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## Chapter ?

### **The concept of systemic-resonance bioinformatics. Resonances and the quest for transdisciplinarity**

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The article is devoted to an important role of the concept of resonances not only in classical and quantum mechanics but also in genetics and biological communication. Matrix representations of oscillators with many degrees of freedom are used to model some phenomena of Mendelian genetics and to analyze structures of genetic-molecular alphabets. To explain phenomena of segregation in these molecular alphabets, the existence of dominant and recessive resonances in nitrogenous bases of DNA and RNA are postulated by analogy with dominant and recessive alleles in Mendelian genetics. Relations of genetic alphabets with modulo-2 addition, dyadic groups of binary numbers and matrices of dyadic shifts are shown. A connection of structures of genetic alphabets with known formalisms of noise-immunity coding (Rademacher and Walsh functions, Hadamard matrices) are discussed taking into account noise-immunity properties of genetic encoding.

#### **1. Introduction**

From an information standpoint, biological organisms are informational essences. They receive genetic information from their ancestors and transmit it to descendants. Science has discovered that all organisms are identical to each other by their basic molecular-genetic structures. Due to this revolutionary discovery, a great unification of all biological organisms has happened in science. A new understanding of life itself has appeared: "*life is a partnership between genes and mathematics*"

[Stewart, 1999]. The question about principles and mathematical bases of genetic informatics became one of the main challenges in mathematical natural sciences today.

It is well known that people use oral speech and singing for a communication due to an inherited ability to tune into resonances and to use resonances as carriers of information. Our voice apparatus is the appropriate oscillatory system with many degrees of freedom. But according to the classics of structural linguistics, 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, Chapter 12]. This is one of reasons to study genetic informatics, including genetic alphabets, from the standpoint of mathematics of resonances.

Moreover any living organism is a huge chorus of coordinated oscillatory processes (mechanical, electrical, piezoelectrical, biochemical, *etc.*), which are connected with their genetic inheritance along chains of generations. Since ancient times, chronomedicine 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, for example, [Gladwell, 2004]). We use matrices to study genetic phenomena.

Genetic molecules DNA and RNA exist on principles of quantum mechanics, but they encode structures of living macroorganisms, which are subjects of classical mechanics. By this reason, mathematics of genetic systems should be appropriate to quantum mechanics and classic mechanics simultaneously. Mathematics of resonances of oscillatory systems is appropriate for quantum mechanics and classic mechanics since such mathematics uses in both cases the same property of matrices to express resonances.

The concept of resonances plays fundamental and interdisciplinary role in science. Quantum mechanics has begun in 1900 due to works by M. Planck, who has analyzed a great set of resonant oscillators inside the cavity and in the result has received his famous law

of electromagnetic radiation emitted by a black body in thermal equilibrium. One can say that Planck has represented the matter as a set of vibrating oscillators and set the task to study the equilibrium established in the result of the exchange of energy between the oscillators and radiation.

Later, after more than 50 years of successful development of quantum mechanics, E. Schrodinger emphasised the basic meaning of resonances: *“The one thing which one has to accept and which is the inalienable consequence of the wave-equation as it is used in every problem, under the most various forms, is this: that the interaction between two microscopic physical systems is controlled by a peculiar law of resonance»* [Schrodinger, 1952, p.115]. In considering an exact balance in nature between bundles of energy, lost by one system and gained by another, he noted: *«I maintain that it can in all cases be understood as a resonance phenomenon»* [ibid, p.114]. He wrote in his resonance concept of quantum interactions, that chemical reactions, including photochemical reactions, can be explained on the base of resonances.

His book [Schrodinger, 1944] said that the chromosome is an aperiodic crystal since its atoms are connected each other by forces of the same nature that atoms in crystals. But vibrations and resonances play a very important role in physics of crystals. One can hope that a resonance approach can usefully serve also in genetics.

L.Pauling used ideas of resonances in quantum mechanical systems in his theory of resonance in structural chemistry. His book [Pauling, 1940] about this theory is the most quoted among scientific books of the XX century. 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 individually.

In classic mechanics, the concept of resonances has also wide theoretical and engineering applications due to vibrational phenomena of a resonant synchronization of oscillatory processes, vibrational separation and structuring of multiphase systems, vibro-transportation of substances, vibro-transmission of energy within systems, *etc.* [Blekhman, 2000; Ganiev et al., 2015]. Our results give a basis for wider use of these phenomena in modeling biological phenomena.

## 2. Background

Matrices possess a wonderful property to express resonances, which sometimes is called as their main quality. Physical resonance phenomenon in classical mechanics 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  $\lambda_i$  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 or resonance frequencies of the system, and the corresponding eigenvectors are defined as its own forms of oscillations (or simply, natural oscillations).

This paper uses the tensor product of matrices, which is denoted by  $\otimes$  and is widely applied in mathematics, physics, informatics, control theory, *etc.* It is applied 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). 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. Quantum physics uses Hermitian matrices (or self-adjoint matrices) with complex entries and real eigenvalues. The tensor product of two Hermitian matrices gives a new Hermitian matrix.

Correspondingly, the tensor product of matrices is used in our researches of genetic systems represented in matrix forms (Petoukhov, 2016).

By definition, the tensor product of two square matrices  $V$  and  $W$  of the orders  $m$  and  $n$  respectively is the matrix  $Q = V \otimes W = \|v_{ij} * w_{kl}\|$  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 tensor product of matrices with fractals [Gazale, 1999, Chapter X].

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  $\lambda_i$  and  $\mu_j$  respectively, then in their tensor product  $Q = V \otimes W$  all eigenvalues are equal to  $\lambda_i * \mu_j$  (figuratively speaking,  $\lambda_i$  and  $\mu_j$  are inherited in this tensor way).

### **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. 1 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  $H$  and  $h$ , gives the (4\*4)-matrix  $Q = V \otimes W$  with its 4 eigenvalues  $H * H$ ,  $H * h$ ,  $H * h$ ,  $h * h$ . In the second case, the tensor product of (4\*4)-matrices, having the same set of eigenvalues  $HB$ ,  $Hb$ ,  $hB$ ,  $hb$ , gives (16\*16)-matrix with 16 eigenvalues, represented in the tabular form.

One can see that the internal content of the table of inheritance in the dihybrid case (Fig. 1 top) is equal to  $[HH, Hh; Hh, hh] \otimes [BB, Bb; Bb, bb]$ ; 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 ( $n=3, 4, \dots$ ) of the tensor hybridization of vibrosystems can be constructed by analogy.

		maternal spectrum	
		H	h
pat. sp.	H	HH	Hh
	h	Hh	hh

		maternal spectrum			
		HB	Hb	hB	hb
pat. sp.	HB	HHBB	HHBb	HhBB	HhBb
	Hb	HHBb	HHbb	HhBb	Hhbb
	hB	HhBB	HhBb	hhBB	hhBb
	hb	HhBb	Hhbb	hhBb	hhbb

  

		maternal gametes	
		H	h
pat. gam.	H	HH	Hh
	h	Hh	hh

		maternal gametes			
		HB	Hb	hB	hb
pat. gam.	HB	HHBB	HHBb	HhBB	HhBb
	Hb	HHBb	HHbb	HhBb	Hhbb
	hB	HhBB	HhBb	hhBB	hhBb
	hb	HhBb	Hhbb	hhBb	hhbb

Fig. 1. 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. «Pat. sp.» and «pat. gam.» mean «paternal spectrum» and «paternal gametes».

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. 1, bottom). 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. By tradition, dominant alleles of genes are represented by uppercase letters and recessive alleles — by lowercase letters.

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

— 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 resonance frequencies 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 vibrational mechanics since the time of C. 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.

The author has put forward and argued the hypothesis that genetic alphabets are based on systems of resonances [Petoukhov, 2016]. Now we describe new results of studying genetic systems from this standpoint.

### **3. Segregations inside genetic alphabets and the Mendel's law of segregation**

Genetics has arisen from the Mendel's discovery of mathematical regularities in phenomena of inheritance of traits in poly-hybrid crosses of organisms. Mendelian genetics explained these phenomenological regularities, which are observed at the level of the whole organisms, on the base of the idea about dominant and recessive alleles of genes from parent reproductive cells — gametes. By analogy with the Mendelian theory, we introduce below a notion of dominant and recessive resonances of genetic molecules to explain some phenomenological regularities of genetic alphabets, which are based in DNA on nitrogenous bases — adenine A, cytosine C, guanine G and thymine T (uracil U in RNA). In particular we will analyze the known phenomenon of segregation of the set of 64 triplets 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; 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

positions; code meanings of triplets with weak roots depend on their third letter (see details in [Petoukhov, 2016]).

Science does not know why the basic alphabet of DNA consists of the four polyatomic letters A, C, G, T of very simple structures. 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 molecular traits or its absence (Fig. 2): 1) C=T & A=G (according to the binary-oppositional traits: “pyrimidine” or “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, that is strong or weak bonds) [Gumbel *et al.*, 2015; Petoukhov, 2008; Stambuk, 1999]. Below we use traditional denotations of these traits: purine — R, pyrimidine — Y, amino — M, keto — K, strong hydrogen bonds — S, weak hydrogen bonds — W.

TRAITS	G	A	C	T(U)
1) purine (R), pyrimidine (Y)	R	R	Y	Y
2) amino (M), keto (K)	K	M	M	K
3) strong hydrogen bonds (S), weak hydrogen bonds (W)	S	W	S	W

Figure 2. The division of the four-letter alphabet of DNA (RNA) into three binary sub-alphabets in accordance with three binary-oppositional traits, which are interpreted as resonances with their symbols R, Y, M, K, S and W.

Each of traits of nitrogenous bases A, C, G, T(U) in Fig. 2 can be interpreted as connected with its own resonance characteristics. For example, it is obvious that purines may have resonances that differ from the resonances 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 oppositional resonance characteristics (Petoukhov, 2016).

The genetic code lies in the bases of living matter. But what kinds of laws lay in the base of the genetic code itself? Attempts of answering on this question have led the author to the idea about special

biological rules («laws») of segregation of molecular-genetic alphabets. These rules are formally similar to the Mendelian law of segregation, which acts at levels of whole organisms, but they act at molecular levels and, from the standpoint of our modeling approach, they are related with resonances of dominant and recessive types in bases A, C, G, T(U) and in their combinations in DNA and RNA. In this Section we give an explanation of the structure of the natural phenomenon of segregation of the set of 16 doublets into two equal sub-sets, the first of which contains 8 strong doublets and the second one contains 8 weak doublets.

Our model approach considers nitrogenous bases C, G, A, T(U) as carriers of pairs of resonant traits since we postulate that the resonant frequencies and the corresponding oscillatory energies are key factors for encoding. One can see from Fig. 2 that for an unambiguous assignment of each of the nitrogenous bases it is enough to take into account two of its three traits. We will characterize each nitrogenous base in terms of its resonances taken from the oppositional pairs of resonances «M or K» and «Y or R». In quantum mechanics, two resonance frequencies of an oscillator with two degrees of freedom lie on the main diagonal of the diagonal (2\*2)-matrix, which characterizes the oscillator. We will use such matrix representation. For example, adenine A is the single nitrogenous base with the pair of resonance traits M and R, therefore, in such bi-resonance representation, one can write adenine  $A = [M, 0; 0, R]$  (for brevity, we will denote this matrix by the symbol MR). Accordingly, for other nitrogenous bases their bi-resonance representations are the following: cytosine  $C = [M, 0; 0, Y]$  (or briefly MY), guanine  $G = [K, 0; 0, R]$  (or KR), thymine  $T = [K, 0; 0, Y]$  (or KY). These diagonal (2\*2)-matrices characterize quantum mechanical state spaces of all of these objects A, C, G, T.

Corresponding state spaces of doublets and triplets are constructed by means of the tensor product of state spaces of their nitrogenous bases, which are subsystems of doublet and triplets. For example, the state space of the doublet CA is characterized by the diagonal matrix (4\*4):  $[M, 0; 0, Y] \otimes [M, 0; 0, R] = [MM, 0, 0, 0; 0, MR, 0, 0; 0, 0, YM, 0; 0, 0, 0, YR]$  and state space of the doublet AC, which has the inverse order of the same letters, is characterized by another diagonal matrix (4\*4):  $[M,$

$0; 0, R] \otimes [M, 0; 0, Y] = [MM, 0, 0, 0; 0, MY, 0, 0; 0, 0, RM, 0; 0, 0, 0, RY]$ . The tensor product is non-commutative operation. By this reason, the difference of these two matrices is not equal to zero. When recording sequences of nitrogenous bases in their bi-resonance representations, we will separate two-letter symbols of adjacent nitrogenous bases by means of vertical dash: for example the doublet CA will be denoted as MY|MR.

CC	CA	AC	AA		
MY MY	MY MR	MR MY	MR MR		
CT	CG	AT	AG		
MY KY	MY KR	MR KY	MR KR		
TC	TA	GC	GA		
KY MY	KY MR	KR MY	KR MR		
TT	TG	GT	GG		
KY KY	KY KR	KR KY	KR KR		

  

		Maternal gametes	
		H	h
Paternal gametes	h	HH	hh
	H	HH	Hh

Fig. 3. The segregation of the set of 16 doublets into subsets of 8 strong doublets (black color) and 8 weak doublets (white color); under each doublet, bi-resonance traits of its two letters are shown. On the right: the Punnet square for monohybrid crosses of organisms; combinations of alleles H and h, which contain at least one dominant allele H, are marked by black color.

Each of two families of 4 doublets with their first letter from the complementary pair C and G contains of 3 strong doublets and 1 weak doublet (Fig. 3, left). In contrary, each of two other families of 4 doublets with their first letter from another complementary pair A and T contains of 1 strong doublet and 3 weak doublets. But the same ratio 3:1 is realized in the Mendel's law of segregation of traits of whole organisms in the case of monohybrid crosses of organisms, whose gametes contain one dominant allele of a corresponding gene and one recessive allele of the same gene (here we mean the situation of complete dominance, when the effect of the dominant allele completely masks the effect of the

recessive allele). This case of crosses of organisms is traditionally shown by means of the Punnett square with the same mosaic ratio 3:1 (Fig. 3).

Based on this analogy — between segregations of traits in the case of molecular doublets and in the case of whole organisms under the law of Mendel —, the author puts forward the following hypothesis:

— The principle of dominant and recessive factors plays its genetic key role in segregation phenomena not only at the level of whole organisms but also at the level of ensembles of genetic molecules; the mentioned resonances of genetic molecules play roles of dominant and recessive factors in laws of segregation of traits in molecular-genetic ensembles.

This hypothesis allows explaining some features of segregations inside genetic alphabets. In addition it allows thinking that Mendel's laws, which are true at supra-chromosome levels, did not come out of nowhere, but they have precursors in form of phenomena of segregation at sub-chromosomal levels. In this case, some analogies of phenomena of segregations in populations of whole organisms (for example, the division into male and female organisms with their sexual interrelations) can exist in the world of biological molecules, including proteins (Petoukhov, 2004). It could lead to new points of view about existence of appropriate oppositional groups of proteins and about similar interrelations among them, *etc.* It seems to be logical that regularities of the world of macro-organisms reproduce regularities of the bio-molecular world for genetic encoding and a survival of organisms in the chain of generations. We show now one of examples of positive applications of this hypothesis.

In Mendelian genetics, those dominant and recessive factors, which are responsible for segregation at the level of organisms, are called "alleles". In our approach — for a terminological unity — those dominant and recessive factors, which are responsible for segregation at the level of molecular-genetic alphabets, will be called "pro-alleles". We suppose that mentioned molecular resonances of nitrogenous bases play the role of such «pro-alleles». Let us show how the idea of dominant and recessive resonances of nitrogenous bases (Fig. 2) explains the segregation of strong and weak doublets inside the mentioned four families of doublets, presented in Fig. 3. It is obvious that inside each of families of 4 doublets

in tabular quadrants (Fig. 3), the second letter in each doublet defines a strong or weak character of the doublet.

Initially one can look at two families of doublets with the first letter C or G in them (they will be called as the C-family and the G-family of doublets). Each of these families contains 3 strong doublets (CC, CT, CG and GC, GT, GG correspondingly) and 1 weak doublet (CA and GA) (Fig. 3, left). In both mentioned doublets CA and GA, their second letter — adenine A — is the carrier of two resonance pro-alleles M and R. By analogy with combinations of dominant and recessive alleles in the case of monohybrid crosses of organisms in Mendelian genetics (Fig. 3, right), one should conclude that — in the C-family and G-family of doublets — the resonances M and R are recessive pro-alleles in the second letters of all the doublets. Correspondingly, two oppositional resonances K and Y play the role of dominant pro-alleles in the second letters of all the doublets. By analogy with the Mendelian scheme of complete dominance, we assume for these families, that any pair of resonance pro-alleles, which contains at least one of dominant pro-alleles K and Y, defines the dominant character of the second letter of a doublet and, by this reason, the dominant character of the doublet as a whole. In each of the C-family and G-family, 3 mentioned doublets contain these dominant resonances K and Y in their second letters (CC, CT, CG and GC, GT, GG) and only 1 doublet does not contain them in its second letter (CA and GA, which are weak doublets).

Now let us turn to other two families of doublets with the first letter A or T in them (the A-family and the T-family of doublets). Each of these families has the opposite ratio of quantities of strong and weak doublets (Fig.3): 3 weak doublets (AA, AT, AG and TA, TT, TG correspondingly) and 1 strong doublet (AC and TC). In both named doublets AC and TC, their second letter — cytosine C — is the carrier of two pro-alleles M and Y, which should be interpreted as recessive pro-alleles. Then two opposite resonances K and R play the role of dominant pro-alleles in the second letters of all doublets of these families. By analogy with the Mendelian scheme of complete dominance, one can again assume that any pair of resonance pro-alleles, which contains at least one of dominant pro-alleles K and R, defines the dominant character of the appropriate second letter of a doublet. In each of the A-family and

T-family, 3 named doublets contain these dominant resonances K and R in their second letters (AA, AT, AG and TA, TT, TG correspondingly) and only 1 doublet does not contain them in its second letter (AC and TC).

It should be specially noted that resonances Y and R correspondingly play the oppositional roles of dominant and recessive pro-alleles in the C-family and G-family of doublets, but in the A-family and T-family, they play the inverse roles of recessive and dominant pro-alleles. But in Mendelian genetics it is well known that dominant and recessive characteristics are not absolute features, but they are relative: the same trait is dominant or recessive depending on the biological environment of its manifestation. For example, a trait of baldness is dominant at men and recessive at women. Therefore, to explain the phenomenon of the reverse segregation concerning strong and weak doublets in these families of doublets, it is sufficient to take by analogy the following. The C-family and G-family of doublets are conditionally "male" families, in which the resonance Y of the second letter of each doublet is one of dominant pro-alleles and the resonance R is one of resonance pro-alleles for the considered phenomenon. In contrast, the A-family and T-family of doublets are conditionally "female" families, in which the same resonances Y and R are correspondingly the recessive and dominant pro-alleles of the second letter of each doublet. In other words, the first letter of each doublet defines, what kind of resonances Y or R in the second letter of the doublet will be dominant or recessive. Our modeling approach has shown that members of the molecular alphabet of 16 doublets are resonance hybrid entities, which are similar to hybrids in Mendelian genetics of organisms.

Modern science explains Mendel's laws on the base of division of pairs of homological chromosomes. Mendel's laws do not be spread to levels below the level of chromosomes. Correspondingly, the rules of segregation of the molecular alphabet of 16 doublets, which are described in our article, have an independent character in relation to Mendel's laws since they cannot be deduced from them [Petoukhov, 2004].

#### **4. Dyadic groups of binary-oppositional resonances, genetic alphabets and hypercomplex numbers**

This Section shows various aspects of logic connections of genetic alphabets with modulo-2 addition and dyadic groups of binary numbers. Modulo-2 addition is utilized broadly in computer technology and the theory of discrete signal processing as the fundamental operation for binary variables. By definition, the modulo-2 addition of two numbers, written in binary notation, is made in a bitwise manner in accordance with the following rules:  $0 \oplus 0 = 0$ ,  $0 \oplus 1 = 0 \oplus 1 = 1$ ,  $1 \oplus 1 = 0$  ( $\oplus$  is the symbol for modulo-2 addition). By means of modulo-2 addition, binary  $n$ -bit numbers form so called dyadic groups, including  $2^n$  members. For example, the set of binary 2-bit numbers 00, 01, 10, 11 forms a dyadic group, in which modulo-2 addition serves as the group operation [Harmuth, 1989]. The distance in this symmetry group is known as the Hamming distance. Below we show that the structural organization of genetic systems is related to logic of modulo-2 addition.

The work [Petoukhov, 2016] noted that the binary-oppositional structure of resonance characteristics of members of the genetic alphabet A, C, G, T(U) (Fig. 2) can be connected with binary numbers for using logic of their dyadic groups in operating genetic binary computers on the base of resonances inside organisms. Correspondingly, each of the pairs of binary-oppositional resonances “R or Y”, “M or K”, “S or W” of this alphabet (Fig. 2) can correspond to its own binary units: Y=0 and R=1; M=0 and K=1; S=0 and W=1.

The theory of discrete signal processing uses so called  $(2^n \times 2^n)$  matrices of dyadic shifts, in each of which three dyadic groups of binary  $n$ -bit numbers are employed for binary numerations of its rows, columns and cells [Ahmed, Rao, 1975]. Fig. 4 shows the simplest examples of such  $(2^n \times 2^n)$  matrices, where  $n = 1, 2$ , for two dyadic groups: 0, 1 and 00, 01, 10, 11. Numeration of any matrix cell is given by modulo-2 addition of numerations of its row and column. Let us use these classical numeric matrices of dyadic shifts to represent the specificity of genetic alphabets, members of which are carriers of the binary-oppositional resonance characteristics.

For matrices of genetic alphabets in Fig. 4, one can denote binary numerations of columns by means of the first pair Y=0 and R=1 and binary numerations of rows – by means of the second pair M=0 and K=1. In this case, we get a coordinate grid, in which each cell contains those nitrogenous bases A, C, G or T, which are carriers of resonances depicted in symbolic numerations of the row and the column of the cell. For example, inside these resonant coordinates, the intersection of resonances M and R from numerations of rows and columns always defines inside appropriate cells adenine A, which is the carrier of this pair of resonances M and R (Fig. 2). In addition, one can see from the (2\*2)-matrix in Fig. 4 that inside cells, each of nitrogenous bases has its own binary representation: C=G=0, A=T=1. From this standpoint, each of doublets inside its cell is represented by a corresponding binary combination: for example, the doublet AG is read as binary number 10, which coincides with the binary numeration of its cell in (4\*4)-matrix in Fig. 4. One can check that such binary readings of all doublets inside their cells in Fig. 4 coincide with binary numerations of their cells in classical matrices of dyadic shifts. The (4\*4)-matrices of doublets in Fig. 3 and 4 are identical.

	Y(0)	R(1)		YY (00)	YR (01)	RY (10)	RR (11)
M(0)	MY	MR	MM	MY MY	MY MR	MR MY	MR MR
	C (0)	A (1)	(00)	CC (00)	CA (01)	AC (10)	AA (11)
K(1)	KY	KR	MK	MY KY	MY KR	MR KY	MR KR
	T (1)	G (0)	(01)	CT (01)	CG (00)	AT (11)	AG (10)
			KM	KY MY	KY MR	KR MY	KR MR
			(10)	TC (10)	TA (11)	GC (00)	GA (01)
			KK	KY KY	KY KR	KR KY	KR KR
			(11)	TT (11)	TG (10)	GT (01)	GG (00)

Figure 4. Matrices of dyadic-group representations of resonance traits for genetic alphabets of 4 monoplets and 16 doublets. Numerations of rows and columns use binary-oppositional resonances (Fig. 2) with the conformity M=0, K=1, Y=0, R=1. Strong doublets are marked by black color.

The distribution of strong and weak doublets inside the alphabet of 16 doublets far from random. In the dyadic-shift matrix of 16 doublets in Fig. 4, one can denote each of strong doublets (black color) by number

+1 and each of weak doublets by opposite number -1. In the result, a numeric matrix  $P$  arises (Fig. 5), each rows of which coincides with one of Rademacher functions known in theory of discrete signal processing. The dyadic-shift decomposition of this matrix  $P$  shows that  $P$  is the sum of four sparse matrices:  $P = P_0 + P_1 + P_2 + P_3$  (Fig. 5). This set of 4 matrices  $P_0, P_1, P_2, P_3$  is unexpectedly closed relative to multiplication: the product of any two matrices from this set gives a matrix from the same set. This property is expressed by the multiplication table coinciding with the multiplication table of hypercomplex numbers known from 1849 year as split-quaternions by J. Cockle (<https://en.wikipedia.org/wiki/Split-quaternion>) (Fig. 5, below). In particular split-quaternions are used in the Poincaré disk model of hyperbolic geometry (Lobachevskian geometry) for the theory of special relativity particularly Minkowski spacetime.

$$P = \begin{vmatrix} 1, -1, 1, -1 \\ 1, 1, -1, -1 \\ 1, -1, 1, -1 \\ -1, -1, 1, 1 \end{vmatrix} = \begin{vmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{vmatrix} + \begin{vmatrix} 0 & -1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 \\ 0 & 0 & 1 & 0 \end{vmatrix} + \begin{vmatrix} 0 & 0 & 0 & -1 \\ 0 & 0 & -1 & 0 \\ 0 & -1 & 0 & 0 \\ -1 & 0 & 0 & 0 \end{vmatrix} + \begin{vmatrix} 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & -1 \\ 1 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 \end{vmatrix}$$
  

*	$P_0$	$P_1$	$P_2$	$P_3$
$P_0$	$P_0$	$P_1$	$P_2$	$P_3$
$P_1$	$P_1$	$-P_0$	$P_3$	$-P_2$
$P_2$	$P_2$	$-P_3$	$P_0$	$-P_1$
$P_3$	$P_3$	$P_2$	$P_1$	$P_0$

*	1	i	j	k
1	1	i	j	k
i	i	-1	k	-j
j	j	-k	1	-i
k	k	j	i	1

Fig. 5. The dyadic-shift decomposition of the matrix  $P = P_0 + P_1 + P_2 + P_3$ , where  $P_0$  is the identity matrix. Bottom: the multiplication table of the sparse matrices  $P_0, P_1, P_2, P_3$  is identical to the multiplication table of split-quaternions (<https://en.wikipedia.org/wiki/Split-quaternion>).

So, the numeric matrix  $P$ , which was received from the genetic matrix based on the idea about dominant and recessive resonances in 16 doublets, represents the split-quaternion with unit coordinates:  $P = 1 + i + j + k$ , where  $i, j, k$  are basis elements of split-quaternions. This unexpected result testifies that the logic of organization of molecular-

genetic systems - in relation to strong and weak doublets - is connected with the multiplication table of split-quaternions.

The alphabet of bases A, C, G, T(U) is divided into two sub-alphabets in the ratio 3:1 in accordance with another phenomenological genetic feature. Thymine T has a unique status and differs from other three letters A, C and G: 1) only thymine T is replaced by another molecule U (uracil) in transferring from DNA to RNA; 2) only thymine T hasn't the functionally important amino group  $\text{NH}_2$ . This binary opposition can be expressed as:  $A = C = G = +1$ ,  $T = -1$ . All letters of each of doublets can be replaced to these numbers for numeric representation of the doublet as the product of these numbers. In the result, the dyadic-shift matrix of 16 doublets (Fig. 4) gets its numeric representation in a form of the Hadamard matrix  $H = [1, 1, 1, 1; -1, 1, -1, 1; -1, -1, 1, 1; 1, -1, -1, 1]$ , rows of which coincide with a complete orthogonal system of Walsh functions for 4-dimensional space.

Hadamard matrices and their Walsh functions are one of main tools in informatics of noise-immunity coding and in digital signal processing. On the basis of Hadamard matrices, 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. Hadamard matrices are used in quantum computers ("Hadamard gates") and in quantum mechanics in the form of unitary operators, *etc.* [Ahmed, Rao, 1975; Seberry, Wysocki, Wysocki, 2005]. Dyadic-shift decompositions of some Hadamard matrices show their connections with systems of hypercomplex numbers (see for example [Petoukhov, 2008a, 2008b, 2010]). Hadamard matrices play basic role in the sequency analysis [Harmuth, 1970, 1977, 1989], which is one of important types of spectral analysis in communication technologies and which has found extensive applications in electronics, acoustics, optics, and so forth. Genetic coding systems provide phenomena of noise-immunity of genetic information, and our results has revealed that genetic systems are phenomenologically connected with Hadamard matrices. (By analogy with the alphabet of 16 doublets, one can show

that phenomenology of the alphabet of 64 triplets is connected with Hadamard (8\*8)-matrices).

### **5. Some concluding remarks**

The concept of resonances is important for information studies and the quest for transdisciplinarity, reflected in books [Burgin, 2010; Hofkirchner, 2013] since it is one of the main concepts in modern science in the whole. This concept serves as a bridge among many scientific fields for their mutual enrichment.

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. In biology there are many interesting works concerning resonances and vibrations. For example, one can note the followings.

L. Pauling (1940) has created the theory of resonance in structural chemistry to explain the formation of hybrid bonds in molecules. The real 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 individually. Pauling supposed that living organisms are chemical in nature, and resonances in their molecules should be very essential for biological phenomena.

S. Ji [2012, 2015] postulates an analogy between enzymic catalysis and blackbody radiation, which was modeled by Planck due to his idea about huge number of resonances. He has noted that some important biological phenomena are described by histograms, which are analogical to histograms of blackbody radiations. This author has proposed a generalization of the Planck equation for modeling many

biological phenomena, having long-tailed histograms. By analogy with the principle of quantization of energy in quantum mechanics, Ji postulates a quantization of free energy levels in enzymes. He also proposes an original theory of molecular machines with using Franck-Condon mechanisms concerning vibronic transitions, which are simultaneous changes in electronic and vibrational energy levels of a molecule. He also proposes an original theory of molecular machines with using Franck-Condon mechanisms concerning vibronic transitions,

Genetic encoding provides innate algorithms of animal motions. For example, newborn turtles and crocodiles, when they hatched from their eggs, crawl due to quite coordinated movements ahead to water without any training from anybody; centipedes crawl by means of coordinated movements of a great number of their legs on the basis of inherited algorithms of control. In these motions, a great number of muscle elements works in a coordinated manner and with economy of energy. We study such problems of dependence of inherited structures and processes from the genetic code by means of the concept of systemic-resonance genetics.

In our opinion, an organism can be seen as a musical synthesizer with multiple settings of inherited resonant modes [Darvas *et al.*, 2012; Petoukhov, 2015]. 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.

In the frame of the concept of systemic-resonance genetics, the author has proposed the bases of “genetic” music on Fibonacci-stages scales [Petoukhov, 2008; Darvas *et al.*, 2012]. This new direction of musical culture is been developing now in the Moscow P.I. Tchaikovsky Conservatory. This Conservatory has represented the first concert of

genetic music on 4 June 2015 in Vienna in the frame of the International conference «IS4IS Summit Vienna 2015». Video of fragments of this concert with some explanations is located at website <http://youtu.be/gagKLDuO9z8>.

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