adequate algebraic apparatus for modeling the set of facts of biological dualism "stochastics-determinism" in the academic language of mathematical natural sciences in connection with features of the molecular-genetic system. The previous author’s works [Petoukhov, 2022a,b] contain descriptions of algebraic interrelations among different sets of probabilities of n-plets in n-plet textual representations of genomic DNAs.

The purpose of this article is to describe the appropriate algebraic apparatus of tensor-unitary transformations proposed by the author. This apparatus is based on the study of the universal stochastic-deterministic features of genomic DNAs. It allows algebraically modeling of a few fundamental biological phenomena, for example, the dualism "stochastics-determinism", gestalt phenomena, multi-reproductions of some structures, phenomena of memory of the past structures, and also of forecast in special formalized situations.

The next section describes tensor-unitary operations, whose idea was originated from

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phenomenological relationships between the probabilities of n-plets and (n+1)-plets in n-text and (n+1)-text representations of genomic DNAs.

2. Tensor-unitary transformations and modeling of biological phenomena

This chapter describes algebraic operations called tensor-unitary transformations.

It is natural to try to model the universal rules of the stochastic organization of genomic DNAs, which are objects of microworld of quantum mechanics, in the language of quantum mechanics and quantum informatics, which are based on the concept of probability. It can be noted here that the concept of a quantum computer first appeared in 1980 in the book of Yu.I. Manin precisely in connection with the analysis of the high-speed processing of DNA information in chromosomes by "*genetic automata*". This book predicted the important role of unitary transformations and tensor products: "*A quantum automaton must be abstract: its mathematical model must use only the most general quantum principles, without prejudging physical realizations. Then the model of evolution is a unitary rotation in a finite-dimensional Hilbert space, and the model of virtual division into subsystems corresponds to the decomposition of space into a tensor product. Somewhere in this picture, an interaction should find its place, which is traditionally described by Hermitian operators and probabilities*" [Manin, 1980, p.15]. Thus, the very birth of quantum informatics was due to the desire to understand the features of genetic informatics and its stochastics!

The first article on quantum biology was published in 1930 by P. Jordan, one of the founders of quantum mechanics, according to the history of its origin [McFadden, Al-Khalili, 2018]. Jordan stated that the missed laws of the living are the rules of probabilities. Works on quantum biology, that is, the modeling of biological phenomena based on the formalisms and ideologies of quantum mechanics and quantum informatics, are intensively developing in our time (see, for example, [Adams, Petruccione, 2020; Biava et al., 2019; Cao et al., 2020; Goh, Tong, Pusparajah, 2020; Karafyllidis, 2017; Khrennikov, Asano, 2020; Laster et al., 2019; Marais et al., 2018; Raghunandan et al., 2019]).

The universal rules of stochastic organization of genomic DNAs, which are presented in our work as multilayer texts written in the languages of tensor interconnected alphabets of DNA n-plets, correspond to the mentioned prediction by Manin and have some connections with quantum mechanics and quantum informatics [Petoukhov, 2022b]. They led to introducing a new concept of "tensor-unitary transformations". One can remind here that in quantum mechanics and quantum informatics, unitary transformations have fundamental meaning: the evolution of closed quantum systems is described by unitary transformations, and all calculations in quantum informatics are based on unitary operators acting as quantum gates [Nielsen, Chuang, 2010]. Unitary transformations (they are orthogonal transformations in the case of real components) of vectors preserve their lengths and also preserve the inner products.

By definition, the proposed tensor-unitary transformations are transformations that preserve the norms (lengths) of vectors when they are tensorial transformed into vectors of a space of increased dimension. Unlike unitary transformations, which transform the original n-dimensional vector into an n-dimensional vector of the same dimension, tensor-unitary transformations transform the original (or "mother") n-dimensional vector into a "daughter" m-dimensional vector of increased dimension ($m > n$) with preserving the length of the mother vector. One can say that they provide the "inheritance" of the vector length into the length of a new tensorial transformed vector belonging a new space of tensorial increased dimension; this new space can be interpreted as the configuration space of a multiparameter system whose number of parameters increases in a course of its development (by analogy with biosystems under their ontogenetic growth).

Applying these tensor-unitary transformations to vectors uses a two-step process. First, the original n-dimensional vector, called the mother vector, is represented as the sum of all its basis vectors with their coordinate weights (for example, the vector [x, y] is represented as [x, 0]+[0, y]

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that is, x[1, 0]+y[0,1]). Then each of these weight basis vectors is tensor-multiplied by the so-called "normvector" (qubit-like vector) ensuring the preservation of the length of the mother vector in the daughter vector of the tensor increased dimension. By definition, a normvector is a *k*-dimensional vector $[\alpha_0, \alpha_1, \alpha_2, \ldots, \alpha_{k-1}]$, whose sum of squares of coordinates is equal to one: $\alpha_0^2 + \alpha_1^2 + \alpha_2^2 + \ldots + \alpha_{k-1}^2 = 1$. Its coordinates can be considered as probability amplitudes.

One can briefly mention that the tensor-unitary transformations can be represented as a very special case of the Hadamard products for block vectors or matrices when it comes to component-wise multiplication of a vector by appropriate number of qubit-like normvectors, whose component sets coincide with the set of probability amplitudes of the corresponding qubit or polyqubit. For the operation of tensor-unitary transformations, a special symbol ⍜ can be proposed (its Unicode 0x235d, https://unicodemap.org/details/0x235D/index.html). This symbol resembles the shape of a thumb with a nail, which is one of the representatives of the biological gestalt-phenomena of the inheritance of a deterministic configurations under conditions of stochastic interactions of individual molecules in cells.

Why universal stochastic rules of genomic DNAs are connected with tensor-unitary transformations? What mathematical features are provided by these transformations? Could they be used for modeling the biological gestalt phenomena and the dualism "stochastics-and-determinism"? Why living nature prefers the usage of tensor-unitary transformations in genetic systems? The main aim of this chapter is to study these questions and present the initial author's results and thoughts about appropriate algebraic tools for modeling the important biological phenomena, which were not been algebraically modeled early but now are been including in the field of mathematical natural science.

2.1. Modeling biological dualism "stochastics-determinism"

Under tensor-unitary transformations, the "qubit-like" property of normvectors provides introducing an element of probability (stochasticity) into the values of individual coordinates of the daughter multi-dimensional vector, whose special groupings of coordinates turn out to be deterministic carriers of memory about the coordinates of the mother vector. Thus, tensor-unitary transformations, being stochastic-deterministic transformations, generate stochastic-deterministic vectors and make it possible to model the biological dualism "stochastics-determinism". Let us explain this with simple examples.

One can consider a simplest mother vector function $[x(t), y(t)] = [x(t), 0] + [0, y(t)]$ and tensor multiplicate its first weighted basis vector $[x(t), 0]$ with the normvector $[\alpha_0, \alpha_1]$, and its second weighted basis vector $[0, y(t)]$ with the normvector $[\beta_0, \beta_1]$ (here $\alpha_0^2 + \alpha_1^2 = 1$, and $\beta_0^2 + \beta_1^2 = 1$):

$$\vec{\boldsymbol{D}}_1 = [x(t), 0] \otimes [\alpha_0, \alpha_1] + [0, y(t)] \otimes [\beta_0, \beta_1] = [x(t)\alpha_0, x(t)\alpha_1, y(t)\beta_0, y(t)\beta_1] \qquad (2.1.1)$$

Using the mentioned symbol ⍜ of the tensor-unitary transformation, this expression can be written also in the following form:

$$[x(t), y(t)] \circledcirc \{[\alpha_0, \alpha_1], [\beta_0, \beta_1]\} = [x(t)\alpha_0, x(t)\alpha_1, y(t)\beta_0, y(t)\beta_1] \qquad (2.1.2)$$

The values of the individual coordinates of the daughter vector function $\vec{\boldsymbol{D}}_1$ (2.1.1) are stochastic since each of them contains one of the probability amplitudes $\alpha_0, \alpha_1, \beta_0, \beta_1$. There exist infinitely many options for the values of $\alpha_0, \alpha_1, \beta_0, \beta_1$, and their random selection changes the values of these individual coordinates but the lengths of the daughter and mother vectors will be equal under all these selections and under each fixed value of the variable t. In other words, using different sets of the values $\alpha_0, \alpha_1, \beta_0, \beta_1$, you get many daughters vector functions $\vec{\boldsymbol{D}}_1$, which differ each other by their coordinates but all of them have the same length under any fixed value of the parameter t.

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This is confirmed by calculating the length $||\vec{\boldsymbol{D}}_1||$ of the vector function (2.1.1) under each fixed value of a variable t:

$$||\mathbf{D_1}|| = \{x^2\alpha_0^2+x^2\alpha_1^2+y^2\beta_0^2+y^2\beta_1^2\}^{0.5} = \\ = \{x^2(\alpha_0^2+\alpha_1^2)+y^2(\beta_0^2+\beta_1^2)\}^{0.5} = (x(t)^2+y(t)^2)^{0.5} \quad (2.1.3)$$

This length (2.1.3) of the daughter 4-dimensional vector $\vec{\boldsymbol{D}}_1$ is equal to the length of the mother 2-dimensional vector function [x(t), y(t)] at any fixed time t. In other words, the daughter vector $\vec{\boldsymbol{D}}_1$, having stochastic coordinates and the increased dimensionality, carries on an exact "memory" of the length of the mother vector function at any fixed moment of time, regardless of the stochasticity of its individual coordinates, and in this respect is a deterministic entity. One can say that here you have stochastics with hidden determinism. Now let us note other deterministic features of this daughter's 4-dimensional vector $\vec{\boldsymbol{D}}_1$, which are connected with its projections on coordinate planes.

A 4-dimensional vector space with a Cartesian system of numbered coordinates $[X_0, X_1, X_2, X_3]$ contains 6 coordinate planes:

$$(X_0,X_1),\ (X_2,X_3),\ (X_0,X_2),\ (X_0,X_3),\ (X_1,X_2),\ (X_1,X_3) \quad (2.1.4)$$

In the plane (X_0,X_1), the daughter vector $\vec{\boldsymbol{D}}_1$ (2.1.1) is represented by its projection vector $\vec{\boldsymbol{M}}_{01} = [x(t)\alpha_0, x(t)\alpha_1, 0, 0]$. Its length $||\mathbf{M_{01}}||$ (2.1.5) is equal to the first coordinate of the mother vector [x(t), y(t)] at any fixed time t:

$$||\mathbf{M_{01}}|| = \{a(t)^2\alpha_0^2 + a(t)^2\alpha_1^2\}^{0.5} = \{a(t)^2(\alpha_0^2 + \alpha_1^2)\}^{0.5} = a(t) \quad (2.1.5)$$

In the plane (X_2,X_3), the daughter vector $\vec{\boldsymbol{D}}_1$ is represented by its projection vector $\vec{\boldsymbol{M}}_{23} = [0, 0, y(t)\beta_0, y(t)\beta_1]$. Its length $||\mathbf{M_{23}}||$ (2.1.6) is equal to the second coordinate of the mother vector [x(t), y(t)] at any fixed time t:

$$||\mathbf{M_{23}}|| = \{y(t)^2\beta_0^2 + y(t)^2\beta_1^2\}^{0.5} = \{y(t)^2(\beta_0^2 + \beta_1^2)\}^{0.5} = y(t) \quad (2.1.6)$$

Expressions (2.1.3, 2.1.5, 2.1.6) indicate that the daughter 4-dimensional vector $\vec{\boldsymbol{D}}_1$, having stochastic coordinates, contains in the groupings of these coordinates the exact "memory" of all coordinates and length of the mother 2-dimensional vector, that is, in this respect it is a deterministic entity.

Thus, tensor-unitary transformations and families of daughter vectors, generated by them, make it possible to model the biological dualism "stochastics-and-determinism", as well as the phenomena of Gestalt biology, in which only relations in groupings of elements are important and meaningful, but not individual elements in themselves. For example, we recognize a musical melody even when it is performed on different instruments and in different frequency ranges with a change in the sound frequencies of individual notes, which turn out to be insignificant, in contrast to the ratios in the groupings of musical frequencies. Since tensor-unitary transformations make it possible to model biological Gestalt phenomena, they can also be conditionally called Gestalt transformations, and the stochastic-deterministic vectors (or vector functions) generated by them can be called Gestalt vectors.

One should emphasize that usually, unitary (or orthogonal) operators are understood as unitary square matrices, but in the case of tensor-unitary transformations, the component-wise tensor product of a mother vector and corresponding number of normvectors is used to get a stochastic-deterministic object (number of normvectors is equal to dimensionality of the mother vector, whose each component should be multiplied by an individual normvector).

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It should be noted that the daughter 4-dimensional vector $\vec{D}_1$ (2.1.1) is not only the carrier of the exact memory of the coordinates of the mother 2-dimensional vector but also the carrier of new information in the planes (X_0, X_2), (X_0, X_3), (X_1, X_2), (X_1, X_3) of 4-dimensional space. In these planes, the daughter vector $\vec{D}_1$ is represented by its projection vectors $\vec{M}_{02} = [x(t)\alpha_0, 0, y(t)\beta_0, 0]$, $\vec{M}_{03} = [x(t)\alpha_0, 0, 0, y(t)\beta_1]$, $\vec{M}_{12} = [0, x(t)\alpha_1, y(t)\beta_0, 0]$, $\vec{M}_{13} = [0, x(t)\alpha_1, 0, y(t)\beta_1]$ whose lengths are not equal to the coordinates of the mother vector. The values of their lengths carry new information, which is entered into them by the stochastic coordinates of the normvectors α_0, α_1, β_0, β_1. These new stochastic components can reflect, for example, the specifics of the stage of ontogenesis or the impacts on the organism from the external environment. Thus, the **tensor-unitary transformation is a memory expansion operation** (while maintaining all the previous memory) for a tensor extended multi-parameter system, which, along with the memory of the "ancestors" parameters, contains many new parameters or information. Correspondingly, tensor-unitary transformations can be used for modeling growing stochastic-deterministic biosystems of morphogenetic, biorhythmic, and other kinds where number of parameters and degrees of freedom is increased step-by-step.

The values of the dot products of two mother vectors - for example, the vectors [x, y] and [s, r] - and of two their daughter vectors are equal only when tensor-unitary transformations of both mother vectors use the same set of normvectors, for example, $[\alpha_0, \alpha_1]$ and $[\beta_0, \beta_1]$. To illustrate this, one can take two mother vectors [x, y] and [s, r], whose dot product is equal to xs+yr. Now let us tensor-unitary transform both mother vectors into their daughter vectors $\vec{P}$ and $\vec{V}$ by using these normvectors $[\alpha_0, \alpha_1]$ and $[\beta_0, \beta_1]$:

$$\begin{aligned} \vec{P} &= [x, y] \circledcirc \{[\alpha_0, \alpha_1], [\beta_0, \beta_1]\} = [x\alpha_0, x\alpha_1, y\beta_0, y\beta_1] \\ \vec{V} &= [s, r] \circledcirc \{[\alpha_0, \alpha_1], [\beta_0, \beta_1]\} = [s\alpha_0, s\alpha_1, r\beta_0, r\beta_1] \end{aligned} \qquad (2.1.7)$$

Calculating the dot product of these two daughter vectors $\vec{P}$ and $\vec{V}$ gives the same value as the dot product of their mother vectors:

$$\begin{aligned} \vec{P} \bullet \vec{V} &= x\alpha_0 s\alpha_0 + x\alpha_1 s\alpha_1 + y\beta_0 r\beta_0 + y\beta_1 r\beta_1 = \\ &= xs(\alpha_0^2 + \alpha_1^2) + yr(\beta_0^2 + \beta_1^2) = xs + yr \end{aligned} \qquad (2.1.8)$$

One can easily check that if components of two mother vectors are tensor multiplied by different normvectors (for example, the mother vector [x, y] is tensor-unitary transformed by normvectors $[\alpha_0, \alpha_1]$ and $[\beta_0, \beta_1]$, and the mother vector [s, r] is tensor-unitary transformed by normvectors $[\gamma_0, \gamma_1]$ and $[\delta_0, \delta_1]$, then the dot product of the daughter vectors are not equal to the dot product of the mother vectors.

Tensor-unitary transformations can be repeatedly applied to generate or develop from a mother vector more and more complex multi-parameter daughter vectors with a step-by-step increase in the dimension of their configuration spaces. In these growing daughter vectors, the connections of parameters from mother vectors and also from previous daughter vectors will be preserved simultaneously with arising of new parameters and relationships. Tensor-unitary transformations make it possible to record a step-by-step history of the development of a tensor growing multi-parametric stochastic-deterministic system in a form of sequences (or a set of the sequences) of daughter vectors corresponding an initial mother vector (or a set of the mother vectors).

Regarding this step-by-step history of development of multi-parametric systems by repeating of tensor-unitary transformations, let us consider an example when the above 4-dimensional daughter vector function $\vec{D}_1$ (2.1.1) is tensor-unitarily transformed into an 8-dimensional daughter vector function $\vec{D}_2$. This example will show that all data about lengths and

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components of the daughter vector function $\vec{D}_1$ are preserved in certain groupings of stochastic coordinates of the daughter vector function $\vec{D}_2$, that is in projections of $\vec{D}_2$ into appropriate subspaces of 8-dimensional space with Cartesian coordinate system. To simplify the notation, we will not constantly indicate that the coordinates of the considered vector functions are functions of time.

To construct $\vec{D}_2$, by analogy with the above, we represent the vector $\vec{D}_1$ as the sum of its weighted basis vectors (2.1.9):

$$\vec{D}_1 = [x\alpha_0, 0, 0, 0] + [0, x\alpha_1, 0, 0] + [0, 0, y\beta_0, 0] + [0, 0, 0, y\beta_1] \quad (2.1.9)$$

Then we tensor multiply each of these four weight basis vectors in (2.1.9) by one of the 4 normvectors (2.1.10):

$$[c_0, c_1], [d_0, d_1], [p_0, p_1], [r_0, r_1], \text{ where } c_0^2+c_1^2 =1,\ d_0^2+d_1^2 =1,\ p_0^2+p_1^2 =1,\ r_0^2+r_1^2 =1 \quad (2.1.10)$$

The resulting 8-dimensional daughter vector $\vec{D}_2$ has the form (2.1.11):

$$\begin{aligned}\vec{D}_2 &= [x\alpha_0, 0, 0, 0]\otimes[c_0, c_1] + [0, x\alpha_1, 0, 0]\otimes[d_0, d_1] + [0, 0, y\beta_0, 0] \otimes [p_0, p_1]+\\ &+ [0,0,0, y\beta_1]\otimes[r_0, r_1] = [x\alpha_0c_0, x\alpha_0c_1, 0,0,0,0,0,0] + [0,0, x\alpha_1d_0, x\alpha_1d_1,\\ &\quad 0,0,0,0] + [0, 0, 0, 0, y\beta_0p_0, y\beta_0p_1, 0, 0] + [0, 0, 0, 0, 0, 0, y\beta_1r_0, y\beta_1r_1] =\\ &= [x\alpha_0c_0, x\alpha_0c_1, x\alpha_1d_0, x\alpha_1d_1, y\beta_0p_0, y\beta_0p_1, y\beta_1r_0, y\beta_1r_1] \quad (2.1.11)\end{aligned}$$

The values of the individual coordinates of this daughter vector $\vec{D}_2$ are also probabilistic in nature, since each of them contains the amplitude of the probabilities, that is, in this aspect, this vector is stochastic.

Calculation of the length $||\mathbf{D}_2||$ of the vector $\vec{D}_2$ (2.1.11), taking into account the relations (2.1.10), gives the following:

$$\begin{aligned}||\mathbf{D}_2|| &= \{(x\alpha_0c_0)^2 + (x\alpha_0c_1)^2 + (x\alpha_1d_0)^2 + (x\alpha_1d_1)^2 + (y\beta_0p_0)^2 +\\ &\quad + (y\beta_0p_1)^2 + (y\beta_1r_0)^2 + (y\beta_1r_1)^2\}^{0.5} =\\ &= \{(x\alpha_0)^2(c_0^2+c_1^2) + (x\alpha_1)^2(d_0^2 + d_1^2) + (y\beta_0)^2(p_0^2 + p_1^2) + (y\beta_1)^2(r_0^2 + r_1^2)\}^{0.5} =\\ &= \{(x^2(\alpha_0^2 + \alpha_1^2) + y^2(\beta_0^2 + \beta_1^2)\}^{0.5} = (x^2 + y^2)^{0.5} \quad (2.1.12)\end{aligned}$$

At any time, this length (2.1.12) of the daughter 8-dimensional vector function $\vec{D}_2$ is equal to the length of the mother 2-dimensional vector function [x(t), y(t)] and the length (2.1.3) of the previous daughter 4-dimensional vector function $\vec{D}_1$. In other words, at any fixed point in time, in the grouping of its coordinates, the daughter vector function $\vec{D}_2$ carries an exact "memory" of the length of the mother vector function, as well as the length of the daughter vector function $\vec{D}_1$, regardless of the stochasticity of its individual coordinates. Accordingly, the stochastic vector function $\vec{D}_2$ in this aspect is a deterministic entity and belongs to the class of stochastically deterministic vector functions (or vectors). We now also note other deterministic features of this daughter vector function $\vec{D}_2$ generated by the tensor-unitary transformation.

We enumerate through X_i the order of coordinates in the 8-dimensional vector space with the Cartesian coordinate system: $[X_0, X_1, X_2, X_3, X_4, X_5, X_6, X_7]$. Let us show that the groupings of 8 weight basis vector functions of $\vec{D}_2$ (2.1.11) contain exact information (memory) about each coordinate of the mother vector function [x(t), y(t)] and each coordinate of the previous daughter 4-dimensional vector function $\vec{D}_1$ at any fixed time.

In the subspace (X_0,X_1,X_2,X_3) the 8-dimensional vector function $\vec{D}_2$ (2.1.11) is represented by the vector function $\vec{V}_{0123} = [x\alpha_0c_0, x\alpha_0c_1, x\alpha_1d_0, x\alpha_1d_1]$. At any time, its length (2.1.13) is equal

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to the length and first coordinate of the mother weight basis vector [x, 0] and the length of the 2-dimensional vector $\vec{M}_{01}$ (2.1.5), which is the projection of the daughter 4-dimensional vector of the previous generation $\vec{D}_1$ (2.1.1):

$$||\vec{V}_{0123}|| = (x^2\alpha_0^2c_0^2 + x^2\alpha_0^2c_1^2 + x^2\alpha_1^2d_0^2 + x^2\alpha_1^2d_1^2)^{0.5} = \{x^2\alpha_0^2(c_0^2 + c_1^2) + x^2\alpha_1^2(d_0^2 + d_1^2)\}^{0.5} = \{x^2\alpha_0^2 + x^2\alpha_1^2\}^{0.5} = x\{\alpha_0^2 + \alpha_1^2\}^{0.5} = x(t) \quad (2.1.13)$$

In the subspace (X_4,X_5,X_6,X_7) the 8-dimensional vector function $\vec{D}_2$ (2.1.11) is represented by the vector function $\vec{V}_{4567} = [y\beta_0p_0, y\beta_0p_1, y\beta_1r_0, y\beta_1r_1]$. At any time, its length (2.1.14) is equal to the length and second coordinate of the mother vector function [x(t), b(t)], as well as the length of the 2-dimensional vector $\vec{M}_{01}$ (2.1.5), which is the projection of the daughter 4-dimensional vector of the previous generation $\vec{D}_1$ (2.1.1):

$$||\mathbf{V}_{4567}|| = \{y^2\beta_0^2p_0^2 + y^2\beta_0p_1^2 + y^2\beta_1^2r_0^2 + y^2\beta_1^2r_1^2\}^{0.5} = \{y^2\beta_0^2(p_0^2 + p_1^2) + y^2\beta_1^2(r_0^2 + r_1^2)\}^{0.5} = \{y^2\beta_0^2 + y^2\beta_1^2\}^{0.5} = y\{\beta_0^2 + \beta_1^2\}^{0.5} = b(t) \quad (2.1.14)$$

Let us now show that the groupings of coordinates of the 8-dimensional daughter vector function $\vec{D}_2$ (2.1.11) also carry the exact memory of all four coordinates of the 4-dimensional daughter vector function of the previous generation $\vec{D}_1$ (2.1.1).

In the plane (X_0,X_1), the 8-dimensional vector function $\vec{D}_2$ (2.1.11) is represented by the vector function $\vec{V}_{01} = [x\alpha_0c_0, x\alpha_0c_1]$. Its length (2.1.15) is equal to the first coordinate of the daughter vector function $\vec{D}_1$ (2.1.1):

$$||\mathbf{V}_{01}|| = (x^2\alpha_0^2c_0^2 + x^2\alpha_0^2c_1^2)^{0.5} = x\alpha_0(c_0^2 + c_1^2)^{0.5} = x\alpha_0 \quad (2.1.15)$$

In the plane (X_2,X_3), the 8-dimensional vector function $\vec{D}_2$ (2.1.11) is represented by the vector function $\vec{V}_{23} = [x\alpha_1d_0, x\alpha_1d_1]$. Its length (2.1.16) is equal to the second coordinate $x\alpha_1$ of the daughter vector $\vec{D}_1$ (2.1.1):

$$||\mathbf{V}_{23}|| = (x^2\alpha_1^2d_0^2 + x^2\alpha_1^2d_1^2)^{0.5} = x\alpha_1(d_0^2 + d_1^2)^{0.5} = x\alpha_1 \quad (2.1.16)$$

In the plane (X_4,X_5), the 8-dimensional vector function $\vec{D}_2$ (2.1.11) is represented by the vector function $\vec{V}_{45} = [y\beta_0p_0, y\beta_0p_1]$. Its length (2.1.17) is equal to the third coordinate $y\beta_0$ of the daughter vector function $\vec{D}_1$ (2.1.1):

$$||\mathbf{V}_{45}|| = (y^2\beta_0^2p_0^2 + y^2\beta_0^2p_1^2)^{0.5} = y\beta_0(p_0^2 + p_1^2)^{0.5} = y\beta_0 \quad (2.1.17)$$

In the plane (X_6,X_7), 8-dimensional vector function $\vec{D}_2$ is represented by the vector function $\vec{V}_{67} = [y\beta_1r_0, y\beta_1r_1]$. Its length (2.1.18) is equal to the fourth coordinate $y\beta_1$ of the daughter vector function $\vec{D}_1$ (2.1.1):

$$||\mathbf{V}_{67}|| = (y^2\beta_1^2r_0^2 + y^2\beta_1^2r_1^2)^{0.5} = y\beta_1(r_0^2 + r_1^2)^{0.5} = y\beta_1 \quad (2.1.18)$$

Thus, indeed, the groupings of the coordinates of the daughter 8-dimensional vector function $\vec{D}_2$, presented in the expressions (2.1.13 - 2.1.18), carry the exact memory of all the coordinates of the mother vector function [x(t), y(t)] and the daughter 4-dimensional vector function of the previous generation $\vec{D}_1$. The set of other groupings of coordinates of the daughter 8-dimensional vector $\vec{D}_2$, for example, in the subspaces (X_0,X_2), (X_1,X_7), (X_1,X_3,X_4,X_5), etc.,

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correspond to vectors whose lengths are not equal to the coordinates of the mother vector and the previous daughter vector $\vec{D}_1$, and can carry new information introduced by the parameters of the normvectors used, which can reflect various factors that affect the complexity of the organism as developing multi-parametric system.

In addition, the following case should be noted. Coordinates of normvectors can be not only fixed numeric values but also normalized functions of time or other variables. The expression (2.1.19) shows an example of the 2-dimensional normvectors $[\alpha_0, \alpha_1]$ whose coordinates are functions of variable t:

$$\overrightarrow{F(t)} = [\alpha_0(t), \alpha_1(t)] / \{ \alpha_0(t)^2 + \alpha_1(t)^2 \}^{0.5} \quad (2.1.19)$$

At any value t, the sum of squares of its coordinates is equal to 1 (2.1.20), that is, the vector function $\overrightarrow{F(t)}$ satisfies the definition of normvectors and can be used in tensor-unitary transformations:

$$\begin{aligned} &\{\alpha_0(t)/(\alpha_0(t)^2 + \alpha_1(t)^2)^{0.5}\}^2 + \{\alpha_1(t)/(\alpha_0(t)^2 + \alpha_1(t)^2)^{0.5}\}^2 = \\ &= \{\alpha_0(t)^2 + \alpha_1(t)^2\} / \{\alpha_0(t)^2 + \alpha_1(t)^2\} = 1 \end{aligned} \quad (2.1.20)$$

In particular, in this case, when the coordinates of the normvectors are normalized functions of time or another variable, the above expressions (2.1.3, 2.1.5, 2.1.6, 2.1.8, 2.1.12 - 2.1.14) about the memory of "ancestors" in vector lengths don't be changed but the expressions (2.1.15 – 2.1.18) about new information acquire forms of essentially new vector functions, which depend on vector functions in used normvectors (2.1.21):

$$\begin{aligned} \|\mathbf{V_{01}}\| &= (x^2\alpha_0^2c_0^2 + x^2\alpha_0^2c_1^2)^{0.5} = x\alpha_0(c_0^2 + c_1^2)^{0.5} = x(t)*\alpha_0(t), \\ \|\mathbf{V_{23}}\| &= (x^2\alpha_1^2d_0^2 + x^2\alpha_1^2d_1^2)^{0.5} = x\alpha_1(d_0^2 + d_1^2)^{0.5} = x(t)*\alpha_1(t), \\ \|\mathbf{V_{45}}\| &= (y^2\beta_0^2p_0^2 + y^2\beta_0^2p_1^2)^{0.5} = y\beta_0(p_0^2 + p_1^2)^{0.5} = y(t)*\beta_0(t), \\ \|\mathbf{V_{67}}\| &= (y^2\beta_1^2r_0^2 + y^2\beta_1^2r_1^2)^{0.5} = y\beta_1(r_0^2 + r_1^2)^{0.5} = y(t)*\beta_1(t) \end{aligned} \quad (2.1.21)$$

This case of using of normvectors, whose coordinates are normalized functions of variables, gives new abilities to model some biological phenomena, for example, cellular differentiations when the cells change to specialized types.

So far, we have been talking about tensor-unitary modeling of growing multi-parameter systems (such as multicellular biosystems in ontogeny). But one can also speak of a similar tensor-unitary modeling of generations of step-by-step expanding families of many computer memory cells. This makes it easier to understand that tensor-unitary transformations can output to a genomorphic-type computer artificial intelligence: such intelligence is based on generations of tensor-unitary expanding families of computer cells, in which some groupings of cells carry information about the states of all cells of families of previous generations, and other groupings of cells carry new information associated with the current influences of the external and internal environment.

Tensor-unitary transformations make it possible to approach the problem of predicting events or states in expanding families of computer memory cells based on function assignments in normalized normvectors, for example, like $[\alpha_0(t), \alpha_1(t)] / \{(\alpha_0(t)^2 + \alpha_1(t)^2)\}^{0.5}$ whose sum of squared coordinates is equal to one (i.e. $\{ \alpha_0^2 + \alpha_1^2\}/\{ \alpha_0^2 + \alpha_1^2\} = 1$).

Let us assume that the functions of this normvector $\alpha_0(t)$, $\alpha_1(t)$ are functions that reflect all the environmental conditions and homeostasis that are significant for the functioning of the body (temperature, pressure, nutrition, illumination, characteristics of sensory perception of the body, characteristics of heartbeat and respiration). If at the next step of repeating the tensor-unitary transformation, the application of the same normvector is repeated (assuming that the above conditions have not practically changed), then it is possible to calculate in advance the state of the

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emerging new extended family of memory cells, and then compare it with the one actually implemented in life, making sure that the states of both families are almost the same.

Memory and the ability to predict are characteristic features of biological intelligence. For this reason, tensor-unitary transformations and the generations of families of stochastic-deterministic vectors generated by them seem to be promising algebraic tools for creating artificial intelligence systems of the genomorphic type.

It should be emphasized that it is the lengths of daughter vectors and their projections into subspaces of the multidimensional configuration space of a multiparameter system that carry the memory of the past and new information. Therefore, in the analysis of genetic diseases, possibly associated with disturbances in the stochastic characteristics of gene sequences, it is necessary to focus on a comparative analysis of the lengths of stochastic vectors and their projections. It is important that for shortened DNA sequences (for example, sequences of separate genes or their combinations), their modeling will be based on component-by-component tensor multiplication not on qubit-like normvectors, but on some other vectors; the use of these new vectors generates daughter vectors of different lengths than the mother vector. The resulting new daughter vectors, received in the case of shortened DNA sequences of genes, can be compared with genomic DNA daughter vectors, paying attention not only to length differences, but also to the values of the dot products between daughter vectors of genes and daughter vectors of genomes. It is not for nothing that there are universal laws of the stochastic organization of genomes, and it is not for nothing that P. Jordan, who was one of the creators of quantum mechanics and the author of the first article on quantum biology, stated that the missed laws of the living are the rules of probabilities [McFadden, Al-Khalili, 2018].

2.2. Tensor-unitary transformations and multi-reproductions of geometric configurations

Tensor-unitary transformations make it possible to simulate multi-reproductions (multi-replications) of geometric configurations. It can be illustrated by the following example. Let the variable coordinates of the mother vector function [x(t), y(t)] correspond to the functions of the parametric definition of the curve (Fig. 2.2.1), called the cardioid (we will call it the mother cardioid):

$$x(t)=\cos(t)*(1+\cos(t)); \quad y(t)=\sin(t)*(1+\cos(t)) \qquad (2.2.1)$$

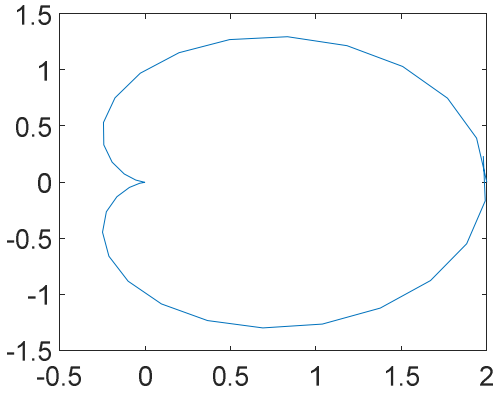

Fig. 2.2.1. Mother cardioid, parametrically specified by the mother vector [x(t), y(t)] where x(t) and y(t) are presented in the expression (2.2.1).

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For simplicity, consider the tensor-unitary transformation of the mother vector function [x(t), y(t)] (where x(t) and y(t) are presented by the expression (2.2.1)), in which both coordinates are tensor multiplied by the same normvector $\vec{W} = [0.5^{0.5}, 0.5^{0.5}]$, giving a daughter vector function $\vec{R}_4(t)$ (2.2.2):

$$\vec{R}_4(t) = [x(t),0] \otimes \vec{W} + [0,y(t)] \otimes \vec{W} = \\ = [x(t)*0.5^{0.5}, x(t)*0.5^{0.5}, y(t)*0.5^{0.5}, y(t)*0.5^{0.5}] \qquad (2.2.2)$$

In the four planes (X_0, X_2), (X_1, X_3), (X_0, X_3) and (X_1, X_2) of the Cartesian coordinate system, this daughter vector function $\vec{R}_4$ is represented by the same projection vector function $[x(t)*0.5^{0.5}, y(t)*0.5^{0.5}]$, whose coordinates correspond the parametric description of the cardioid (Fig. 2.2.2). Thus, in these four different 2-dimensional subspaces of the 4-dimensional configuration space of the multi-parameter system, four identical daughter cardioids are generated, which are slightly reduced copies of the mother cardioid (2.2.1). This fact illustrates the general proposition that **tensor-unitary transformations can serve as multi-reproduction operations for structures** given by the mother vector. In other words, these tensor-unitary operations, prompted by the universal rules of the stochastic organization of genomic DNAs, make it possible to model in the matrix-tensor language not only the biological dualism "stochastics-determinism" with its gestalt phenomena, but also, for example, the phenomena of cell division under processes of mitosis and meiosis.

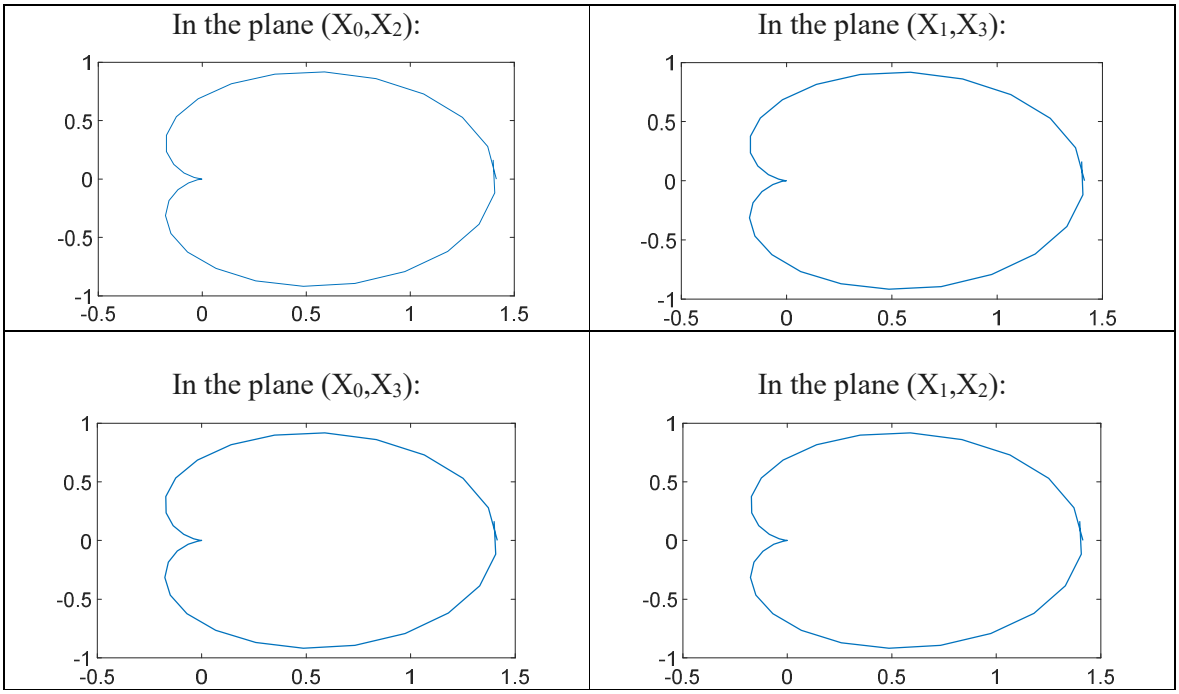

Fig. 2.2.2. Cardioids described parametrically by the projections of the daughter 4-dimensional vector function $\vec{R}_4(t)$ (2.2.2) in the planes (X_0,X_2), (X_0,X_3), (X_1,X_2) and (X_1,X_3) of the Cartesian system coordinates of 4-dimensional space.

If the named normvector has different signs for its coordinates of the same magnitude, for example, $[0.5^{0.5}, -0.5^{0.5}]$, then under the tensor-unitary transformation of the same parent vector,

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instead of the daughter vector function (2.2.2), another 4-dimensional daughter vector function $\vec{S}_4(t)$ (2.2.3) arises:

$$\vec{S}_4(t) = [x(t), 0] \otimes [0.5^{0.5}, -0.5^{0.5}] + [0, y(t)] \otimes [0.5^{0.5}, -0.5^{0.5}] = \\ = [x(t)*0.5^{0.5},\ -x(t)*0.5^{0.5},\ y(t)*0.5^{0.5},\ -y(t)*0.5^{0.5}] \qquad (2.2.3)$$

In the plane (X_0,X_2), from this vector function $\vec{S}_4(t)$ there is a vector projection $[x(t)*0.5^{0.5},\ y(t)*0.5^{0.5}]$.
In the plane (X_0,X_3), from the vector function $\vec{S}_4(t)$ there is a vector projection $[x(t)*0.5^{0.5},\ -y(t)*0.5^{0.5}]$.
In the plane (X_1,X_2), from the vector function $\vec{S}_4(t)$ there is a vector projection $[-x(t)*0.5^{0.5},\ y(t)*0.5^{0.5}]$.
In the plane (X_1,X_3), from the vector function $\vec{S}_4(t)$ there is a vector projection $[-x(t)*0.5^{0.5},\ -y(t)*0.5^{0.5}]$.

Fig. 2.2.3 shows the parametrically specified cardioids corresponding to these projections. It shows that this change in the sign of one of the coordinates of the normvector leads to the fact that the set of the four planes (X_0,X_2), (X_1,X_3), (X_0,X_3) and (X_1,X_2) of the 4-dimensional space splits into pairs of planes, in which there are mirrored cardioids (in contrast to identical cardioids in Fig. 2.2.2). This is one example of the fact that in algebraic biology, tensor-unitary transformations make it possible to model the appearance of mirror-symmetric structures in the described reproduction of images from the mother vector function.

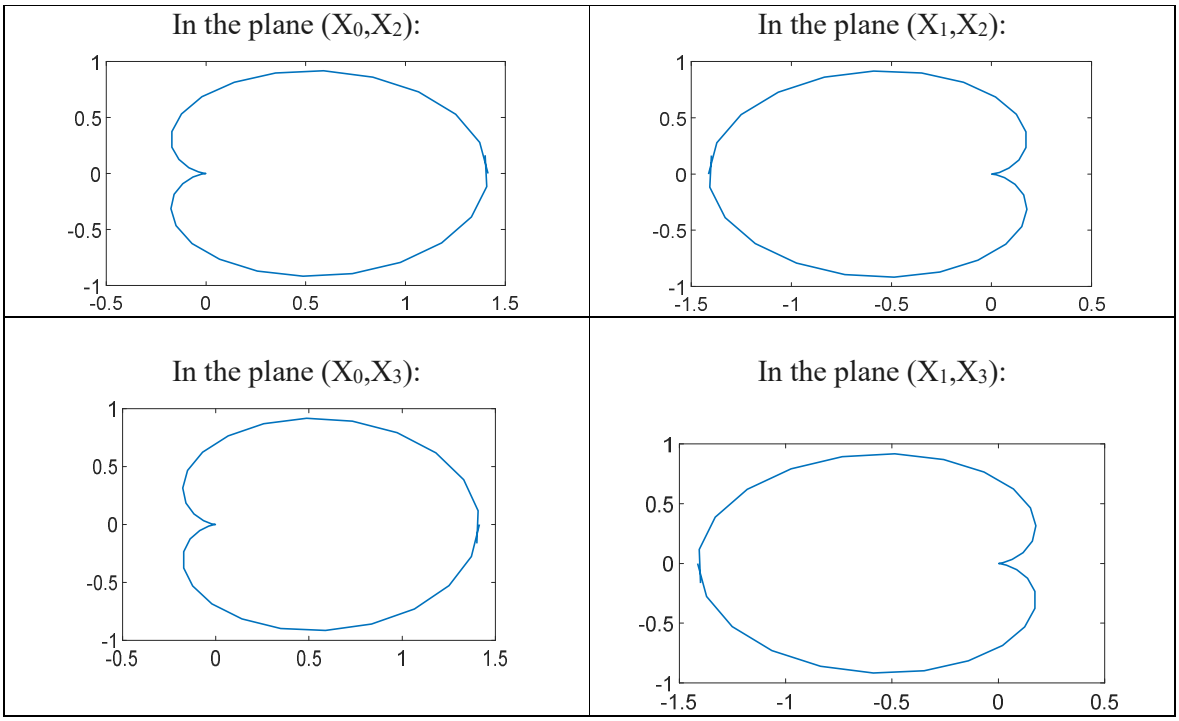

Fig. 2.2.3. Mirrored pairs of cardioids parametrically described by vector projections of the daughter 4-dimensional vector function $\vec{S}_4(t)$ (2.2.3) in the planes (X_0,X_2), (X_0,X_3), (X_1,X_2), and (X_1,X_3) of the Cartesian coordinate system of 4-dimensional space.

Let us now consider an example of the case when, under a tensor-unitary transformation, each coordinate of the mother 2-dimensional vector function [x(t), y(t)] is tensor multiplied by an

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individual 2-dimensional normvector with unequal coordinates. For example, let the first coordinate of this mother vector function be tensor multiplied by the normvector $[\alpha_0, \alpha_1]$, $\alpha_0 \neq \alpha_1$, $\alpha_0^2 + \alpha_1^2 = 1$, and the second coordinate by the normvector $[\beta_0, \beta_1]$, $\beta_0 \neq \beta_1$, $\beta_0^2 + \beta_1^2 = 1$. The tensor-unitary transformation of the mother vector function [x(t), y(t)] using such normvectors generates a 4-dimensional daughter vector function $\vec{W}_4(t)$ (2.2.4):

$$\vec{W}_4(t) = [x(t), 0] \otimes [\alpha_0, \alpha_1] + [0, y(t)] \otimes [\beta_0, \beta_1] = \\ = [x(t)\alpha_0, x(t)\alpha_1, y(t)\beta_0, y(t)\beta_1] \quad (2.2.4)$$

In a 4-dimensional space with a Cartesian coordinate system (X_0,X_1,X_2,X_3) in the planes (X_0,X_2), (X_1,X_3), (X_0,X_3), and (X_1,X_2) the following vector projections of this daughter vector function $\vec{W}_4$ exist:

$$[x(t)\alpha_0, y(t)\beta_0], \ [x(t)\alpha_1, y(t)\beta_1], \ [x(t)\alpha_0, y(t)\beta_1], \ [x(t)\alpha_1, y(t)\beta_0] \quad (2.2.5)$$

Since the mother vector [x(t), y(t)] parametrically defines some "mother" curve (for example, a cardioid), then each of these four vectors (2.2.5) also defines a certain parametrically defined curve in its plane. Each of such curves is a repetition of the mother curve, but with deformation due to scaling of the coordinate axes.

One can turn now to the phenomena of coordinated biocycles. The organism is a huge chorus of coordinated cyclic processes, whose number increases as it develops ontogenetically from the embryonic to the mature state with step-by-step receiving new and new degrees of freedom, which are coordinated with already existing. For example, in an adult human body, this number reaches enormous values, since it contains approximately 100 trillion cells participating in these sets of coordinated cycles. Moreover, all these cyclic processes occur through stochastic interactions between individual molecules in cells. According to the provisions of ancient chronomedicine, all our diseases are the result of violations in this coherence.

But how to simulate such development of huge sets of coordinated cyclic processes under conditions of stochasticity of individual parameters of an organism and a huge step-by-step increase in the dimension of its configuration space? Tensor-unitary transformations allow us to offer a model answer to this question since they generate stochastic-deterministic vector functions; in these vector functions, with a purely stochastic nature of the values of individual coordinates, sets of coordinated stable cycles on certain groupings of coordinates can be represented, i.e. on certain groupings of subspaces of the configuration space of a developing multi-parametric organism. As it is known, in mathematics, the tensor product of matrices is used to increase the dimension of a vector space. The genetic coding system, together with the family of DNA alphabets, is structured specifically for the tensor product of matrices, which links, for example, matrix representations of different DNA alphabets into a single tensor family of matrices [Petoukhov, He, 2010].

One can add that tensor-unitary transformation can be applied not only in the case of the algebra of real numbers but also in cases of different systems of multidimensional numbers: complex numbers, hyperbolic numbers, quaternions by Hamilton, split-quaternions by Cockle, etc.

In quantum mechanics, unitary transformations describe the evolution of closed quantum systems. The author believes that tensor-unitary transformations are useful for the development of quantum mechanics of non-closed quantum systems that develop with an increase in their multicomponent composition like biological bodies that develop in the course of onto- and phylogenesis.

Speaking of modeling a set of coordinated cyclic processes in an organism, one should also recall the connection between structured DNA alphabets and a family of matrices (2.2.6), which is described in [Petoukhov, 2021a]:

$$[1, 1; 1, 1]^{(n)} \otimes [1, 1, -1, -1; 1, 1, -1, -1; 1, -1, 1, -1; -1, 1, -1, 1] \quad (2.2.6)$$

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There are interesting actions of such matrices (2.2.6) to voluntary 2^n-dimensional vectors having arbitrary coordinates $a_i(t)$, which can be, for example, cyclic functions of time. In a general case, actions of (2^n*2^n)-matrices (2.2.6) to a voluntary 2^n-dimensional vector with coordinates unrelated to each other gives a new block-structured vector with interrelated coordinates combined in pairs by a binary-oppositional principle. If coordinates of an initial vector of a system are cyclic or wave functions, then the received new vector have block-structured sets of coordinates whose blocks are equal to each other up to the sign, and their cyclic changes are synchronized in time (that is, cyclic behavior of the considered system in its different configuration subspaces becomes strongly interrelated). Figuratively speaking, these matrix operators create order out of chaos (see details in [Petoukhov, 2021a]).

2.3. Gestalt vectors and projection operators based on genetic matrices

In accordance with Section 2.1, we call gestalt vector functions (or gestalt vectors) those daughter stochastic-deterministic vector functions that result from tensor-unitary transformations of mother vector functions. For example, the above daughter vector functions $\vec{\boldsymbol{D}}_1$ (2.1.1) and $\vec{\boldsymbol{D}}_2$ (2.1.11) are examples of gestalt vector functions (or briefly, gestalt vectors) obtained by tensor-unitary transformations from the mother vector function [x(t), y (t)]. This name is due to the fact that, as described above, the gestalt vectors model the features of biological gestalt phenomena, the content of which is determined by the relationship between the groupings of their elements, while the meanings of individual elements are not significant (by analogy with the gestalt phenomena of the perception of a musical melody, recognizable when performed in different frequency ranges, that is, precepted largely independent of the frequency value of each individual musical note).

As described in Section 2.1 using the examples of gestalt vector functions $\vec{\boldsymbol{D}}_1$ (2.1.1) and $\vec{\boldsymbol{D}}_2$ (2.1.11), part of the set of possible groupings of coordinates in gestalt vectors carries the memory of the past states of the developing multicomponent system (that is, knowledge of the coordinates of the parent vector and child gestalt vectors of previous generations), and the other part of the groupings of coordinates in gestalt vectors carries new information that appeared only at this stage in the development of the system and of its multidimensional configuration space. For algebraic selection of certain groupings of coordinates in genetic gestalt vectors, projection operators are needed. Are there any projection operators in the structures of the genetic coding system?

The answer to this question is positive. It turns out that there is an extensive set of tensorial interconnected projection operators based on matrix representations of structured DNA alphabets. This set of mutually related genetic matrices that meet the criteria of projection operators and are associated with universal projection rules for the stochastic organization of genomic DNAs is described in [Petoukhov, 2021a, Figs. 9.1-9.7].

In particular, there in Fig. 9.1 the (4*4)-matrices of oblique projection operators are described: $\mathbf{P_0}$ = [1 0 1 0; 1 0 1 0; 0 0 0 0], $\mathbf{P_1}$ = [0 0 0 0; 0 0 0 0; 0 1 0 1; 0 1 0 1], $\mathbf{P_2}$ = [0 1 0 1; 0 1 0 1; 0 0 0 0; 0 0 0 0]; $\mathbf{P_3}$ = [0 0 0 0; 0 0 0 0; 1 0 1 0; 1 0 1 0]. What are the results of the action of these genetic projection operators on the gestalt vectors of the corresponding dimension? Let us give an example of their action on the 4-dimensional gestalt vector $\vec{\boldsymbol{D}}_1$ = [x(t)α_0, x(t)α_1, y(t)β_0, y(t)β_1], described above, shown in expression (2.1.1):

$$\vec{\boldsymbol{D}}_1 * \mathbf{P_0} = [x(t)\alpha_0(t) + y(t)\beta_0(t), \quad 0, \quad x(t)\alpha_0(t) + y(t)\beta_0(t), \quad 0] \qquad (2.3.1)$$

The new vector function (2.3.1) formed as a result of this action has an interesting property: its non-zero first and third coordinates are identical, and therefore synchronized in time (if the

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parameter t denotes time). This means that the resulting vector function consists of two synchronized parts, regardless of what variables or constant values $\alpha_0(t)$ and $\beta_0(t)$ are used in the coordinates of the normvector of the tensor-unitary transformation. In many respects, similar results are obtained when the same vector function $\vec{D}_1$ is subjected to skew genetic projections that give the expressions $\vec{D}_1*P_1$, $\vec{D}_1*P_2$, $\vec{D}_1*P_3$. This synchronization of parts of each vector function thus formed is useful for modeling a number of developing biosystems containing synchronized subsystems.

For the case of 8-dimensional Gestalt vectors, for example, $\vec{D}_2$ (2.1.11), there is a whole family of genetic (8*8)-matrices of oblique projection operators shown in Figures 9.3-9.7 in [Petoukhov, 2021a]. An example from this family is the matrix P_8 = [1 0 1 0 1 0 1 0; 1 0 1 0 1 0 1 0; 0 0 0 0 0 0 0 0; 0 0 0 0 0 0 0 0; 0 0 0 0 0 0 0 0; 0 0 0 0 0 0 0 0; 0 0 0 0 0 0 0 0; 0 0 0 0 0 0 0 0]. Its action on the 8-dimensional vector $\vec{D}_2$ = [$x\alpha_0c_0$, $x\alpha_0c_1$, $x\alpha_1d_0$, $x\alpha_1d_1$, $y\beta_0p_0$, $y\beta_0p_1$, $y\beta_1r_0$, $y\beta_1r_1$] (2.1.11) generates the 8-dimensional vector function (2.3.2):

$$\vec{D}_2*P_8 = [x(t)\alpha_0c_0+x(t)\alpha_0c_1,\ 0,\ x(t)\alpha_0c_0+x(t)\alpha_0c_1,\ 0,\ x(t)\alpha_0c_0+x(t)\alpha_0c_1,\ 0,\ x(t)\alpha_0c_0+x(t)\alpha_0c_1,\ 0] \quad (2.3.2)$$

In this vector function, the non-zero first, third, fifth, and seventh coordinates are identical and synchronized in time (if the parameter t denotes time). All other coordinates are equal to zero. This means that the generated vector function consists of four synchronized parts, regardless of what variables or constant values are used in the coordinates of the normvectors of the tensor-unitary transformation. In many respects, similar results are obtained when the same vector function $\vec{D}_2$ is affected by other genetic oblique projectors presented in [Petoukhov, 2021a, Figs. 9.3-9.7].

Passing to the cases of Gestalt vectors of even higher dimension and acting on them with the corresponding genetic matrices of oblique projections, we obtain vector functions with an increasing number of non-zero identical coordinates (all other coordinates are equal to zero).

In connection with the presented doctrine of evolution based on bio-antenna arrays, it should be noted that the theory of antenna arrays in technology is associated with projection operators. Correspondingly, for the search words "projection operators and antenna arrays", the browser gives many publications. Therefore, the presence of projection operators in the above-mentioned genetic matrices, as well as the existence of universal projection rules in the stochastic organization of genomic DNAs, can be considered as additional evidences in favor of the adequacy of this doctrine.

In addition, we note that the concept of tensor-unitary transformations was introduced by the author as a result of his development of the doctrine of energy-information evolution based on bio-antenna arrays [Petoukhov, 2022a,b]. In this doctrine, the ability of molecules to function as antennas plays an important role. To this doctrine, here one can additionally note that the ability of molecules to work as antennas has long been known in chemistry using the example of dendrimer molecules, articles about which are often referred them to as antennas [Bar-Haim, Klafter, 1998].

3. Regarding biological fractals and vegetative propagation

In the previous section, it was noted that each genomic DNA is a fractal-like system of many interrelated quantum information mandalas, where each of the cellules at its different tiers can be represented by its individual stochastic fractal-like mandala.

Thus, these genomic mandalas are fractal-like in nature, similar to the long-known fractal-like structures of morphogenesis: fern, spruce with its multi-tiered needle structures, cabbage *Brassica oleracea*, etc. (Fig. 3.1) Each next part of such a structure is potentially capable to produce again a similar fractal-like structure in the developing multi-parametric body whose

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number of freedom degrees and a dimensionality of the configuration space are increased correspondingly more and more. In our opinion, this fundamental possibility of separate parts of a growing biological body generate new parts having analogical structures is one of the most important secrets of living Nature.

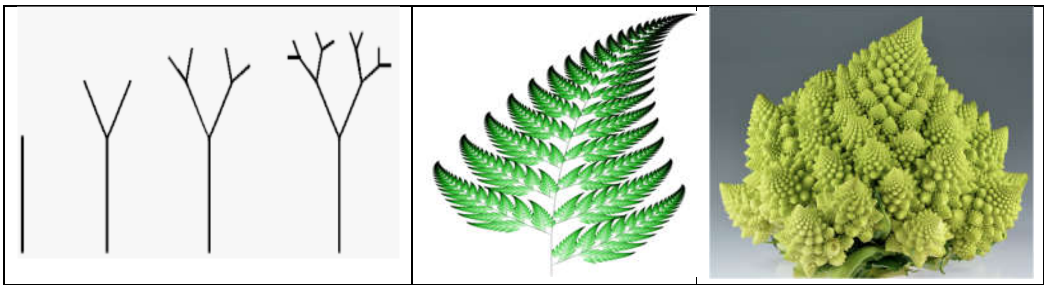

Fig. 3.1. Examples of biological fractals. At the left: a step-by-step development of a dichotomic fractal-like structure, when each new part of the structure with dichotomous branching generates a new dichotomous branching at the next step in the development of the system. At the middle: a fractal model of fern (from https://en.wikipedia.org/wiki/Barnsley_fern; the image is available to share and distribute under the Creative Commons Attribution-Share Alike 4.0 International license). At the right: cabbage *Brassica oleracea* (from https://en.wikipedia.org/wiki/Romanesco_broccoli; the image is available to share and distribute under the Creative Commons Attribution-Share Alike 4.0 International license).

The features of the genomic mandalas testify about fractal-like organization of genomic DNAs. They testify that already at the deepest level of biological organization - at the level of genomic DNAs associated with quantum informatics - fractal principles work, which totally permeate the overlying inherited biostructures and which are also connected to stochastic mechanisms of Gestalt biology.

Mandelbrot introduced the following definition of fractals: "*A fractal is a rough or fragmented geometric shape that can be split into parts, each of which is (at least approximately) a reduced-size copy of the whole*" [Mandelbrot, 1983]. In accordance with this definition, literary sources usually describe a creation of fractals by recursion algorithms inside a 2-dimensional space or inside other spaces of fixed dimensions. Well-known examples of such fractals are 2-dimensional Sierpiński carpet (https://en.wikipedia.org/wiki/Sierpi%C5%84ski_carpet) and 3-dimensional Menger sponge (https://en.wikipedia.org/wiki/Menger_sponge). If one considers biological bodies (for example, trees or seashells) as ready structures in 3-dimensional physical space, their configurations can be frequently interpreted as fractal-like ones in accordance with Mandelbrot's definition. But if you consider a step-by-step ontogenetic development of multi-parametric living bodies, whose number of parameters and degrees of freedom become more and more and whose configuration spaces are correspondingly grown in dimensionalities, such definition is not applicable since you have another situation: a dimensionality of a space is not fixed but is tensor growing. A theory of such biological fractals, whose similar fragments are distributed in different subspaces of a tensor growing configuration space, should be constructed in the future.

It seems that for studying of stochastic organization of genomic DNAs, stochastic fractals of Schramm-Löwner evolution can be useful [Lawler, Schramm, Werner, 2004]. They are connected with conformally invariant fractal curves that arise in critical two-dimensional models of statistical mechanics, such as the Ising model and percolation.

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4. Stochastic determinism as an antipode to deterministic chaos

Our world is full of random events. The life and development of genetically inherited bio-bodies are inextricably linked with random interactions of molecules, against which the inherited deterministic macrostructures with the parental traits are realized. So, hidden determinism and the corresponding laws of stochastic determinism exist behind these accidents. The important role of probabilities in Nature is reflected in quantum mechanics based on the concept of probabilities. At the same time, as the Nobel laureate in physics R. Feynman stated, that nobody really understands quantum mechanics. The studies of the biological dualism “stochastics-determinism” and the universal rules of the stochastic organization of genomic DNAs, presented in this paper, draw attention to the need to develop the theory of “stochastic determinism” (or “chaotic determinism”) as an antipode to the well-known theory of “deterministic chaos”. In the author's opinion, in the future theory of stochastic determinism, a prominent place will be occupied by the tensor-unitary transformations described above, which model the named dualism, biological gestalt phenomena, and tensor reproduction of biostructures. Let's look at the differences between these two theories.

The theory of deterministic chaos (or dynamic chaos) has been developed by the works of a large number of mathematicians and physicists. It has been the subject of a large number of publications (see, for example, [Bishop, 2017; Cattani, 2017; Skiadas, 2016; Weinberger, 2019]. Deterministic chaos is a phenomenon and a part in the theory of dynamical systems, in which the behavior of a nonlinear system looks random, despite the fact that it is determined by deterministic laws. The reason of this phenomenon is instability (sensitivity) with respect to the initial conditions and parameters: a small change in the initial condition over time leads to arbitrarily large changes in the dynamics of the system. A well-known example of a system of deterministic chaos is Sinai billiards [https://mathworld.wolfram.com/SinaiBilliards.html].

What is the difference between stochastic determinism, represented in the phenomena of biological dualism "stochastics-determinism", and deterministic chaos? Fig. 4.1 shows the main differences.

№	Deterministic chaos	Stochastic determinism
1	The birth of the random from the non-random is observed. A completely deterministic system generates unpredictable states that have the properties of a random process.	The birth of the deterministic (non-random) from the random is observed. A system characterized by random interactions of molecules at the cellular level gives rise to deterministic biological forms.
2	A small change in the initial condition leads to arbitrarily large changes in the dynamics of the system over time (it is instability or sensitivity of the system with respect to the initial conditions).	Random interactions among molecules at the beginning of the biosystem development have little effect on the final deterministic result of its development (stability or insensitivity with respect to initial conditions).
3	In systems of deterministic chaos, it is customary to consider multi-parameter systems with a fixed dimension of their configuration spaces (for example, Sinai billiards).	In the stochastic determinism of biological systems, systems are considered with tensor development of the dimension of their configuration spaces (for example, when sets of interconnected billiards of Sinai are born tensorically in the course of development).

Fig. 4.1. The main differences between stochastic determinism and deterministic chaos.

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One of the distinguishing features of the living is the presence of forms of constant movement in it. No wonder they say that "*life is movement*". Correspondingly, a living cell can always be distinguished from a dead one by this feature: in almost all biological tissues, cells move continuously, albeit slowly, or at least change shape. But it is not at all a thermal, Brownian motion. On the contrary, "*Brownian motion in a eukaryotic cell is a sign of its death*" [Fulton, 1984, p. 7].

Taking into account all having materials about biological dualism "stochastics-determinism", the author puts forward the following hypothesis: in living bodies, a special type of stochastic (or stochastic-deterministic) motions exist, the study of which is important for understanding biological stochastic-deteministic phenomena. It is probably that this kind of motions has its own princilpes of minimization and conservation laws. The algebraic toolkit described above can be useful in these future studies and in developing the theory of stochastic determinism as well.

Some concluding remarks

The stochastic organization of genomic DNAs must give pieces of evidence about special interconnections between formalisms of antenna arrays and formalisms of quantum informatics described above. Correspondingly the doctrine of evolution on bio-antenna arrays is connected with formalisms of quantum informatics and quantum mechanics. The described tensor-unitary transformations are useful for modeling dualism “stochastics-determinism”. They can be also useful for creation of quantum mechanics of tensorial development of multiparametric systems like biosystems and for creation of artificial intelligence of genomorphic type based on families of enlarging sets of computer memory cells.

The theory of stochastic determinism as an antipode to deterministic chaos should be developed. Vibrational synchronization and vibrational mechanics can be one of the participants in ensuring the biological dualism "stochastics-determinism". The theory of vibrational mechanics itself should be further developed to cover vibrational phenomena in tensor developing multiparameter systems.

The described algebraic tools and results are useful for development of our knowledge about “genetic intelligence”. By genetic intelligence, we understand that part of the intellectual potentialities of living organisms, which allows, on the basis of genetic information in DNA and RNA molecules, to build, for example, from one fertilized cell an organism, having trillions of cells, where parental characteristics are reproduced by a multichannel noise-resistant manner, despite strong noises and constantly changing conditions of nutrition and external influences. This building is accompanied by a systematic increase, in the course of ontogenesis, of the number of body parameters and a corresponding increase in the dimension of its configuration space of states. In mathematics, the tensor product of matrices is used to increase the dimension of a vector space. The genetic coding system, together with the family of DNA alphabets, is structured in accordance with the tensor product of matrices, which links, for example, matrix representations of different DNA alphabets into a single tensor family of matrices [Petoukhov, 2021a].

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