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Review Article

The system-resonance approach in modeling genetic structures

Sergey V. Petoukhov

Institute of Machines Studies, Russian Academy of Sciences, 101990 Moscow, Russia

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ABSTRACT

The founder of the theory of resonance in structural chemistry Linus Pauling established the importance of resonance patterns in organization of living systems. Any living organism is a great chorus of coordinated oscillatory processes. From the formal point of view, biological organism is an oscillatory system with a great number of degrees of freedom. Such systems are studied in the theory of oscillations using matrix mathematics of their resonance characteristics. This study is devoted to a new approach for modeling genetically inherited structures and processes in living organisms using mathematical tools of the theory of resonances. This approach reveals hidden relationships in a number of genetic phenomena and gives rise to a new class of bio-mathematical models, which contribute to a convergence of biology with physics and informatics. In addition some relationships of molecular-genetic ensembles with mathematics of noise-immunity coding of information in modern communications technology are shown. Perspectives of applications of the phenomena of vibrational mechanics for modeling in biology are discussed.

Contents

1. Introduction

The idea about the structural pattern of the observed world, including living matter, on the basis of vibrations arises to Ancient China and Ancient India. Among many works about resonances in different systems, the theory of resonance of Linus Pauling takes an important place. His book (Pauling, 1940) about this theory in structural chemistry is the most quoted among scientific books of the XX century. Its first Chapter is titled «Resonance and chemical bond». The theory was developed to explain the formation of hybrid bonds in molecules. The actual molecule, as Pauling proposed, is a sort of hybrid, a structure that resonates between the two alternative extremes; and whenever there is a resonance between the two forms, the structure is stabilized. His theory uses the fundamental principle of a minimal energy because – in resonant combining of parts into a single unit – each of members of the ensemble requires less energy for performing own work than when working

E-mail address: spetoukhov@gmail.com

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individually. Pauling claimed that living organisms are chemical in nature, and resonances in their molecules should be very essential for biological phenomena.

This study continues the approach developed by Pauling and his followers in applications to some single molecules, about an important role of resonances in living organisms. The new in the paper is a detection of crossing the world of genetic phenomena with the world of classical mathematics of resonance spectra of vibration systems with many degrees of freedom. On this basis, a unified mathematical approach is developed to the analysis of a number of systems of genetic coding and genetic phenomena. This approach reveals hidden relationships and regularities in these systems and leads to a new class of bio-mathematical models using matrices of resonances. These results support the feasibility of understanding the genetic system and genetic phenomena on the basis of mathematics of special systems of resonances. Energetic principles of biological organization are also under attention in this approach because frequency characteristics of vibro-systems are associated with energetics.

The proposed approach is correlated with the following situation in modern science. In the past century, science has discovered that the molecular basis of genetic coding (DNA structures, etc.) is identical in all species of organisms. A new understanding of life appeared: «*Life is a partnership between genes and mathematics*» (Stewart, 1999). All physiological systems of the body should be structurally coordinated with the genetic code for their reproductions in descendants to avoid extinction. It is obvious that unifying mathematical approaches are needed for the simulation of the genetic unity of different structures of organism. Every organism is endowed with the inherited ability to tune into resonances and to use resonances as carriers of information. Our speech and singing are examples of this because they use resonances of our voice apparatus, which is the oscillatory system with many degrees of freedom. According to the classics of structural linguistics (Roman Jakobson and others), our language did not come out of nowhere, but it is a superstructure over the oldest language – the genetic language (Jakobson, 1987, 1999; Petoukhov and He, 2010). This is one of the reasons to investigate the genetic system, including genetic alphabets, from the standpoint of mentioned mathematics of resonances.

The genetic coding has noise-immunity properties. According to Mendel's law of independent assortment, information from microworld of genetic molecules dictates macrostructures of living organisms, despite of strong noise and interference, through many independent channels (for instance, colors of hair, eye and skin are inherited independently from each other). This determinism is carried out by means of unknown algorithms of multi-channel noise-immunity coding. Consequently, every organism is an algorithmic machine of multi-channel noise-immunity coding.

To study this genetic machine it is advisable to use the theory of noise-immunity coding, which is based on the mathematics of matrices and which is used in engineering to solve similar problems. An example of this is the noise-immune transmission of high-quality photographs of the surface of Mars to Earth – on the base of mathematics of matrices – in conditions of strong distortions of carrier electromagnetic signals passing through millions of kilometers of interference. This is one of reasons for attention to the matrix analysis of structures of the genetic code, including an analysis of the possibility of using genetic systems of resonances for the transmission of hereditary information. The presented concept of resonance genetics brings together biology with physics and informatics since systems of resonances allow providing a reception and transmission of information (our inherited abilities of acoustic communication through speech and singing are examples of this). This study reveals that the molecular genetic ensembles are structurally related to known formalisms of the mathematical theory of noise-immunity coding of information (functions of Rademacher and Walsh, Hadamard matrices, etc.).

This study pays its main attention to matrices of vibrosystems since we analyze organism as a set of heritable systems of resonances. Vibration mechanics has many applications in engineering due to its phenomena of a resonant synchronization of oscillatory processes, vibratory separation and structuring of multiphase systems, vibro-transportation of substances, vibro-transmission of energy within systems and so on (Blekhman, 2000; Ganiev et al., 2015). Our results give a basis for wider use of these phenomena in modeling biological phenomena. They can also pull together genetics and quantum mechanics, which is based on taking into account frequencies and resonant characteristics of objects of the quantum-mechanical world.

2. Background

The background of this study includes well-known genetic and physiological phenomena, such as Mendel's laws, molecular structures of the genetic code and psychophysical Weber–Fechner law.

The main research method to study the mentioned phenomena is their mathematical modeling by means of classical mathematics of theory of oscillations, allowing analyzing the resonant characteristics of oscillatory systems with many degrees of freedom. Our unified approach on the basis of matrix representations of resonances allows to reveal hidden relationships in different genetic and inherited physiological phenomena, and to discover new possibilities of convergence of biology with physics and informatics.

2.1. Oscillatory processes and matrix representations of resonances

Any living organism is a great chorus of coordinated oscillatory processes (mechanical, electrical, piezoelectrical, biochemical, etc.), which are connected with their genetic inheritance along chains of generations. In the ontogenetic development of an organism from embryo to adult, the number of oscillatory processes in the chorus is greatly increased while maintaining their mutual consistency not only at each stage of development, but also at different stages. Since ancient times, chrono-medicine believes that all diseases are the result of disturbances in the ordered set of oscillatory processes.

From a formal point of view, a living organism is an oscillatory system with a great number of degrees of freedom. Theory of oscillations uses mathematics of matrices to study resonant characteristics of oscillatory systems with many degrees of freedom (see, e.g., Gladwell, 2004). We use matrices to study genetic phenomena.

Matrices possess a wonderful property to express resonances, which sometimes is called as their main quality (Bellman, 1960; Balonin, 2000, p. 21, 26). Physical resonance phenomenon is familiar to everyone. The expression $y = A^*S$ models the transmission of a signal S via an acoustic system A, represented by a relevant matrix A. If an input signal is a resonant tone, then the output signal will repeat it with a precision up to a scale factor $y = \lambda^*S$ by analogy with a situation when a musical string sounds in unison with the neighboring vibrating string. In the case of a matrix A, its number of resonant tones S_i corresponds to its size. They are called its eigenvectors, and the scale factors λ_i with them are called its eigenvalues or, briefly, spectrum A. Frequencies $\omega_i = \lambda_i^{0.5}$ (Gladwell, 2004, p. 61) are defined as natural frequencies of the system, and the corresponding eigenvectors are defined as its own forms of oscillations (or simply, natural oscillations).

These free undamped oscillations occur in the system in the absence of the friction forces in it and in the absence of external excitation forces. Behavior of the system in conditions of free

$$A = \begin{vmatrix} 4, & 0.6 \\ 0.6 & 2 \end{vmatrix}$$

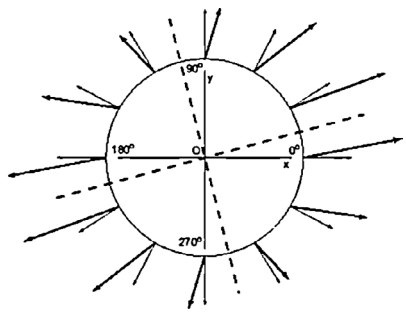


Fig. 1. Illustration of actions of the matrix A by vectors $[x, y]$ (from Zharov (2002)).

oscillations determines by its behavior in many other conditions. In this context, one of the main tasks of the theory of oscillations is a determination of natural frequencies (mathematically, eigenvalues of operators) and the natural forms of oscillations of bodies. To find all the eigenvalues λ_i (i.e., spectrum system A) and eigenvectors of the matrix A, which are defined by the matrix equation $A^*s = \lambda^*s$, the "characteristic equation" of the matrix A is analyzed: $\det(A - \lambda E) = 0$, where E – the identity matrix. The characteristic equation together with its eigenvalues and eigenvectors is fundamental in the theory of mechanical, electrical and other oscillations at macroscopic or microscopic levels. The theory of oscillations is described in many books with some terminological differences in them sometimes. In preparing this article, the author relied mainly on a detailed book (Gladwell, 2004), which additionally contained many examples of matrix analysis of oscillatory systems.

Let us remind the essence of the eigenvalues and eigenvectors by means of the matrix A on Fig. 1, which acts on vectors $[x, y]$. In this case almost any vector is transformed into a new vector $[x, y]^*A$ with changing its direction. The exceptions are those vectors $[x, y]$, which belong to two orthogonal dotted lines and are called "eigenvectors" of the matrix A; they conserve their direction under action of the matrix A, but their lengths are scaled with factors λ_i, which are called "eigenvalues" of the matrix A (each eigenvalue corresponds to its own direction of eigenvectors).

Not all square matrices represent vibrational systems. Matrices, which are relevant to the various problems of the theory of oscillations, are usually symmetrical real matrices (Gladwell, 2004, p. 178). Such matrices have real eigenvalues and their eigenvectors are orthogonal.

This paper considers the spectra of $(2^n{*}2^n)$ matrices, which are generated in the result of tensor products of initial (2*2) matrices and which are used for modeling genetic phenomena and structures. The tensor product of matrices, denoted by $\otimes$, is widely applied in mathematics, physics, informatics, control theory, etc. It is used for algorithmic generation of higher dimensional spaces on the basis of spaces with smaller dimensions (reminding a growth of degrees of freedom in the ensemble of cells of growing organism in the result of their division). By definition, the tensor product of two square matrices V and W of the orders m and n respectively is the matrix $Q = V \otimes W = ||v_{ij}{*}W||$ with the order $m{*}n$ (Bellman, 1960). The tensor product has the property of inheritance of mosaic structure of the original matrix under its tensor exponentiation. This property connects the operation with fractals (Gazale, 1999, Chapter X). Fig. 2 shows an example of the formation of fractal patterns, the type of which depends on the mosaic of the original matrix.

The tensor product of matrices is also endowed with the property of "inheritance" of their eigenvalues: if the original matrix V and W have the eigenvalues λ_i and μ_j respectively, then in their tensor product $Q = V \otimes W$ all eigenvalues are equal to $\lambda_i{*}\mu_j$ (figuratively speaking, λ_i and μ_j are inherited in this tensor way).

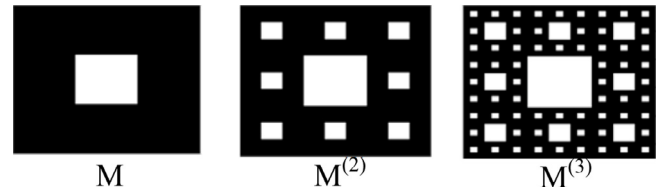


Fig. 2. The example of a fractal carpet of Sierpinski produced in the tensor family of matrices $M^{(n)} = [1,1,1;\ 1,0,1;\ 1,1,1]^{(n)}$, where (n) means tensor power. Black and white elements of mosaics correspond to elements 1 and 0.

		maternal spectrum	
		A	a
paternal spectrum	A	AA	Aa
	a	aA	aa

		maternal spectrum			
		AB	Ab	aB	ab
pat. sp.	AB	AABB	AABb	AaBB	AaBb
	Ab	AABb	AAbb	AaBb	Aabb
	aB	AaBB	AaBb	aaBB	aaBb
	ab	AaBb	Aabb	aaBb	aabb

		Maternal gametes	
		A	A
paternal gametes	A	AA	Aa
	a	aA	Aa

		maternal gametes			
		AB	Ab	aB	ab
pat. gam.	AB	AABB	AABb	AaBB	AaBb
	Ab	AABb	AAbb	AaBb	Aabb
	aB	AaBB	AaBb	aaBB	aaBb
	ab	AaBb	Aabb	aaBb	aabb

Fig. 3. Comparison of Punnett squares and tables of inheritance of eigenvalues of matrices under the tensor product. Top row: examples of tables of inheritance of eigenvalues under the tensor product in cases of (2*2)-matrices (left) and (4*4)-matrices (cases of monohybrid and dihybrid hybridizations). Bottom row: examples of Punnett squares for monohybrid and dihybrid crosses of organisms under the laws of Mendel. Abbreviations «pat. sp.» and «pat. gam.» mean «paternal spectrum» and «paternal gametes».

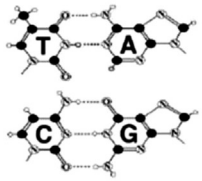
3. The analogy between Punnett squares and tables of the tensor inheritance of eigenvalues of matrices

Features of the tensor inheritance of eigenvalues of the original matrices (or "parental" matrices) in the result of their tensor product can be conveniently represented in the form of "tables of inheritance". The top row of Fig. 3 shows the example of two simplest cases, conventionally referred to as monohybrid and dihybrid cases of a tensor hybridization of vibrosystems. In the first case, the tensor product of two (2*2)-matrices V and W, which have the same set of eigenvalues A and a, gives the (4*4)-matrix $Q = V \otimes W$ with its 4 eigenvalues A*A, A*a, A*a, a*a. In the second case, the tensor product of (4*4)-matrices, having the same set of eigenvalues AB, Ab, aB, ab, gives (16*16)-matrix with 16 eigenvalues, represented in the tabular form.

One can see that the internal content of the table of inheritance for the dihybrid case (Fig. 3 top) is equal to [AA, Aa; Aa, aa]⊗[BB, Bb; Bb, bb]; in other words, the spectrum of the dihybrid vibrosystem is equal to the tensor product of spectra of two monohybrid vibrosystems. Similar tables of inheritance for n-hybrid cases ($n = 3, 4, \ldots$) of the tensor hybridization of vibrosystems can be constructed by analogy.

The author notes that these tables of the tensor inheritance for spectra of vibrosystems are identical to Punnett squares for poly-hybrid crosses of organisms (Fig. 3). In genetics from 1906 year, Punnett squares represent Mendel's laws of inheritance of traits under poly-hybrid crosses. Only in Punnett squares, instead of eigenvalues of matrices and their combinations, exist similar combinations of dominant and recessive alleles of genes from parent reproductive cells – gametes.

This formal analogy – between Punnett squares of combinations of alleles and tables of tensor inheritance of eigenvalues of matrices of vibrosystems – generates the following idea:



TRAITS	G	A	T	C
1) pyrimidine (C,T), purine (A,G)	0_1	0_1	1_1	1_1
2) amino (A,C), keto (G,T)	0_2	1_2	0_2	1_2
3) complementarity (C,G) and (A,T) with 3 or 2 hydrogen bonds	1_3	0_3	0_3	1_3

Fig. 4. Three binary sub-alphabets according to three kinds of binary-opposite traits in a set of nitrogenous bases G, A, T, C. Left: the molecular structure of these bases of DNA. Right: the partition of the four-letter alphabet of DNA on three binary sub-alphabets in accordance with three binary-oppositional traits. Inside each binary sub-alphabet, equivalent letters are marked by the symbol 1 or 0.

- alleles of genes and their combinations can be interpreted as eigenvalues of (2^n*2^n)-matrices from tensor families of matrices of oscillatory systems. For genetic systems, this model approach focuses an attention on the possible importance of a particular class of mutually related resonances from tensor families of matrices, which play the role of biological "matrix archetypes."

In this modeling approach, each allele of a gene, which has a polyatomic structure, is characterized by a single number: an eigenvalue of a matrix of an oscillatory system with a corresponding number of degrees of freedom. It resembles the phenomenon, known in vibration mechanics since the time of Christiaan Huygens, of self-synchronization of a plurality of pendulums mounted on a common movable platform: the self-synchronization provides that all the pendulums begin to oscillate with a single common frequency, although initially each of them could have its own natural frequency of oscillation.

This approach is also associated with dyadic groups of binary numbers and matrices of dyadic shifts, known in the theory of digital signal processing (Ahmed and Rao, 1975; Harmuth, 1970, 1977): taking into account binary-oppositional attributes of homozygosity and heterozygosity for alleles of genes, one can represent combinations of individual alleles by means of symbols "0" and "1". This generates numerical representations of Punnett squares as matrices of dyadic shifts (Petoukhov, 2011, 2014). But it is known that, if a system shows its connection with dyadic shifts, it indicates a connection of its structural organization (in our case, it is the genetic system) with modulo-2 addition, which is the logical basis of modern computers.

4. Genetic alphabets and tensor systems of resonances

The author puts forward the hypothesis that genetic alphabets are based on systems of resonances, or, more precisely, on systems of eigenvalues and eigenvectors of tensor families of [2^n*2^n]-matrices. From the standpoint of this hypothesis, we represent one of variants of a relevant representation of genetic alphabets, which testifies in favor of this hypothesis.

The molecules of heredity (DNA) contain sequences of four nitrogenous bases in the role of four "letters" of the basic genetic alphabet of DNA: adenine A, cytosine C, guanine G, thymine T. The genetic code encodes sequences of 20 amino acids in proteins using 64 triplets representing all possible combinations of these four types of the letters: CAG, GCT, ATC, ... The system of genetic coding is based on sets (alphabets) of n-plets: the set of 4 monoplets (nitrogenous bases A, C, G, T); the set of 4^2 = 16 doublets (AA, AC, . . .); the set of 4^3 = 64 triplets. (The same numbers 4, 16, 64 are realized in Punnett squares and tables of inheritance of eigenvalues).

Let us assume that four nitrogenous bases of DNA are eigenvalues of some matrices and so they can be located on diagonals of the corresponding diagonal matrices. In this case the following known facts are useful: (1) any square matrix with distinct eigenvalues λ_i is transformed into its diagonal form (due to selection of the basis), in which all its eigenvalues lie on its diagonal, and all other entries are equal to zero; (2) the tensor product of diagonal matrices always generates a diagonal matrix.

Science does not know why the basic alphabet of DNA consists of the four polyatomic letters A, C, G, T of very simple structure. But it is known that the set of these four structures is not quite heterogeneous, but it carries on itself the symmetric system of binary-oppositional traits. The system of such traits divides the genetic four-letter alphabet into various three pairs of letters, which are equivalent from a viewpoint of one of these traits or its absence (Fig. 4): (1) C = T & A = G (according to the binary-opposite traits: "pyrimidine" or "non-pyrimidine", that is purine); (2) A = C & G = T (according to the traits: amino or keto); (3) C = G & A = T (according to the traits: three or two hydrogen bonds are materialized in these complementary pairs) (Gumbel et al., 2015; Petoukhov, 2008; Stambuk, 1999).

To study phenomenological properties of the alphabet of 64 triplets, one can continue this natural scheme of division into sub-alphabets on the base of the principle of paired letters. Imagine, for example, the amino-pair A and C and the keto-pair G and T in the role of diagonal members of two diagonal (2*2)-matrices, i.e. in the role of their eigenvalues (Fig. 5). Tensor products of these two diagonal matrices $[C, A]_d$ and $[T, G]_d$ in all possible combinations in three represent the entire alphabet of 64 triplets in the ordered form of diagonals of 8 diagonal (8*8)-matrices (the octet of diagonals in Fig. 5 below; the index "d" after the brackets we use for short notation of diagonal matrices). Here each triplet is one of eigenvalues of one of eight (8*8)-matrices and corresponds to its own eigenvector.

It is known that code values of triplets are dependent on the order of letters in them. For example, triplets AAC, ACA and CAA, which are identical in their letter composition and which belong to the first of octets in Fig. 5, encode different amino acids. In our approach, each of triplets has its own personality, because it plays the role of one of eigenvalues of one of the above (8*8)-matrices and it belongs to its individual eigenvector, which is one of 8 basic vectors of an appropriate 8-dimensional space. It means that in this model approach three triplets AAC, ACA, CAA are essentially different each from other because each of them is connected with its eigenvector, i.e. with its own form of oscillations inside an oscillatory system with 8 degrees of freedom.

Each of traits of nitrogenous bases A, C, G, T in Fig. 4 can be interpreted as connected with its own resonance characteristics. For example, it is obvious that purines may have resonance characteristics that differ from the resonance characteristics of pyrimidines due to differences in the structure of the purine and pyrimidine molecules. In this light, each of mentioned pairs of binary-oppositional traits can be treated as a pair of binary-oppositional kinds of resonance characteristics. In this case, numeric symbols 0 and 1 in each of binary sub-alphabets in Fig. 4 are representations of binary-oppositional kinds of resonance characteristics. This idea connects physical concepts of resonances of vibrosystems with abstract binary-numeric systems of computer technology and mathematics, including dyadic groups of binary numbers. For comparison, we recall that in computer technology binary elements 0 and 1 are physically realized through using two types of

$$\begin{vmatrix} C, 0 \\ 0, A \end{vmatrix} = [C, A]_d\,; \quad \begin{vmatrix} T, 0 \\ 0, G \end{vmatrix} = [T, G]_d$$

$$[C,A]_d \otimes [C,A]_d \otimes [C,A]_d = [CCC, CCA, CAC, CAA, ACC, ACA, AAC, AAA]_d$$
$$[C,A]_d \otimes [C,A]_d \otimes [T,G]_d = [CCT, CCG, CAT, CAG, ACT, ACG, AAT, AAG]_d$$
$$[C,A]_d \otimes [T,G]_d \otimes [C,A]_d = [CTC, CTA, CGC, CGA, ATC, ATA, AGC, AGA]_d$$
$$[C,A]_d \otimes [T,G]_d \otimes [T,G]_d = [CTT, CTG, CGT, CGG, ATT, ATG, AGT, AGG]_d$$
$$[T,G]_d \otimes [C,A]_d \otimes [C,A]_d = [TCC, TCA, TAC, TAA, GCC, GCA, GAC, GAA]_d$$
$$[T,G]_d \otimes [C,A]_d \otimes [T,G]_d = [TCT, TCG, TAT, TAG, GCT, GCG, GAT, GAG]_d$$
$$[T,G]_d \otimes [T,G]_d \otimes [C,A]_d = [TTC, TTA, TGC, TGA, GTC, GTA, GGC, GGA]_d$$
$$[T,G]_d \otimes [T,G]_d \otimes [T,G]_d = [TTT, TTG, TGT, TGG, GTT, GTG, GGT, GGG]_d$$

Fig. 5. Representations of nitrogenous bases and triplets in the form of eigenvalues of matrices. Above: the original diagonal (2*2)-matrices with pairs of letters C and A, T and G. Bottom: the alphabet of 64 triplets in the form of 8 diagonals from 8 diagonal matrices with sizes (8*8).

signal amplitudes (e.g. oppositional in polarity) or two kinds of laser beams etc., but in the considered genetic case, the binary opposition of the resonance characteristics gives an opportunity to consider genetic systems as binary computers on resonances.

4.1. Symmetric properties of the eight octets of triplets and their code values

Until now, nothing has been said about amino acids and stop-codons, which are encoded by triplets and which are not taken into account in the formalistic construction of the eight octets of triplets based on the tensor product of alphabetic (2*2)-matrices. Consider now mosaics of placing amino acids and stop-codons inside these octets of eigenvalues of the diagonal matrices.

Note that the huge quantity $64! \approx 10^{89}$ of variants exists for dispositions of 64 triplets in 8 octets, i.e. in 64 cells. For a comparison, the modern physics estimates a duration of existence of the Universe in 10^{17} s. Obviously, the random arrangement of 20 amino acids and of corresponding triplets in 64 cells almost never gives symmetry in such set of octets.

But unexpectedly the location of amino acids and triplets, having different phenomenological properties, shows fine symmetries of properties in this set of 8 octets in Fig. 5. These symmetries in the molecular-genetic system testify the existence of hidden patterns. One can demonstrate six examples of hidden symmetries and laws related to the resonance approach.

4.1.1. The first example of hidden regularities inside the eight octets

Substitution into the octets of triplets those amino acids and stop-codons, which are encoded by triplets, detects a hidden symmetry in this octet organization: the entire set of 8 octets shows itself as a complect of 4 pairs of adjacent octets with identical lists of amino acids and stop-codons in each pair (Fig. 6).

4.1.2. The second example of hidden regularities inside the eight octets

It is known that the alphabet of 64 triplets is divided by nature into two equal sub-sets on the basis of strong and weak roots, i.e., the first two positions in triplets (Rumer, 1968): (a) 32 triplets with strong roots, i.e., with 8 "strong" doublets AC, CC, CG, CT, GC, GG, GT, TC on their first positions (such triplets are denoted by black color on Figs. 7 and 8); (b) 32 triplets with weak roots, i.e., with 8 "weak" doublets AA, AG, AT, GA, TA, TT, TG.

Code meanings of triplets with strong roots do not depend on the letters on their third position; code meanings of triplets with weak roots depend on their third letter (Fig. 7).

The phenomenological location of 32 triplets with strong roots (black color) and 32 triplets with weak roots (white color) has the symmetric character in these octets (Fig. 8, left): (1) the black-and-white mosaic of each octet is mirror-antisymmetric in its left and right halves and it has a meander-like character; (2) the whole set of 8 octets is divided into a pair of adjacent octets with identity mosaics; (3) each octet contains 4 triplets with strong roots and 4 triplets with weak roots.

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

Fig. 6. Inside any of the four pairs of octets 1-2, 3-4, 5-6, 7-8, both octets are identical in their lists of encoded amino acids and stop-codons (an appropriate amino acid or stop-codon are shown under each triplet for the case of the Vertebrate Mitochondrial Code, which is the most symmetric among known dialects of the genetic code).

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

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

Fig. 7. The partition of the alphabet of 64 triplets into sub-alphabets of 32 triplets with strong roots (the left column, black color) and of 32 triplets with weak roots (the right column) in cases of the Standard Code and the Vertebrate Mitochondrial Code. All initial data are taken from the NCBI's web-site http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi.

[CCC, CCA, CAC, CAA,	ACC, ACA, AAC, AAA]$_d$	[+1,+1, -1,-1,+1,+1, -1,-1]$_d$
[CCT, CCG, CAT, CAG,	ACT, ACG, AAT, AAG]$_d$	[+1,+1, -1,-1,+1,+1, -1,-1]$_d$
[CTC, CTA, CGC, CGA,	ATC, ATA, AGC, AGA]$_d$	[+1,+1,+1,+1,-1, -1, -1,-1]$_d$
[CTT, CTG, CGT, CGG,	ATT, ATG, AGT, AGG]$_d$	[+1,+1,+1,+1,-1, -1, -1,-1]$_d$
[TCC, TCA, TAC, TAA,	GCC, GCA, GAC, GAA]$_d$	[+1,+1, -1,-1,+1,+1, -1,-1]$_d$
[TCT, TCG, TAT, TAG,	GCT, GCG, GAT, GAG]$_d$	[+1,+1, -1,-1,+1,+1, -1,-1]$_d$
[TTC, TTA, TGC, TGA,	GTC, GTA, GGC, GGA]$_d$	[-1, -1,-1,-1, +1,+1,+1,+1]$_d$
[TTT, TTG, TGT, TGG,	GTT, GTG, GGT, GGG]$_d$	[-1, -1,-1,-1, +1,+1,+1,+1]$_d$

Fig. 8. The symmetric location of triplets with strong and weak roots in the 8 octets of triplets. Meander character of sequences of black and white triplets in each octet is shown. Right: the representation of each octet in the form of a Rademacher function consisting of elements of "+1" and "−1".

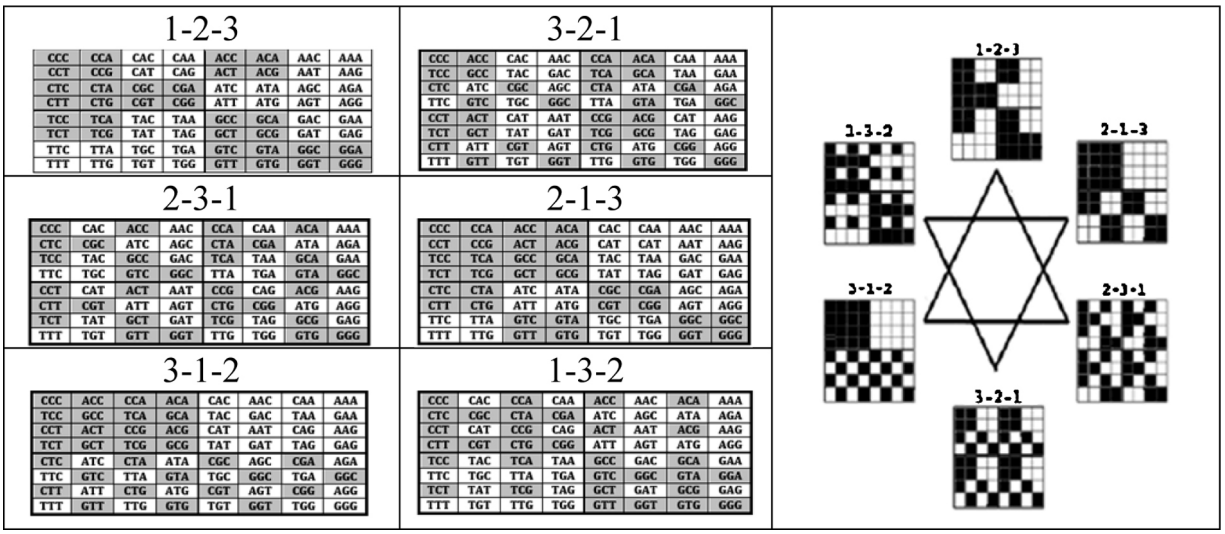


Fig. 9. Changes of 8 octets of triplets with strong roots (black color) and weak roots (white color) from Fig. 8 in the case of all possible variants of simultaneous permutations of positions in all triplets. Right: the general scheme of relations of the 6 sets of 8 octets of triplets. Each of two triangles in the six-pointed star corresponds to its own cases of circular permutations: 1-2-3→2-3-1→3-1-2 (direct reading of triplets) and 3-2-1→2-1-3→1-3-2 (inverse reading).

But such odd meander functions are well known in signal processing theory and probability theory under the name "Rademacher functions": $r_n(x) = \mathrm{sign}(\sin 2^n \pi x)$. Rademacher functions, containing only the elements "+1" and "−1", are phenomenologically associated with the genetic alphabet: each of the 8 octets of triplets is one of Rademacher functions if every black (white) triplet is interpreted as an element "+1" ("−1"). These phenomenological symmetries speak additionally about structural connections of the alphabet of 64 triplets with formalisms of mathematics of digital signal processing.

4.1.3. *The third example of hidden regularities inside the eight octets*

Works of many authors are devoted to relations between genetic coding and circular codes, which concern questions of reading frame (Arquès and Michel, 1996; Michel, 2007, 2013; Michel and Seligmann, 2014; Seligmann, 2011, 2015; Stambuk, 1999). In this section, cyclic permutations of positions in triplets are taken into account. The set of 8 octets from Fig. 8 have an interesting property in relation to simultaneous permutations of positions in all triplets (Fig. 9).

Let us consider all possible variants of such cyclic permutations, where 3 variants exist for a direct reading of each triplet (1-2-3→2-3-1→3-1-2) and 3 variants for an inverse reading (3-2-1→2-1-3→1-3-2). Fig. 9 shows that each of these 6 variants changes all octets and their black-and-white mosaics described above on Fig. 8. In the result of the permutations, 5 new sets of octets of triplets appear, where unexpectedly each of new 40 octets (5*8 = 40) has again a meander character of its mosaic, which is characterized by one of Rademacher functions. These results

[CCC, CCA, CAC, CAA, ACC, ACA, AAC, AAA]$_d$	[+1, +1,+1, +1, +1, +1, +1, +1]$_d$
[CCT, CCG, CAT, CAG, ACT, ACG, AAT, AAG]$_d$	[-1, +1, -1, +1, -1, +1, -1, +1]$_d$
[CTC, CTA, CGC, CGA, ATC, ATA, AGC, AGA]$_d$	[-1, -1, +1, +1, -1, -1, +1, +1]$_d$
[CTT, CTG, CGT, CGG, ATT, ATG, AGT, AGG]$_d$	[+1, -1, -1, +1, +1, -1, -1, +1]$_d$
[TCC, TCA, TAC, TAA, GCC, GCA, GAC, GAA]$_d$	[-1, -1, -1, -1, +1, +1, +1, +1]$_d$
[TCT, TCG, TAT, TAG, GCT, GCG, GAT, GAG]$_d$	[+1, -1, +1, -1, -1, +1, -1, +1]$_d$
[TTC, TTA, TGC, TGA, GTC, GTA, GGC, GGA]$_d$	[+1, +1, -1, -1, -1, -1, +1, +1]$_d$
[TTT, TTG, TGT, TGG, GTT, GTG, GGT, GGG]$_d$	[-1, +1, +1, -1, +1, -1, -1, +1]$_d$

Fig. 10. The numeric representation of the 8 octets of triplets coincides with a complete orthogonal system of Walsh functions for the 8-dimensional case, if the unique status of thymine T is taken into account within digitizing of triplets. Black color corresponds to triplets represented by "+1".

testify that the Nature divided the set of 64 triplets into the subsets of 32 triplets with strong roots and of 32 triples with weak roots by the very special way in a connection with cyclic permutations.

4.1.4. *The fourth example of hidden regularities inside the eight octets*

Among the four DNA bases – A, C, G, T – the letter T contrasts phenomenologically with three other letters of the alphabet: (1) only the letter T is transformed into another letter U (uracil) in the transition from DNA to RNA; (2) only the letter T (and its substitute U) does not have the functionally important amino group NH_2 in contrast of other three letters (see Fig. 4, left).

This binary opposition can be expressed in a digital form as: A = C = G = + 1 and T = −1. Then each triplet under replacing its letters on these numbers (A = C = G = + 1, T = −1) can be represented as the product of these numbers. For example, the triplet CAT is represented as 1*1*(−1) = −1 and the triplet TGT – as (−1)*1 *(−1) = +1. In the result, the 8 octets of triplets obtain numerical representations

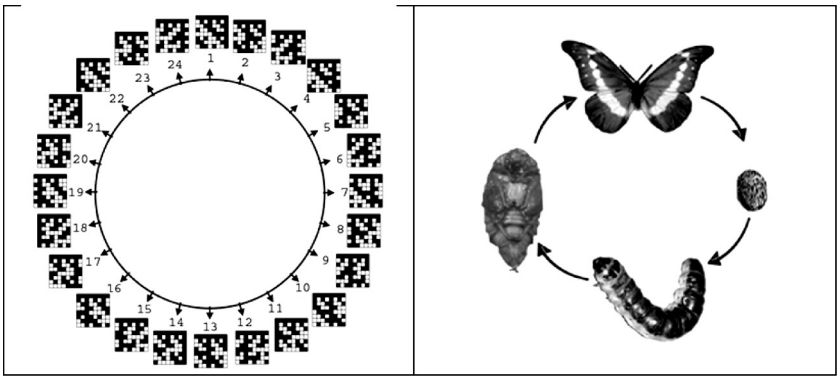


Fig. 11. Cyclic changes. Left: iterative cyclic shifts of the first letters of all 8 octets (from Fig. 10) into last positions of the same octets give 24 sets of 8 octets, whose mosaics correspond to 24 complete sets of Walsh functions for 8-dimensional space (black color means +1, white color means −1). Right: metamorphosis of butterflies.

as sequences of elements +1 and −1 (these elements are correspondingly marked by black and white colors on Fig. 10). The set of these sequences coincide with the complete system of orthogonal Walsh functions for an 8-dimensional space (Fig. 10, right).

These Walsh functions, containing only the elements of "+1" and "−1", are widely used in digital signal processing and noise-immunity coding. Completeness of the system of 8 Walsh functions means that any 8-dimensional vector can be represented as their superposition (i.e., decomposed on their base). On the basis of complete systems of Walsh functions, noise-immunity coding of information is used on the spacecrafts "Mariner" and "Voyager" for transmission to Earth photos of Mars, Jupiter, Saturn, Uranus and Neptune. Complete systems of Walsh functions form Hadamard matrices, which are used in quantum computers ("Hadamard gates"); Hadamard matrices are used in quantum mechanics in the form of unitary operators, etc. (Ahmed and Rao, 1975; Seberry et al., 2005). Walsh functions play basic role in the sequency analysis (Harmuth, 1970, 1977, 1981), which is one of important types of spectral analysis in communication technologies on discrete signals and which has found extensive application in electronics, acoustics, optics, and so forth. The sequency analysis spawned entirely new communication system, instant imaging device, a high-speed underwater acoustic cinema, receivers and transmitters of non-sinusoidal electromagnetic waves. In particular, on the base of sequency analysis the problem of absorption of radio waves and acoustic waves that important for bioinformatics is bypassed (Soroko, 1979). In our approach, these systems of Walsh functions are representatives of the genetic alphabet: each of the 8 functions of the complete Walsh system is the diagonal of one of the genetic (8*8)-matrices of the diagonal type, i.e., a spectrum of eigenvalues of an oscillation system with 8 degrees of freedom.

In addition, we note the following. Matrices $[C, A]_d$ and $[T, G]_d$, tensor products of which gave 8 octets of triplets in Fig. 5, were associated with the binary sub-alphabet on the trait "amino-keto" (Fig. 4). If we turn to the other two sub-alphabets in Fig. 4, it is possible to similarly consider the other two pairs of diagonal matrices: $[C, G]_d$ and $[T, A]_d$; $[C, T]_d$ and $[G, A]_d$. Each of these pairs gives rise to other 8 octets of triplets by means of tensor products of its matrices in all possible combinations in threes (analogous to the table in Fig. 5 below). Each of these two new sets of 8 octets of triplets also has its numerical representation in the form of new (individual) sets of Rademacher and Walsh functions for the same binary-oppositional traits of triplets: (1) strong and weak roots of triplets; (2) the special status of the letter T.

These results support the following:

- Alphabets of the genetic code are alphabets of eigenvalues and eigenvectors of matrices of oscillatory systems (figuratively speaking, the genetic code is the code of systems of resonances); accordingly, one can think, that genetic texts are written in the language of the resonances.

From this standpoint it follows that a living body is a choir of coordinated oscillatory processes.

4.1.5. *The fifth example of hidden regularities inside the eight octets*

The 8 octets with their black-and-white mosaics on Fig. 10 have additional cyclic properties. Each octet contains 24 nitrogenous bases (or letters). One can cyclically shift the first letters of octets into the last position in their octets. In this case a new set of 8 octets appears with new mosaics. Repeating this cyclic shift of the first letters of all octets into the last positions of their octets again and again, we receive 192 octets inside 24 sets of 8 octets with individual mosaics (Fig. 11). One can check that the mosaic of each of 192 octets corresponds again to one of Walsh functions. Moreover each of 24 sets of octets corresponds again to a complete set of Walsh functions for 8-dimensional space of signals and to an appropriate Hadamard (8*8)-matrix. It confirms that the Nature has built genetic alphabets in connection with cyclic shifts.

Such cyclic metamorphoses in the family of 24 complete sets of Walsh functions (Fig. 11, left), which are related with phenomenological features of the alphabet of triplets, lead to an association with the famous doctrine of Ancient Chinese medicine. The last connects chrono-cyclic processes in biological organisms with chrono-cycles of the surrounding world, first of all, with the solar cycles of the changing of days and nights. The duration of such solar cycles is divided traditionally into 24 equal parts (24 h) in accordance with a cyclic activity of inherited physiological organs (Petoukhov, 2001). This scheme is used intensively in recipes of acupuncture, in methods of pulse-diagnostics, etc. Modern medicine supports this Ancient doctrine (Wright, 2002).

Many significant examples of cyclic genetic organizations of biological bodies are given by metamorphoses of animals. For instance, butterflies have four stages of cyclic metamorphoses in their life: egg → larva (the caterpillar stage) → pupa (the chrysalis phase) → adult butterfly → egg → . . . (Fig. 11, right). All these 4 different organisms possess the identical DNA-molecules, but – in the cyclic transition from one organism to another – algorithms of the implementation of DNA-information are cyclically changed, that is accompanied by the expression of other sets of genes in a temporal chain of developmental stages. One can additionally note that in the chrysalis phase the organism does not eat at all; consequently its atomic content is not changed practically, but its atomic-molecular configurations are reformed cardinally by means of complex permutations of chemical elements to generate finally a butterfly. Such

cyclic phenomena make up a large puzzle, for the solution of which one should research cyclic properties of molecular-genetic structures.

4.1.6. The sixth example of symmetries inside the eight octets

The nitrogenous bases have different molecular parameters: adenine A ($C_5H_5N_5$) has molar mass 135 g, its quantity of protons is equal to 70; cytosine C ($C_4H_5N_3O$) has molar mass 111 g, its quantity of protons is equal to 58; guanine G ($C_5H_5N_5O$) has molar mass 151 g, its quantity of protons is equal to 78; thymine T ($C_5H_6N_2O_2$) has molar mass 126 g, its quantity of protons is equal to 66 (amounts of protons in complementary pairs C—G and A—T are both equal to 136).

The set of 8 octets of triplets on Fig. 5 has a few numerical symmetries in their molecular parameters including the followings:

- In all the 4 pairs of octets 1-8, 2-7, 3-6 and 4-5, which are located symmetrically in relation to the middle horizontal line on Fig. 5, amounts of molar masses of their 24 triplets are equal to 6276 g;
- In all the 4 pairs of octets 1-8, 2-7, 3-6 and 4-5, amounts of protons of their 24 triplets are equal to 3264;
- Each of octets comprises 12 representatives of each complementary pairs C—G and A—T; correspondingly its amount of their hydrogen bonds is equal to 60 (=12*3 + 12*2);
- Each octet contains of 12 purines A, G and 12 pyrimidines C, T.

These results can be also related to the question about arithmetic inside the genetic code (Shcherbak, 2003).

5. Vibrational mechanics and biological phenomena

Mechanical and electrical oscillations in living bodies are closely connected because many tissues are piezo-electrical (nucleic acids, bone, actin, dentin, tendons, etc.). Mathematics of mechanical and electrical oscillations is analogical (so called "electro-mechanical analogies" are well-known). Vibrational mechanics is widely used in engineering and is full of amazing phenomena of vibrational separation and structuring of multiphase media, vibro-transportation of substances, vibro-transfer of energy and so forth (Blekhman, 2000; Ganiev et al., 2015). The concept of resonance genetics draws attention to a possible value of phenomena of vibrational mechanics in physiology with its complex phenomena of coordinated actions of many parts, for example, within division of cells, etc. Practically invisible vibrations can provide, for example, the following phenomena: the upper position of the inverted pendulum becomes stable; heavy metal ball "floats" in a layer of sand; a rope takes a form of a vertical stem if a corresponding vibration acts on its base. Inside fluids, vibrating bodies can attract or repel each other (vibrating forces of Bjerknes) and pulsating gas bubbles may coalesce or divide.

Mutual synchronization of many physiological processes is important for a living body, including phenomena of its symmetric organization (Petoukhov, 1981, 1989). Vibrational mechanics gives the known example of resonant self-synchronization of plurality of oscillating pendulums mounted on a common movable platform (Harvard demonstration – http://www.youtube.com/watch?v=Aaxw4zbULMs). Inside a living organism, its structural water apparently plays the role of such common mobile platform, which is required for synchronization. Illustrative example of morphogenetic and general physiological role of structural water is given by jellyfish, which consists of 99% water, but despite of this its morphology implements heritable phyllotaxis phenomena: tentacles, canals and zooids of some jellyfish exactly correspond to phyllotaxis laws (Jean, 1994, Chapter 12.3.3). This structural water is also a candidate for the role of a unifying vibro-platform for vibro-transfer of energy among different parts of a living body. The physical features of structural water, associated with resonance interactions in it, are currently being studied in laboratories around the world. An important role in vibro-connections among parts of an organism belongs also to cytoskeleton that works in coordination with boundary water and membranes (Igamberdiev, 2012).

The phenomenon of vibro-transfer of energy among parts of an oscillatory system is known: a rotary electromotor operates stably, when it is disconnected from the power electrosupply, if it is standing on a mutual vibro-platform with another rotary electromotor of similar resonant characteristics, which is connected to a power supply (self-synchronization by resonant interactions). Taking into account possibilities of such energy transferring, living organisms can be seen as resonance consumers of energy of surrounding electromagnetic waves coming from space and the depths of the earth. Photosynthesis, which is based on absorbing solar energy of light waves, is probably only one of examples of the biological consumption of energy from external wave sources on the basis of resonant mechanisms (a resonant "vampirism" of energy and information in organisms). A lot of data from homeopathy and physiological phenomena of ultraweak influences testifies in favor of resonant organization of living matter.

Vibrational mechanics also allows simulating the evolutionary coordination and selection in the problem of a creation of a single organism from many pieces. Let us return to the example of rotary motors on a total mobile platform. Around a single electric motor connected to the power supply one can set – on the total mobile platform – many other rotary motors without the electrical power supply, which have different resonance characteristics. Through the self-synchronization by resonant interactions, only those motors, which are capable to resonance coordination with the base motor, will work as parts of a single functional colony, and the remaining motors will not work and will be correspondingly eliminated from such total working ensemble. Resonant combining parts into a single whole is based on the fundamental physical principle of minimum of energy: each of members of the ensemble requires less energy for performing own work than when working individually. The principle of energetic minimum in resonance processes has some correlations with the principle of relaxation in morphogenetic processes proposed in (Igamberdiev, 2012). The concept of resonance genetics has also some interrelations with the idea of Bauer (1935) that living systems work in expense of non-equilibrium, and the external energy is used not directly to perform work but to support the stable non-equilibrium state; most of this energy is transformed into the kinetic energy.

The morphological variability follows certain rules that can be called nomothetical laws and analyzed as symmetrical transformations (Meyen, 1973). The nomothetical laws and morphogenetic phenomena are related with the known idea about existence of a morphogenetic field, a possible nature and bases of which are discussed by many authors (Beloussov, 1998, 2012; Igamberdiev, 2014; Meyen, 1973). The book of D'Arcy Thompson (1917) remains the most comprehensive compendium of nomothetical laws operating in the course of biological transformations.

Our concept of resonance genetics proposes a new approach to simulate inherited biological surfaces, which typically have curvilinear forms. Curvilinear 2-dimensional surfaces inside 3-dimensional Euclidean spaces are described in Riemann geometry by means of fields of metric tensors, which are represented by symmetrical nonsingular (2*2)-matrices [g_{11}, g_{12}; g_{21}, g_{22}], where $g_{12} = g_{21}$ (Gallot et al., 2004; Rashevsky, 1964). But symmetrical (2*2)-matrices represent also vibro-systems with two degrees of freedom. It means that resonance characteristics of such vibro-systems can be used to define (or encode) corresponding metric tensors. This coincidence of symmetrical (2*2)-matrices from

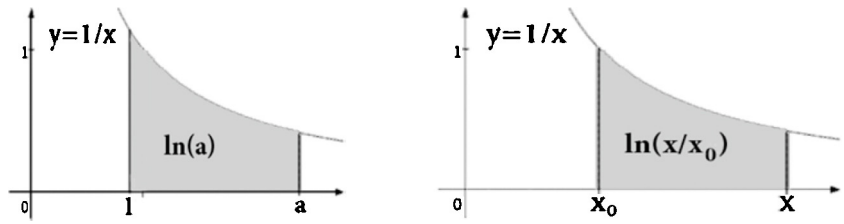


Fig. 12. Natural logarithm as a square under hyperbola $y = 1/x$. Left: $\ln(a)$ is equal to the square under the hyperbola from 1 to a. Right: $\ln(x/x_0)$ is equal to the square under the hyperbola from x_0 to x.

Riemann geometry and from theory of oscillations has led the author to the idea about so called "morphoresonance" field as a new version of morphogenetic field (Petoukhov, 2015b,c). By definition, the morphoresonance field, which exists inside a living organism and which develops in time, is a tensor field of oscillation processes with coordinated resonance frequencies of many oscillatory systems with many degrees of freedom. In this notion we do not suppose existence of physical fields or forces unknown to science. This version of the morphogenetic field for the first time links the morphogenetic field with the features of molecular genetic systems (on basis of resonance spectra). The idea about fields of metric tensors, which are defined (or are encoded) by means of fields of corresponding resonance spectra, can be used in particular to simulate Euclidean and Non-Euclidean bio-symmetries (Igamberdiev, 2012; Petoukhov, 1989, 2015b,c). We suppose that morphogenesis is a system-resonance phenomenon. Basic principles of the theory of the morphoresonance field are connected with conformal bio-symmetries (Petoukhov, 1989) and their generalization up contact bio-symmetries on the base of the group of contact transformations known in optics and mechanics in the following topics: the optical-mechanical analogy; Huygens' principle; canonical equations of Hamilton, etc. On this way the question about characteristical (generating) functions of morphogenetic medium is studied. One can add that tensor fields are widely used in physics. For instance, Albert Einstein identified the gravitational field with the field of metric tensors of Riemann geometry. Tensor fields of Riemann geometry are used to describe physical quantities characterizing the elastic, optical, thermodynamic, dielectric, piezomagnetic and other properties of anisotropic bodies.

An organism during its life on genetic basis should solve algorithmic problems of two types: (1) informational, providing coordinated energy processes; (2) energetic, providing information processes. Systems of resonances can be used as a common basis of such "two-faced" algorithms since resonances are associated both with oscillatory energy and with informatics of communications among objects.

It is profitable for an organism, which is a single whole, to have the same typical algorithms at different levels of its functioning for a mutual optimal coordination of its parts. By this reason we study possibilities to simulate different innate phenomena on the general basis of formalisms of the theory of resonances of vibro-systems with many degrees of freedom. Here we can mention, for example, the basic psychophysical Weber–Fechner law, to which different types of inherited sensory perception are subordinated: sight, hearing, smell, touch, taste, etc. The Weber–Fechner law declares the following: the intensity of the perception is proportional to the logarithm of stimulus intensity; it is expressed by the equation

$$p = k * \ln(x/x_0) = k * \{\ln(x) - \ln(x_0)\}, \quad (1)$$

where p – the intensity of perception, x – stimulus intensity, x_0 – threshold stimulus, ln – natural logarithm, k – a weight factor. Because of this law, the power of sound in technology is measured on a logarithmic scale in decibels.

This logarithmic law (1) is simply modeled on the base of natural resonance frequencies of a particular class of oscillatory systems with 2 degrees of freedom. As known (Klein, 2004), the natural logarithm can be defined for any positive real number "a" as the area under the hyperbola $y = 1/x$ from 1 to a (Fig. 12, left). It means that two points of the hyperbola with their coordinates $(x, 1/x)$ and $(x_0, 1/x_0)$, where $x > 1$, $x_0 > 1$, define values of natural logarithms $ln(x)$ and $ln(x_0)$. Subtraction $ln(x) - ln(x_0)$ gives the intensity of perception p in the expression (1) of the Weber–Fechner law (Fig. 12, right). But the same points $(x, 1/x)$ and $(x_0, 1/x_0)$ are defined by diagonal matrices $[x, 0; 0, 1/x]$ and $[x_0, 0; 0, 1/x_0]$ of two vibro-systems with eigenvalues, which are related reciprocally (correspondingly, natural resonance frequencies in every of the vibro-systems are also reciprocal to each other).

Here one can also recall the known phenomenon of conformational fluctuations of enzyme macromolecules on frequencies of sound waves and other frequencies. In connection with this phenomenon, the possible importance for life "*fantastic pictures of musical interactions of biochemical systems, cells, organs*" related to "*biochemical aesthetics*" has been noted in (Shnoll, 1979, p. 75).

Our research is associated with "biochemical aesthetics". An organism can be seen as a musical synthesizer with multiple settings of inherited resonant modes (Darvas et al., 2012; Petoukhov, 2015a,b). Music is a game with acoustic resonances, to which people are remarkably predisposed. Throughout tens of thousands of years, people create musical instruments, adjusting them to specific systems of resonances. Over the centuries, people have learned to combine individual instruments and singers into orchestras and choirs as coordinated oscillating systems with an increased number of degrees of freedom. Gottfried Leibniz declared that music is arithmetic of soul, which computes without being aware of it. Taking into account that music is represented by systems of resonances, one can reformulate this declaration: systems of resonances are the arithmetic of soul, which computes without being aware of it.

6. Some concluding remarks

Max Planck wrote: «We thus find that it is a characteristic of every new idea occurring in science that it combines in a certain original manner two distinct series of facts» (Planck, 1936). The general idea that knowledge is a search for analogies is recognized in science at least since the time of B. Bolzano. Accordingly, the concept of system-resonance genetics is appeared in the result of the author's discovery of structural analogies between genetic phenomena and the mathematical theory of resonances of vibro-systems with many degrees of freedom. Due to this, promising intersections of biology with physics and informatics were revealed.

All natural objects possess resonance properties. From the standpoint of our model approach, genetic physiology is associated with a relatively narrow class of systems of resonances, which are related with eigenvalues and eigenvectors of

(2^n*2^n)-matrices from tensor families based on tensor products of (2*2)-matrices. Our results argue in favor of specificity of the biological system of inherited varieties of resonances expanding during ontogeny.

Genetic molecules belong to the microworld and therefore are subordinated to the principles of quantum mechanics. Quantum mechanics operates with frequency and resonance characteristics of quantum-mechanical objects; its mathematics uses eigenvalues of matrices. In general, quantum mechanics was emerged and developed largely as a science about resonances in microworld. Thus, the concept of system-resonance genetics (or spectral-resonance genetics) creates models of genetic phenomena on the same language of frequencies and resonances, on which models in quantum mechanics are based. In addition to this, it uses the same matrix language, on which "matrix mechanics" of Werner Heisenberg has been created; it is historically the first form of quantum mechanics, which retains its value to this day. In quantum physics, Hermitian matrices (or self-adjoint matrices) with complex entries play an important role. In our matrix approach to genetic systems, Hermitian matrices are attracted a special attention because of the following: (1) they have real eigenvalues; (2) the tensor product of two Hermitian matrices gives a new Hermitian matrix; (3) in quantum physics, in considering the quantum system consisting of two subsystems, its state space is constructed in the form of the tensor product of state spaces of the subsystems. Taking these into account, all data mentioned above in our article about tensor families of matrices with real eigenvalues can be also interpreted from the standpoint of tensor families of Hermitian matrices. The study of such interpretation and its consequences can lead to interesting results and to new questions. For example, the question is possible: what of kinds of Hermitian operators stands behind genetic diagonal matrices such as [C, 0; 0, A] and [T, 0; 0, G] (Fig. 5), which can be represented in numerical forms, including forms of numeric block matrices? Is it a new kind of Hermitian operators, which plays a role in genetics, or not?

The concept of resonance genetics can facilitate a convergence of biology and quantum mechanics, possibility of which is studied by many authors (see e.g. Igamberdiev, 2014). The creator of the theory of resonance in structural chemistry L. Pauling was right when he supposed an important meaning of resonances in organization of living matter (Pauling, 1940).

In the past century, science has discovered that molecular-genetic bases of all living organisms are the same (alphabets of DNA, RNA, etc.) and that they are very simple. A hope arises that the algorithmic foundations of organisms, which are subordinated to genetic laws such as Mendel's laws, are also very simple and are unified for all living things. Identifying these algorithms of living matter is important. We assume that the algorithms of resonant matching and ordering subsystems play one of key roles in living matter.

The author believes that the development of modern theoretical biology – as a branch of mathematical natural science – can go on the same way as the development of modern theoretical physics, which, according to P. Dirac, should be by the following recipe. "*Start with a beautiful mathematical theory. "If it is really beautiful* – he believed – *it is sure to be an excellent model of important physical phenomena. So you need to search for these phenomena to develop applications of beautiful mathematical theory and interpret them as predictions of new laws of physics" – in such way, according to Dirac, the whole new physics is built – relativistic and quantum*" (quote from Arnold (2006)). This article shows that beautiful mathematical theory of eigenvalues and eigenvectors of tensor families of matrices gives models of important genetic phenomena and structures with revealing their deep connection with the theory of resonances of oscillatory systems with many degrees of freedom.

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References

Ahmed, N., Rao, K., 1975. Orthogonal Transforms for Digital Signal Processing. Springer-Verlag Inc., NY.
Arquès, D.G., Michel, C.J., 1996. A complementary circular code in the protein coding genes. J. Theor. Biol. 182, 45–58.
Arnold, V.I., 2006. Public lecture at Mathematical Institute by V.A Steklov (Publichnaya lektsiia v Matematicheskom institute imeni V.A. Steklova), http://elementy.ru/lib/430178/430281 (in Russian).
Balonin, N.A., 2000. New course on the theory of motion control (Novyi kurs teorii upravleniia dvizheniem). Saint Petersburg State University, Saint Petersburg (in Russian).
Bauer, E.S., 1935. Theoretical Biology. VIEM, Moscow/Leningrad (in Russian Bauer, E.S., 1982. Theoretical Biology, with English translation. Akadémiai Kiadó, Budapest, 1982).
Bellman, R., 1960. Introduction to Matrix Analysis. MacGraw-Hill Book Company, New York.
Beloussov, L.V., 1998. The Dynamic Architecture of a Developing Organism. Kluwer, Dordrecht.
Beloussov, L.V., 2012. Morphogenesis as a macroscopic self-organizing process. Biosystems 109, 262–279.
Blekhman, I.I., 2000. Vibrational Mechanics. World Scientific, Singapore, 509 p.
D'Arcy Thompson, W., 1917. On Growth and Form. Cambridge University Press, London.
Darvas, G., Koblyakov, A., Petoukhov, S., Stepanyan, I., 2012. Symmetries in molecular-genetic systems and musical harmony. Symmetry Cult. Sci. 23 (3–4), 343–375.
Gallot, S., Hulin, D., Lafontaine, J., 2004. Riemannian Geometry. Springer Verlag, Berlin, New York.
Ganiev, R.F., Ganiev, S.R., Kasilov, V.P., Pustovgar, A.P., 2015. Wave Technology in Mechanical Engineering. Scrivener Publishing LLC, Massachusetts.
Gazale, M.J., 1999. Gnomon. From Pharaohs to Fractals. Princeton University Press, New Jersey, 280 p.
Gladwell, G.M.L., 2004. Inverse Problems in Vibration. Kluwer Academic Publishers, London, 452 p.
Gumbel, M., Fimmel, E., Danielli, A., Strüngmann, L., 2015. On models of the genetic code generated by binary dichotomic algorithms. Biosystems 128, 9–18.
Harmuth, H.F., 1970. Transmission of Information by Orthogonal Functions. Springer, Berlin.
Harmuth, H.F., 1977. Sequency Theory. Foundations and Applications. Academic Press, NY.
Harmuth, H.F., 1981. Nonsinusoidal Waves for Radar and Radio Communication. Academic Press, NY.
Igamberdiev, A.U., 2012. Biomechanical and coherent phenomena in morphogenetic relaxation processes. Biosystems 109, 336–345.
Igamberdiev, A.U., 2014. Time rescaling and pattern formation in biological evolution. Biosystems 123, 19–26.
Jakobson, R., 1987. Language in Literature. MIT Press, Cambridge.
Jakobson, R., 1999. Texts, Documents, Studies. RGGU, Moscow (in Russian).
Jean, R., 1994. Phyllotaxis. A Systemic Study in Plant Morphogenesis. Cambridhe University Press.
Klein, F., 2004. Elementary Mathematics from an Advanced Standpoint: Arithmetic, Algebra, Analysis. Dover Publications, London.
Meyen, S.V., 1973. Plant morphology in its nomothetical aspects. Bot. Rev. 39, 205–260.
Michel, C.J., 2007. Circular codes in genes, http://dpt-info.u-strasbg.fr/~c.michel/Circular_Codes.pdf.
Michel, C.J., 2013. Circular code motifs in transfer RNAs. Comput. Biol. Chem. 45, 17–29.
Michel, C.J., Seligmann, H., 2014. Bijective transformation circular codes and nucleotide exchanging RNA transcription. Biosystems 118, 39–50.
Pauling, L., 1940. The Nature of the Chemical Bond and the Structure of Molecules and Crystals: An Introduction to Modern Structural Chemistry, 2nd ed. Oxford University Press, London, 664 p.
Petoukhov, S.V., 1981. Biomechanics, Bionics and Symmetry. Nauka, Moscow, 239 p. (in Russian).
Petoukhov, S.V., 1989. Non-Euclidean geometries and algorithms of living bodies. Comput. Math. Appl. 17, 505–534.
Petoukhov, S.V., 2001. Genetic Codes II: numeric rules of degeneracy and a chronocyclic theory. Symmetry Cult. Sci. 12 (3–4), 275–306.
Petoukhov, S.V., 2008. Matrix Genetics, Algebras of the Genetic Code, Noise Immunity (Matrichnaya genetika, algebry geneticheskogo koda,

pomekhoustoychivost). Publishing House "Regular and Chaos Dynamics", Moscow, 315 p. http://petoukhov.com/matrix-genetics-petoukhov-2008.pdf (in Russian).
Petoukhov, S.V., 2011. Matrix genetics and algebraic properties of the multi-level system of genetic alphabets. Neuroquantology 9 (4), 60–81.
Petoukhov, S.V., 2014. Matrix genetics: algebra of projection operators, cyclic groups and inherited ensembles of biological cycles. In: Dragovich, B., Panajotović, R., Timotijević, D. (Eds.), Proceedings of 2nd International Conference on Theoretical Approaches to BioInformation Systems. 17–22 September 2013, Belgrade, Serbia. Institute of Physics, Belgrade, pp. 189–204, www.tabis2013.ipb.ac.rs/tabis2013.pdf.
Petoukhov, S.V., 2015a. Music and the modeling approach to genetic systems of biological resonances. In: Lecture at the International Conference on ISIS Summit Vienna 2015. The Information Society at the Crossroads, 3–7 June 2015, Vienna, Austria, http://sciforum.net/conference/70/paper/2812.
Petoukhov, S.V., 2015b. The concept of resonances in genetics ("resonance bioinformatics"). In: Selected Works of the VII International Congress on The Weak and Super-Weak Fields and Radiation in Biology and Medicine, 7–11 September 2015, St. Petersburg, Russia, pp. 1–41, http://www.biophys.ru/lib/sci/resonance/460-resonance-00001 (in Russian).
Petoukhov, S.V., 2015c. The concept of resonances in genetics ("resonance genetics") and genetic music. In: Abstracts of the 2nd International Conference on Physics of Living Systems: Past, Present and Future, 10–11 September 2015. Moscow Institute of Physics and Technology (State University), p. 38.
Petoukhov, S.V., He, M., 2010. Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications. IGI Global, Hershey, USA, 271 p.
Planck, M., 1936. Scientific ideas, their origin and effects. In: Planck, M. (Ed.), The Philosophy of Physics. W.W. Norton & Company, USA.
Rashevsky, P.K., 1964. Riemannian Geometry and Tensor Analysis. Nauka, Moscow (in Russian).
Rumer, Yu.B., 1968. Codon systematization in the genetic code (Sistematizatsiia kodonov v geneticheskom kode). Dokl. Akad. Nauk SSSR 183 (1), 225–226 (in Russian).
Seberry, J., Wysocki, B.J., Wysocki, T.A., 2005. On some applications of Hadamard matrices. Metrica 62, 221–239.
Seligmann, H., 2011. Two genetic codes, one genome: frameshifted primate mitochondrial genes code for additional proteins in presence of antisense antitermination tRNAs. Biosystems 105, 271–285.
Seligmann, H., 2015. Phylogeny of genetic codes and punctuation codes within genetic codes. Biosystems 129, 36–43.
Shcherbak, V.I., 2003. Arithmetic inside the universal genetic code. Biosystems 70, 187–209.
Shnoll, S., 1979. Physico-Chemical Factors of Biological Evolution (Fiziko-himicheskie factory biologicheskoy evolutsii). Nauka, Moscow, 263 p. (in Russian).
Soroko, L.M., 1979. The sequency analysis in engineering and physics. Uspekhi Fizicheskih Nauk 129 (10), 355–357.
Stambuk, N., 1999. Circular coding properties of gene and protein sequences. Croat. Chem. Acta 72 (4), 999–1008.
Stewart, I., 1999. Life's Other Secret: The New Mathematics of the Living World. Penguin, NY.
Wright, K., 2002. Times of our lives. Sci. Am. 287 (3), 58–65.
Zharov, V.E., 2002. Spherical Astronomy. RFFI, Friazino.