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Hyperbolic Numbers in Modeling Genetic Phenomena

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Abstract. The article is devoted to applications of 2-dimensional hyperbolic numbers and their algebraic 2^n-dimensional extensions in modeling some genetic and cultural phenomena. Mathematical properties of hyperbolic numbers and of their bisymmetric matrix representations are described in a connection with their application to analyze the following structures: alphabets of DNA nucleobases; inherited phyllotaxis phenomena; Punnett squares in Mendelian genetics; the psychophisical Weber-Fechner law; long literary Russian texts (in their special binary representations). New methods of algebraic analysis of the harmony of musical works are proposed, taking into account the innate predisposition of people to music. The hypothesis is put forward that sets of eigenvectors of matrix representations of basis units of 2^n-dimensional hyperbolic numbers play an important role in transmitting biological information and that they can be considered as one of foundations of coding information at different levels of biological organization. In addition, the hypothesis about some analogue of the Weber-Fechner law for sequences of spikes in single nerve fibers is formulated. The proposed algebraic approach is connected with the theme of a grammar of biology and applications of bisymmetric doubly stochastic matrices. Applications of hyperbolic numbers reveal hidden interrelations between structures of different biological and physical phenomena. They lead to new approaches in mathematical modeling genetic phenomena and innate biological structures.

Keywords: hyperbolic numbers, matrix, eigenvectors, genetics, Punnett squares, Fibonacci numbers, phyllotaxis, music harmony, literary texts, doubly stochastic matrices

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1 Introduction

Living bodies are a huge number of various molecules interconnected by quantum-mechanical and stochastic relationships. These sets of molecules have an amazing ability to inherit the biological characteristics of organisms to next generations. G. Mendel, in his experiments with plant hybrids, found that the transmission of traits during the crossing of organisms occurs in accordance with certain algebraic rules, despite the colossal heterogeneity of molecular structures of their bodies. In genetics textbooks, these algebraic rules of polyhybrid crossbreeding are presented since 1906 in the form of Punnett squares resembling mathematical square matrices in their structure. Mendel also proposed a model for explanation of the observed rules, introducing the idea of binary-oppositional forms of the existence of factors of inheritance of traits: dominant and recessive forms.

This article continues the search for algebraic models of the natural features of genetic structures and of inherited macrobiological phenomena. As known, the key difference between living and inanimate objects is as follows: inanimate objects are controlled by the average random movement of millions of their particles, while in a living organism, genetic molecules have a dictatorial effect on the entire living organism. By this reason, the author focuses on studing of the system of genetic alphabets and of the genetic code in the form of mathematical matrices constructed on binary-oppositional features of DNA alphabets.

On this way the article addresses the issues of coding information in the genetic system. In a broad sense, code is usually understood as correspondence between two sets of characters. For example, from this point of view a usual phone book can be considered as a coding system, in which its phone numbers encodes names of people. But this article considers analogies of the genetic code with more complex kinds of codes termed as algebraic codes and algebra-geometric codes, which are widely used in modern communication technologies for algorithmic providing a noise-immunity transfer of information. Obviously, the genetic coding of information has noise immunity, which allows the transfer of genetic information from

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ancestors to descendants along the generation chain in very difficult and different living conditions of organisms. The study of possible algorithms for noise-immunity transfer of genetic information is an important scientific task, the successful solution of which can give a lot of useful for engineering, medical, biotechnological and othersciences. It is about unraveling the bioinformational patents of living matter.

This article draws special attention to structural analogies of the molecular system of genetic coding with one of known types of multidimensional hypercomplex numbers commonly called hyperbolic numbers (although other their names are also used in the literature: double numbers, Lorentz numbers, etc.). As known, this type of hypercomplex numbers can be represented by bisymmetric matrices, which - in special cases - are doubly stochastic matrices having many applications in linear programming, theory of games and optimisations, etc. and interesting for their apllication in algebraic biology.

The main task of mathematical natural sciences is the creation of mathematical models of natural systems. Development of models and formalized theories depends highly on those mathematical notions and instruments, on which they are based. Modern science knows that different natural systems could possess their own individual geometries and their own individual arithmetic [Kline, 1982]. Various kinds of multi-dimensional numbers – complex numbers, hyperbolic numbers, dual numbers, quaternions and other hypercomplex numbers – are used in different branches of modern science. They have played the role of the magic tool for development of theories and calculations in problems of heat, light, sounds, fluctuations, elasticity, gravitation, magnetism, electricity, current of liquids, quantum-mechanical phenomena, special theory of relativity, nuclear physics, etc. For example, in physics thousands of works - only in XX century – were devoted to quaternions of Hamilton (their bibliography is in [Gsponer, Hurni, 2008].

The idea about special mathematical peculiarities of living matter exists long ago. For example V.I. Vernadsky put forward the hypothesis on a non-Euclidean geometry of living nature [Vernadsky, 1965]. It seems an important task to investigate what systems of multi-dimensional numbers are connected or can be connected with ensembles of parameters of the genetic code and inherited biological peculiarities. Some results of such investigation are presented in this article. They are connected with hyperbolic numbers and their algebraic extensions, matrix forms of which give a new class of mathematical models in biology. Author's results described in this article are related in particularly to works by O. Bodnar who noted that ontogenetic transformations of phyllotaxis lattices in plants can be formaly modelled by hyperbolic rotations, which are particular cases of hyperbolic numbers and are well known in the special theory of relativity (Lorentz transformations) [Bodnar, 1992, 1994]. On this basis he stated that geometry of living bodies has structural relations with the Minkovsky geometry. Another evidence in favor of structural relaltions of inherited biological phenomena with hyperbolic rotations was shown in the work [Smolyaninov, 2000], which analyzed problems of locomotion control and put forward ideas of the "locomotor theory of relativity".

It is obvoius that all physiological systems must be argued with a genetic coding system in order to be genetically encoded for their survival and inheritance into next generations. For this reason, the structural organization of physiological systems can bear the imprint of the structural features of molecular genetic systems. Our study aims to identify such relationships of inherited physiological structures with the molecular genetic system. Taking into account

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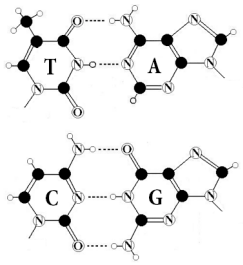
known data about ratios of musical harmony in parametric organization of DNA molecules, new algebraic approaches are proposed for analyzing hidden harmony of musical pieces.

2 Matrix representations of DNA alphabets and hyperbolic numbers

In DNA molecules DNA genetic information is written in sequences of 4 kinds of nucleobases: adenine A, cytosine C, guanine G and thymine T. They form a DNA alphabet of 4 monoplets. In addition, DNA alphabets of 16 doublets and 64 triplets also exist. It is known [Fimmel, Danielli, Strüngmann, 2013; Petoukhov, 2008; Petoukhov, He, 2010; Stambuk, 1999] that these four nucleobases A, C, G and T are interrelated due to their symmetrical peculiarities into the united molecular ensemble with its three pairs of binary-oppositional traits or indicators (Fig. 2.1):

1) Two letters are purines (A and G), and the other two are pyrimidines (C and T). From the standpoint of these binary-oppositional traits one can denote C = T = 0, A = G = 1;
2) Two letters are amino-molecules (A and C) and the other two are keto-molecules (G and T). From the standpoint of these traits one can designate A = C = 0, G = T = 1;
3) The pairs of complementary letters, A-T and C-G, are linked by 2 and 3 hydrogen bonds, respectively. From the standpoint of these binary traits, one can denote C = G = 0, A = T = 1.



№	Binary Symbols	C	A	G	T/U
1	$\mathbf{0_1}$ — pyrimidines $\mathbf{1_1}$ — purines	$\mathbf{0_1}$	$\mathbf{1_1}$	$\mathbf{1_1}$	$\mathbf{0_1}$
2	$\mathbf{0_2}$ — amino $\mathbf{1_2}$ — keto	$\mathbf{0_2}$	$\mathbf{0_2}$	$\mathbf{1_2}$	$\mathbf{1_2}$
3	$\mathbf{0_3}$ — three hydrogen bonds; $\mathbf{1_3}$ — two hydrogen bonds	$\mathbf{0_3}$	$\mathbf{1_3}$	$\mathbf{0_3}$	$\mathbf{1_3}$

Fig. 2.1. Left: the four nitrogenous bases of DNA: adenine A, guanine G, cytosine C, and thymine T. Right: three binary sub-alphabets of the genetic alphabet on the basis of three pairs of binary-oppositional traits or indicators.

Taking into account the phenomenological fact that each of DNA-letters C, A, T and G is uniquely defined by any two kinds of mentioned binary-oppositional indicators (Fig. 2.1), these genetic letters can be represented by means of corresponding pairs of binary symbols, for example, from the standpoint of two first binary-oppositional indicators. It is convenient for us - for the further description - use at the first position of each of letters its binary symbol from the second pair of binary-oppositional indicators (the indicator "amino or keto": C=A=0, T=G=1) and at the second positions of each of letters its binary symbol from the first pair of binary-oppositional indicators (the indicator "pyrimidine or purine": C=T=0, A=G=1). In this case the letter C is represented by the binary symbol 0_20_1 (that is as 2-bit binary number), A – by the symbol 0_21_1, T – by the symbol 1_20_1, G – by the symbol 1_21_1. Using

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these representations of separate letters, each of 16 doublets is represented as the concatenation of the binary symbols of its letters (that is as 4-bit binary number): for example, the doublet CC is represented as 4-bit binary number $0_20_10_20_1$, the doublet CA – as 4-bit binary number $0_20_10_21_1$, etc. By analogy, each of 64 triplets is represented as the concatenation of the binary symbols of its letters (that is as 6-bit binary number): for example, the triplet CCC is represented as 6-bit binary number $0_20_10_20_10_20_1$, the triplet CCA – as 6-bit binary number $0_20_10_20_10_21_1$, etc. In general, each of n-plets is represented as the concatenation of the binary symbols of its letters (below we will not show these indexes 2 and 1 of separate letters in binary representations of n-plets but will remember that each of positions corresponds to its own kind of indicators from the first or from the second set of indicators in Fig. 2.1).

It is convenient to represent DNA-alphabets of 4 nucleotides, 16 doublets, 64 triplets, … 4^n n-plets in a form of appropriate square tables (Fig. 2.2), which rows and columns are numerated by binary symbols in line with the following principle. Entries of each column are numerated by binary symbols in line with the first set of binary-oppositional indicators in Fig. 2.1 (for example, the triplet CAG and all other triplets in the same column are the combination "pyrimidine-purin-purin" and so this column is correspondingly numerated 011). By contrast, entries of each of rows are numerated by binary numbers in line with the second set of indicators (for example, the same triplet CAG and all other triplets in the same row are the combination "amino-amino-keto" and so this row is correspondingly numerated 001). In such tables (Fig. 2.2), each of 4 letters, 16 doublets, 64 triplets, … takes automatically its own individual place and all of them are arranged in a strict order.

It is essential that these 3 separate genetic tables form the joint tensor family of matrices since they are interrelated by the known operation of the tensor (or Kronecker) product of matrices [Bellman, 1960]. So they are not simple tables but matrices. By definition, under tensor multiplication of two matrices, each of entries of the first matrix is multiplied with the whole second matrix. The second tensor power of the (2*2)-matrix [C, A; T, G] of 4 DNA-letters gives automatically the (4*4)-matrix of 16 doublets; the third tensor power of the same (2*2)-matrix of 4 DNA-letters gives the (8*8)-matrix of 64 triplets with the same strict arrangement of entries as in Fig. 2.2. In this tensor construction of the tensor family of genetic matrices, data about binary-oppositional traits of genetic letters C, A, T and G are not used at all. So, the structural organization of the system of DNA-alphabets is connected with the algebraic operation of the tensor product. It is important since the operation of the tensor product is well known in mathematics, physics and informatics, where it gives a way of putting vector spaces together to form larger vector spaces. The following quotation speaks about the crucial meaning of the tensor product: «*This construction is crucial to understanding the quantum mechanics of multiparticle systems*» [Nielsen, Chuang, 2010, p. 71].

	0	1
0	C	A
1	T	G

	00	01	10	11
00	CC	CA	AC	AA
01	CT	CG	AT	AG
10	TC	TA	GC	GA
11	TT	TG	GT	GG

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	000	001	010	011	100	101	110	111
000	CCC	CCA	CAC	CAA	ACC	ACA	AAC	AAA
001	CCT	CCG	CAT	CAG	ACT	ACG	AAT	AAG
010	CTC	CTA	CGC	CGA	ATC	ATA	AGC	AGA
011	CTT	CTG	CGT	CGG	ATT	ATG	AGT	AGG
100	TCC	TCA	TAC	TAA	GCC	GCA	GAC	GAA
101	TCT	TCG	TAT	TAG	GCT	GCG	GAT	GAG
110	TTC	TTA	TGC	TGA	GTC	GTA	GGC	GGA
111	TTT	TTG	TGT	TGG	GTT	GTG	GGT	GGG

Fig. 2.2. The square tables of DNA-alphabets of 4 nucleotides, 16 doublets and 64 triplets with a strict arrangement of all components. Each of tables is constructed in line with the principle of binary numeration of its column and rows on the basis of binary-oppositional traits of the nitrogenous bases (see explanations in the text).

In the DNA double helix, complementary nucleobases C and G are connected by 3 hydrogen bonds and complementary nucleobases A and T are connected by 2 hydrogen bonds. One can denote their typical connections with hydrogen bonds by expressions C=G=3 and A=T=2. Replacing in the (2*2)-matrix [C, A; T, G] (Fig. 2.2) symbols C, A, T and G by their numbers of hydrogen bonds 3 and 2, a numeric matrix [3, 2; 2, 3] appears (Fig. 2.3). The second and the third tensor powers of this matrix $[3, 2; 2, 3]^{(n)}$, where n = 2, 3, generate numeric (4*4)- and (8*8)-matrices in Fig. 2.3, which automatically represent symbolic matrices of 16 doublets and 64 triplets in Fig. 2.2 from the standpoint of the product of their numbers of hydrogen bonds. For example the doublet CA is replaced by number 3*2=6 and the triplet AGT is replaced by number 2*3*2=12. These genetic matrices are closely connected by their structures with so called matrices of dyadic shifts, which are known in digital information technology of noise immune coding and which are described below in the Appendix I. See also some thematic details and argumentations for using 2^n-dimensional hyperbolic numbers and dyadic shifts in matrix genetics and algebraic biology in ([Petoukhov, 2019 c]).

3	2
2	3

9	6	6	4
6	9	4	6
6	4	9	6
4	6	6	9

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27	18	18	12	18	12	12	8
18	27	12	18	12	18	8	12
18	12	27	18	12	8	18	12
12	18	18	27	8	12	12	18
18	12	12	8	27	18	18	12
12	18	8	12	18	27	12	18
12	8	18	12	18	12	27	18
8	12	12	18	12	18	18	27

Fig. 2.3. Numeric representations of the tensor family of symbolic matrices (Fig. 2.2) of 4 monoplets, 16 doublets and 64 triplets from the standpoint of their numeric characteristics of hydrogen bonds C=G=3 and A=T=2.

Fig. 2.4 shows that the matrix [3, 2; 2, 3] is decomposed into sum of two sparse matrices, one of which is the identity matrix (j_0 = [1, 0; 0, 1]) and the second matrix j_1 = [0, 1; 1, 1]) represents imaginary unit of hyperbolic numbers since $j_1^2 = j_0$. The set of these matrices j_0 and j_1 is closed relative to multiplication and defines the multiplication table of algebra of hyperbolic numbers (Fig. 2.4, right).

$$\begin{vmatrix} 3, 2 \\ 2, 3 \end{vmatrix} = 3*\begin{vmatrix} 1, 0 \\ 0, 1 \end{vmatrix} + 2*\begin{vmatrix} 0, 1 \\ 1, 0 \end{vmatrix} = 3*j_0 + 2*j_1;$$

*	1	j_1
1	1	j_1
j_1	j_1	1

Fig. 2.4. The decomposition of the matrix [3, 2; 2, 3] into two sparse matrices, where matrices j_0 and j_1 are matrix representations of real and imaginary units of algebra of hyperbolic numbers with the shown multiplication table of these units.

Here we should remind that two-dimensional hyperbolic numbers are written in linear notation as $m_1 = a*\mathbf{1}+b*\mathbf{j}$ (where **1** is the real unit; **j** is the imaginary unit with the property $\mathbf{j} \neq \pm\mathbf{1}$ but $\mathbf{j}^2 = \mathbf{1}$; *a*, *b* are real coefficients). These numbers are used in physics and mathematics and they have also synonimical names: "split-complex numbers", “double numbers” and "perplex numbers". The collection of all hyperbolic numbers forms algebra over the field of real numbers [Harkin, Harkin, 2004; Kantor, Solodovnikov, 1989]. The algebra is not a division algebra or field since it contains zero divisors. Addition and multiplication of hyperbolic numbers are defined by (2.1):

$$(x+jy)+(u+jv)=(x+u)+j(y+v); \quad (x+jy)(u+jv)=(xu+yv)+j(xv+yu) \qquad (2.1)$$

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This multiplication is commutative, associative and distributes over addition.

A hyperbolic number has its matrix form of representation: [a, b; b, a] = a*[1, 0; 0, 1] +b*[0, 1; 1, 0] where [1, 0; 0, 1] is the identity matrix representing real basis unit; [0, 1; 1, 0] represents imaginary basis unit. Fig. 2.4 shows the matrix representation of hyperbolic numbers a***1**+b***j** for the case a = 3 and b = 2. The symmetric matrices [1, 0; 0, 1] and [0, 1; 1, 0] representing these real and imaginary unites are orthogonal matrices.

If a^2-b^2 = 1, then the matrix [a, b; b, a] defines hyperbolic rotations known in the special theory of relativity as Lorentz transformations. Hyperbolic rotations are usually expressed by a symmetric matrix (2.2) through hyperbolic cosine «cosh» and hyperbolic sine «sinh» since $\cosh^2 x - \sinh^2 x = 1$ [Collins Concise Dictionary, 1999; Shervatov, 1954; Stakhov, 2009]:

$$\begin{vmatrix} \cosh x, & \sinh x \\ \sinh x, & \cosh x \end{vmatrix} \qquad (2.2)$$

Symmetric matrices that represent hyperbolic numbers have real eigenvalues and orthogonal eigenvectors (which distinguishes them from non-symmetic matrix representations of complex numbers). Such symmetric matrices form the basis of the theory of resonances of oscillatory systems with many degrees of freedom, and are also metric tensors from the point of view of Riemannian geometry.

The second tensor power of the bisymmetric matrix [a, b; b, a], which represents hyperbolic numbers, is decomposed into 4 sparse matrices e_0, e_1, e_2 and e_3 with real coefficients *aa, ab ba* and *bb* (Fig. 2.5). The used decomposition is based on the known principle of dyadic shifts described below in the Appendix I.

The set of matrices e_0, e_1, e_2 and e_3 is closed relative to multiplication and satisfies to the multiplication table in Fig. 2.5. The set of these (4x4)-matrices corresponds to algebra of 4-dimensional numbers $aa*e_0 + ab*e_1 + ba*e_2 + bb*e_3$, where the matrix e_0 represents the real unit 1 and matrices e_1, e_2 and e_3 represent imaginary units. These 4-dimensional numbers are algebraic extensions of 2-dimensional hyperbolic numbers and for simplicity they can be termed "4-dimensional hyperbolic numbers" (in our previous publications we termed them "hyperbolic matrions" [Petoukhov, 2008; Petoukhov, He, 2010]). Each of matrices e_0, e_1, e_2 and e_3 is an orthogonal matrix with its determinant +1.

By comparing Fig. 2.3 and Fig. 2.5, one can see that the numeric (4*4)-matrix of hydrogen bonds in Fig. 2.3 represents 4-dimensional hyperbolic number $9e_0+6e_1+6e_2+4e_3$ where e_0 is the identity matrix representing real unit 1. By analogy, the numeric (8*8)-matrix in Fig. 2.3 represents 8-dimensional hyperbolic number $27j_0+18j_1+18j_2+12j_3+18j_4+12j_5+12j_6+8j_7$ where j_k are basis units of 8-dimensional hyperbolic numbers.

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$$\begin{vmatrix} a, b \\ b, a \end{vmatrix}^{(2)} = \begin{vmatrix} aa, ab, ba, bb \\ ab, aa, bb, ba \\ ba, bb, aa, ab \\ bb, ba, ab, aa \end{vmatrix} = aa \begin{vmatrix} 1\,0\,0\,0 \\ 0\,1\,0\,0 \\ 0\,0\,1\,0 \\ 0\,0\,0\,1 \end{vmatrix} + ab \begin{vmatrix} 0\,1\,0\,0 \\ 1\,0\,0\,0 \\ 0\,0\,0\,1 \\ 0\,0\,1\,0 \end{vmatrix} + ba \begin{vmatrix} 0\,0\,1\,0 \\ 0\,0\,0\,1 \\ 1\,0\,0\,0 \\ 0\,1\,0\,0 \end{vmatrix} +$$

$$+ bb \begin{vmatrix} 0\,0\,0\,1 \\ 0\,0\,1\,0 \\ 0\,1\,0\,0 \\ 1\,0\,0\,0 \end{vmatrix} = aa*\mathbf{1} + ab*e_1 + ba*e_2 + bb*e_3 .$$

*	**1**	e_1	e_2	e_3
1	**1**	e_1	e_2	e_3
e_1	e_1	**1**	e_3	e_2
e_2	e_2	e_3	**1**	e_1
e_3	e_3	e_2	e_1	**1**

Fig. 2.5. The decomposition of the matrix [a, b; b, a]$^{(2)}$, representing 4-dimensional hyperbolic numbers, into 4 sparse matrices, the set of which is closed relative to multiplication. The multiplication table for this set is shown at the right. The symbol **1** denotes the identity matrix e_0.

In a general case, 2^n-dimensional hyperbolic (or double) numbers are hypercomplex numbers and they possess, by definition, the following features. They contain 2^n basis units e_k (one real unit and 2^n-1 imaginary units), which are interrelated by a symmetric table of their mutual multiplication where all $e_k^2 = +1$ ($k = 0, 1, 2,..., 2^n$-1).

By analogy with Figs. 2.4 and 2.5, the higher tensor powers n = 3, 4, 5, … of the bisymmetric matrix [a, b; b, a] produce bisymmetric matrices [a, b; b, a]$^{(n)}$, which can be also decomposed into 2^n sparse matrices, the set of which is closed relative to multiplication and which define appropriate multiplication tables of algebras of 2^n-dimensional hypercomplex numbers m_n (which were termed "hyperbolic matrions" of the order n in our previous publications [Petoukhov 2008; Petoukhov, He, 2010]). These decompositions use a structural similarity of the matrices [a, b; b, a]$^{(n)}$ with matrices of dyadic shifts described below in the Appendix I.

It is useful to rewrite the multiplication table in Fig. 2.5 into a form where all decimal indexes of basis units e_0, e_1, e_2 and e_3 are shown in their binary notations: e_{00}, e_{01}, e_{10} and e_{11} (Fig. 2.6).

*	e_{00}	e_{01}	e_{10}	e_{11}
e_{00}	e_{00}	e_{01}	e_{10}	e_{11}
e_{01}	e_{01}	e_{00}	e_{11}	e_{10}
e_{10}	e_{10}	e_{11}	e_{00}	e_{01}
e_{11}	e_{11}	e_{10}	e_{01}	e_{00}

Fig. 2.6. The multiplication table in algebra of 4-dimensional hyperbolic numbers where indexes of basis units are shown in their binary notations e_{00}, e_{01}, e_{10} and e_{11} in contrast to their decimal notations e_0, e_1, e_2 and e_3 in Fig. 2.5.

One can see from Fig. 2.6 that in all cases a result of the product of two basis units ($e_p*e_k = e_s$) is equal to that basis unit e_s whose binary index s is equal to a result of modulo-2 addition for binary indexes p and k of the factors e_p and e_k (under the operation of modulo-2

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addition the following rules are true: 0+0=0, 1+1=0, 0+1=1, 1+0=1). In other words the following equation (2.3) for bimary indexes is true:

$$e_p * e_k = e_{p+k} \quad (2.3)$$

For example, a result of the product e_2*e_3 is equal to e_1 since decimal indexes 2 and 3 are expressed by binary numbers 10 and 11 whose modulo-2 addition gives the binary number 01 refered to decimal number 1. This method of binary operations with indexes to calculate a result of the product of any two basis units is true not only for 4-dimensional hyperbolic numbers but also for other 2^n-dimensional hyperbolic numbers. The equation (2.3) is especially useful in cases of high values n when it is difficult to address to multiplication tables having 2^n*2^n sizes each time when you need to know a result e_s of the product of basis units $e_p*e_k = e_s$. (For example, the Appendix II contains matrix representations of basis units of 32-dimensional hyperbolic numbers, which are useful for mathematical musicology).

For this you should represent indexes p and k in their binary notation (inside a complete set of n-bit binary numbers) and calculate their binary sum $p+k$ on the basis of the known operation of modulo-2 addition where the following rules are true: 0+0=0, 1+1=0, 0+1=1, 1+0=1. The result of such modulo-2 addition is a searched index s in its binary notation. For example, if you multiplicate two 2^3-dimensional hyperbolic numbers each other, the complete set of 3-bit binary numbers is the following: 000, 001, 010, 011, 100, 101, 110, 111 (they correspond decimal numbers 0, 1, 2, 3, 4, 5, 6, 7). To calculate a result of multuplication of basis units e_3*e_5, you take decimal indexes 3 and 5 in their binary notation 011 and 101. Their modulo-2 addition gives binary number 110, which corresponds decimal number 6. In such way we get the search result: $e_3*e_5=e_6$.

3 Hyperbolic and Fibonacci numbers in phyllotaxis modeling

Fibonacci numbers F_n form an additive sequence such that each number is the sum of the two preceding ones: $F_n = F_{n-1} + F_{n-2}$ (Table 3.1).

Table 3.1. The Fibonacci sequence.

n	1	2	3	4	5	6	7	8	9	10	…
F_n	1	1	2	3	5	8	13	21	34	55	…

Fibonacci numbers are strongly related to the golden ratio $\varphi = (1+5^{0.5})/2$. Binet's formula (3.1) expresses the nth Fibonacci number in terms of n and the golden ratio, and implies that the ratio of two consecutive Fibonacci numbers tends to the golden ratio as n increases:

$$F_n = (\varphi^n - (-\varphi^{-1}))/5^{0.5} \quad (3.1)$$

In biology, it has long been known that, for example, in many plant objects the spiral arrangement of their bioorganisms form ordered patterns (shoots of plants and trees, seeds in the heads of sunflowers, scales of coniferous cones and pineapples, etc.). These patterns are

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determined by overlapping left and right oriented spiral lines - parastichies. To characterize phyllotaxis of such botanical objects, usually indicate two parameters: number of left spirals and number of right spirals, which are observed on the surface of phyllotaxis objects. Phyllotaxis of structures with such patterns is described by ratios of neighboring Fibonacci numbers:

$$F_{n+1}/F_n: \quad 2/1, 3/2, 5/3, 8/5, 13/8, 21/13, 34/21, \ldots \tag{3.2}$$

$$(F_{n+1}/F_n) \rightarrow (F_{n+2}/F_{n+1}): 2/1 \rightarrow 3/2 \rightarrow 5/3 \rightarrow 8/5 \rightarrow 13/8 \rightarrow 21/13 \rightarrow \ldots \tag{3.3}$$

The sequence (3.2) is termed the "parastichic sequence" [Jean ,2006; Petoukhov, 1981]. It seems natural to use 2-dimensional hyperbolic numbers for modeling these 2-parametric patterns in phyllotaxis objects and their ontogenetic transformations. In this approach, proposed by the author, the sequence (3.2) of phyllotaxis ratios is transformed into additive sequences (3.4, 3.5) reflecting linear notation of appropriate hyperbolic numbers and their matrix representations (we call sequences (3.4, 3.5) as parastichic sequences of hyperbolic numbers):

$$F_{n+1} + jF_n: \ 2 + j, 3 + j2, 5 + 3j, 8 + 5j, 13 + 8j, 21 + 13j, 34 + 21j, \ldots. \tag{3.4}$$

$$\left|\begin{matrix} F_{n+1}, F_n \\ F_n, F_{n+1} \end{matrix}\right| : \left|\begin{matrix} 2, 1 \\ 1, 2 \end{matrix}\right|, \left|\begin{matrix} 3, 2 \\ 2, 3 \end{matrix}\right|, \left|\begin{matrix} 5, 3 \\ 3, 5 \end{matrix}\right|, \left|\begin{matrix} 8, 5 \\ 5, 8 \end{matrix}\right|, \left|\begin{matrix} 13, 8 \\ 8, 13 \end{matrix}\right| \ldots \tag{3.5}$$

In this approach, to define a hyperbolic number u+jv, which transforms a hyperbolic number $F_{n+1} + jF_n$ into its neighboring hyperbolic number $F_{n+2} + jF_{n+1}$ from the sequence (3.4), the following simple equation (3.6) should be solved:

$$(F_{n+1} + jF_n)(u + jv) = (F_{n+2} + jF_{n+1}) \tag{3.6}$$

The solution to this equation (3.6) gives the following expressions (3.7) for components of the desired hyperbolic number u + jv:

$$u = F_{n+1}/F_n + (-1)^{n+1} * F_{n-1} / (F_n * (F_n^2 - F_{n-1}^2)), \quad v = (-1)^n / (F_n^2 - F_{n-1}^2) \tag{3.7}$$

In the case of such components (3.7), $u^2 - v^2 \neq 1$ and the appropriate matrix [u, v; v, u] does not present a hyperbolic rotation in the sense of expression (2.2). But this matrix can be rewriting into the form (10) where the matrix of a hyperbolic rotation (in the sense of expression (2.2)) is multiplied by a coefficient $(u^2 - v^2)^{0.5}$:

$$[u, v; v, u] = (u^2 - v^2)^{0.5} [u(u^2 - v^2)^{-0.5}, v(u^2 - v^2)^{-0.5}; v(u^2 - v^2)^{-0.5}, u(u^2 - v^2)^{-0.5}] \tag{3.8}$$

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Now let us describe results of the author's study of eigenvalues of the symmetric matrices in the parastichic sequence (3.5). Each of these matrices $[F_{n+1}, F_n; F_n, F_{n+1}]$ has two eigenvalues, which are equal to two Fibonacci numbers again: F_{n+2} and F_{n-1}. One can noted that these eigenvalues are the sum and the difference of the Fibonacci components of the original hyperbolic number $F_{n+1} + jF_n$ since $F_{n+2} = F_{n+1} + F_n$ and $F_{n-1} = F_{n+1} - F_n$. The ratio F_{n+2}/F_{n-1} of such eigenvalues defines a new sequence (11) of Fibonacci ratios, which tend to φ^3 as n increases:

$$F_{n+2}/F_{n-1}: \quad 3/1, 5/1, 8/2, 13/3, 21/5, 34/8, 55/13, \ldots. \qquad (3.9)$$

By analogy with expressions (3.2, 3.4, 3.5) such pair of eigenvalues F_{n+2} and F_{n-1} can be considered as components of a new hyperbolic number $F_{n+2} + jF_{n-1}$. In this case the sequence of ratios (3.9) is transformed into additive sequences (3.10, 3.11) reflecting linear notation of appropriate hyperbolic numbers and their matrix presentations:

$$F_{n+2} + jF_{n-1}: \quad 3 + j, 5 + j, 8 + j2, 13 + j3, 21 + j5, 34 + j8, 55 + j13, \ldots. \qquad (3.10)$$

$$\left| \begin{matrix} F_{n+2}, F_{n-1} \\ F_{n-1}, F_{n+2} \end{matrix} \right| : \left| \begin{matrix} 3, 1 \\ 1, 3 \end{matrix} \right|, \left| \begin{matrix} 5, 1 \\ 1, 5 \end{matrix} \right|, \left| \begin{matrix} 8, 2 \\ 2, 8 \end{matrix} \right|, \left| \begin{matrix} 13, 3 \\ 3, 13 \end{matrix} \right|, \left| \begin{matrix} 21, 5 \\ 5, 21 \end{matrix} \right| \ldots \qquad (3.11)$$

Each of symmetric matrices $[F_{n+2}, F_{n-1}; F_{n-1}, F_{n+2}]$ of the sequence (3.11) has two eigenvalues, which are again equal to two Fibonacci numbers multiplied by a factor 2 (twice the Fibonacci numbers): $2F_{n+1}$ and $2F_n$. Ratios $2F_{n+1}/2F_n$ of such eigenvalues form a sequence, which is identical to the initial parastichic sequence (3.2). Using the Binet's formula (3.1), all members of these sequences can be additionally expressed through the golden ratio φ in integer powers. This procedure of analysis of the eigenvalues of new and new sequences of symmetric matrices, representing hyperbolic numbers by analogy with sequences (3.4, 3.5, 3.10, 3.11), can be repeated as long as desired, obtaining a hierarchy of eigenvalues of the matrices based on Fibonacci numbers multiplied by a factor 2 at corresponding steps of the iterative procesure.

The following important point should be emphasized. In contrast to the traditional additive series of one-dimensional Fibonacci numbers, the author introduces an additive series of two-dimensional hyperbolic numbers and an additive series of (2*2)-matrices representing these numbers and defining an additional additive series of eigenvalues of these matrices (3.4, 3.5, 3.10, 3.11). As far as we know, such Fibonacci series of two-dimensional numbers have not been described in the literature by anyone, and therefore they can be considered new in the extensive subject matter of Fibonacci numbers and their applications (some of author's results of the study of additive series of 4-dimensional hyperbolic Fibonacci numbers will be presented below).

Similar results are obtained by considering the additive series of two-dimensional hyperbolic Lucas numbers and the additive series of their matrix representations, which

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determine the additive series of eigenvalues of these symmetric matrices (these results are been publishing in a separate article). Here one can remind that one-dimensional Lucas numbers form the series $L_{n+2} = L_n + L_{n+1}$: 2, 1, 3, 4, 7, 11, 18, ... , which is also known in phyllotaxis laws [Jean, 2006]. A study of additive series of complex numbers, whose components are Fibonacci numbers, and of their ordinary representations by non-symmetric matrices gives also interesting additive series of their eigenvalues but in form of complex numbers.

It should be noted that the study of the eigenvalues of symmetric matrices has special meaning due to the fact that in the theory of oscillations symmetric matrices are matrix representations of oscillatory systems with many degrees of freedom. Moreover, the eigenvalues of such a matrix determine the resonant frequencies of the corresponding oscillatory system. The described results on the properties of inherited phyllotaxis phenomena with their Fibonacci ratios, represented by symmetric matrices and their matrix eigenvalues, are important, in particular, for the concept of multi-resonance genetics, which connects structural features of molecular-genetic systems with resonances of oscillatory systems [Petoukhov, 2016].

4 Fibonacci sequences of 2^n-dimensional hyperbolic numbers

This Section continues the theme of additive series of hyperbolic numbers, coordinates of which are Fibonacci numbers. Now we turn to algebraic extensions of hyperbolic numbers in forms of 2^n-dimensional hyperbolic numbers. Let us consider an additive sequence (4.1) of 4-dimensional hyperbolic numbers $F_{n+3}e_0+F_{n+2}e_1+F_{n+1}e_2+F_ne_3$ with Fibonacci coordinates from (Table 3.1). In this sequence, each member is equal to the sum of two previous members:

$$3e_0+2e_1+1e_2+1e_3;\ 5e_0+3e_1+2e_2+1e_3;\ 8e_0+5e_1+3e_2+2e_3;\ 13e_0+8e_1+5e_2+3e_3;\ \ldots \quad (4.1)$$

A corresponding matrix representation of each member from (4.1) has 4 eigenvalues, which can be considered again as coordinates of a new 4-dimensional hyperbolic number. The author reveals that these new 4-dimensional hyperbolic numbers form a new additive sequence (4.2):

$$1e_0+1e_1+3e_2+7e_3;\ 1e_0+3e_1+5e_2+11e_3;\ 2e_0+4e_1+8e_2+18e_3;\ 3e_0+7e_1+13e_2+29e_3;\ldots \quad (4.2)$$

The sequence (4.2) combines Fibonacci and Lucas sequences in the following sense. In its 4-dimensional hyperbolic numbers, coordinates of basis elements e_0 and e_2 are Fibonacci numbers and coordinates of basis elements e_1 and e_3 are Lucas numbers: 3, 1, 4, 7, 11, 18, 29, … . Such aggregation of Fibonacci and Lucas numbers resembles a phyllotaxis-like locations of amino acid residues in the helices of polypeptides for various molecular chains - 11/3, 18/5, 29/8, 47/13; here fraction numerators are Lucas numbers and fraction denominators are

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Fibonacci numbers. These bio-molecular phenomena of polypeptides configurations are described in the fundamental book [Frey-Wissling, Muhlethaler, 1965].

A matrix representation of each member of the sequence (4.2) has 4 eigenvalues, which can be considered again as coordinates of a new 4-dimensional hyperbolic number. These 4-dimensional hyperbolic numbers form a new additive sequence (4.3):

$$-8e_0-4e_1+4e_2+12e_3;\ -12e_0-8e_1+4e_2+20e_3;\ -20e_0-12e_1+8e_2+32e_3;\ -32e_0-20e_1+12e_2+32e_3;..\quad (4.3)$$

Comparing sequences (4.1) and (4.3) reveals that a set of coordinates of each member of the sequence (4.3) repeats - with a factor 4 - a set of coordinates of the corresponding member of the sequence (4.1) with accuracy up to signs and a cyclic permutation of coordinates. For example, the first member of (4.1) contains coordinates 3, 2, 1, 1 and the first member of (4.3) contains coordinates -4*2, -4*1, 4*1, 4*3. This procedure of calculating repeating additive sequences of 4-dimensional hyperbolic numbers associated with Fibonacci and Lucas numbers can be repeated as long as desired. Similar results are received for additive sequences of 2^n-dimensional hyperbolic numbers with Fibonacci coordinates in cases $n = 3, 4, \ldots$.

5 Hyperbolic numbers and the Weber-Fechner law

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 differentinnate phenomena on the general basis of hyperbolic numbers and its algebraic extensions. This Section is devoted to the main psychophysical law by Weber-Fechner and its structural connection with phyllotaxis laws through hyperbolic numbers. The innate Weber-Fechner law states that the intensity of the perception is proportional to the logarithm of stimulus intensity; it is expressed by the equation (5.1):

$$p = k*\ln(x/x_0) = k*\{\ln(x) - \ln(x_0)\} \qquad (5.1)$$

where p - the intensity of perception, x – stimulus intensity, x_0 - threshold stimulus, ln – natural logarithm, k – a weight factor. It is known that different types of inherited sensory perception are subordinated to this law: sight, hearing, smell, touch, taste, etc. Because of this law, the power of sound in physics and engineering technologies is measured on a logarithmic scale in decibels.

One can suppose that the innate Weber–Fechner law is the law especially for nervous system. But it is not so since its meaning is much wider because it holds true in many kinds of lower organisms without a nervous system in them: "*this law is applicable to chemo-tropical, helio-tropical and geo-tropical movements of bacteria, fungi and antherozoids of ferns, mosses and phanerogams ... . The Weber-Fechner law, therefore, is not the law of the nervous system and its centers, but the law of protoplasm in general and its ability to respond to stimuli*" [Shults, 1916, p.126]

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Let us show that hyperbolic numbers are related to the Weber-Fechner law, which is based on the natural logarithm (5.1). Historically the natural logarithm was formerly termed the hyperbolic logarithm, as it corresponds to the area under a hyperbola [Klein, 2004; Shervatov, 1954]. History of hyperbolic logarithms is described for example in the book [Klein, 2004]. As known, 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. 5.1, left). It means that two points of the hyperbola with their coordinates $(x, 1/x)$ and $(x_0, 1/x_0)$, where $x > 1$ and $x_0 > 1$, define values of natural logarithms $\ln(x)$ and $\ln(x_0)$. Subtraction $\ln(x) - \ln(x_0) = \ln(x/x_0)$ expresses the intensity of perception p in the expression (5.1) of the Weber–Fechner law (Fig. 5.1, right). A change of a stimulus intensity x_1 into a new stimulus intensity x_2 corresponds to a hyperbolic rotation, which transforms points of this hyperbola each into other and defines an appropriate change of intensity of perception: $\Delta p = k*\ln(x_2/x_1)$. One can add that each point $(x, 1/x)$ of this hyperbola, where $x \geq 1$, can be naturally interpreted as hyperbolic number with positive coordinates $x+x^{-1}j$, which is represented by a bisymmetric matrix with positive entries (such matrices coincide with doubly stochastic matrices under an appropriate matrix normalization; see below Section 12 on doubly stochastic matrices and their applications).

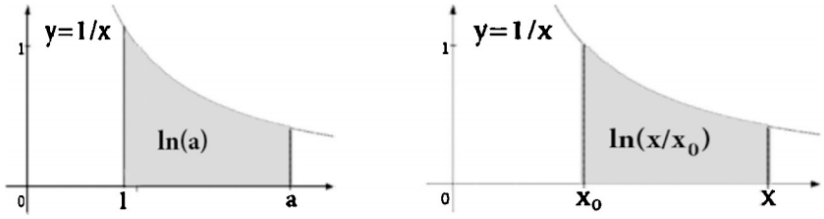

Fig. 5.1. Natural logarithm as the area under the hyperbola $y = 1/x$. Left: $\ln(a)$ is equal to the area under the hyperbola from 1 to a. Right: $\ln(x/x_0)$ is equal to the area under the hyperbola from x_0 to x.

Hyperbolic rotations are particular cases of 2-dimensional hyperbolic numbers. This analysis gives evidences that our sensory perception obeys the same structural principles as morphogenesis with its phyllotaxis laws and that these principles can be effectively modelling on the basis of hyperbolic numbers.

Phyllotaxis laws are related with the golden ratio (or the golden section) $\varphi = (1+5^{0.5})/2 = 1{,}618\ldots$. Here one can attract attention to the well-known phenomenon of human visual perception, which consists in the aesthetic preference for proportions of the golden ratio. People are endowed with an aesthetic feeling that allows them to prefer certain proportions and forms in specific situations (review materials can be found in the book [Petoukhov, 1981, Appendix 1]). A classic example is given by the proportion of the golden section, which is featured for a long time in architecture and theoretical works on aesthetics, although it sometimes causes criticism due to the efforts of some authors to absolutize its significance. The famous American neurophysiologist and one of the founders of cybernetics McCalloch specially studied the aesthetics of this proportion [McCulloch, 1965, c. 395]. He wrote that he spent two years measuring the person's ability to bring an adjustable oblong object to a preferred shape, because he did not believe that human persons prefer the golden ratio or that they could recognize it. They prefer and they can! In repeated experimental constructing the

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most pleasant forms, human persons come to the preference of the golden ratio and they can establish it. As McCulloch concluded one who is able to detect a difference in the twentieth of the length, area or volume, exposes this difference to 1:1,618, and not to 1:1,617 or 1:1,619.

Obviously, if in the ratio 1:1,618 for the smaller and larger sides of a rectangle, the length of the larger side is redenoted as 1, then the relative length of the smaller side will become equal to φ^{-1}=0,618. In other words, these values φ and φ^{-1} in the aesthetics of proportions for our visual perception always go in pairs and therefore they can be considered - in the frame of our approach - as two parts of the single hyperbolic number $\varphi+j*\varphi^{-1}$ whose matrix presentation is $[\varphi, \varphi^{-1}; \varphi^{-1}, \varphi]$. But this hyperbolic number $\varphi+j*\varphi^{-1}$ is related with hyperbolic number 3+j*2, which was shown above as connected with the molecular-genetic system (see Figs. 2.3 and 2.4). Really, $(\varphi+j*\varphi^{-1})^2 = 3+j*2$ or in their matrix presentations:

$$\begin{vmatrix} \varphi, & \varphi^{-1} \\ \varphi^{-1}, & \varphi \end{vmatrix}^2 = \begin{vmatrix} 3, & 2 \\ 2, & 3 \end{vmatrix}$$

Fig. 5.2. The relation of 2-dimensional hyperbolic numbers $\varphi+j*\varphi^{-1}$ and 3+j*2

Below we'll meet again the hyperbolic number 3+j*2 in Sections on relations of hyperbolic numbers with musical harmony and the quint ratio 3/2 (or the pure perfect fifth).

The end of this article contains one additional paragraph with the hypothesis that some analogue of the Weber-Fechner law exists in single nervous fibers for encoding time intervals among action potentials, whose sequences carry information in nervous system.

6 The alphabets of orthogonal vector bases associated with basis units of 2^n-dimensional hyperbolic numbers

Let us remind the essence of the eigenvalues and eigenvectors by means of the matrix A on Fig. 6.1, 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).

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

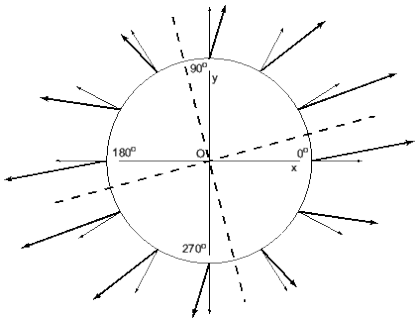

Fig. 6.1. Illustration of actions of the matrix A on vectors [x, y] (from [Zharov, 2002])

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Each basis unit of 2^n-hyperbolic numbers is represented by a corresponding symmetric (2^n*2^n)-matrix, which is an orthogonal matrix and has its own set of orthogonal eigenvectors. This orthogonal set is a corresponding vector basis of 2^n-dimensional space. For example in the case of any 2-dimensional hyperbolic number a*j_0 +b*j_1 (Fig. 2.4) its real component aj_0 is presented by the matrix a*[1, 0; 0 1], which has two orthogonal eigenvectors [1, 0] and [0, 1] independently on value of the coefficient a ($a \neq 0$). This pair of eigenvectors defines the first vector basis of the 2-dimensional space of existance of hyperbolic numbers. The imaginary term bj_1 is presented by the matrix b*[0, 1; 1, 0] (Fig. 2.4), which has another pair of orthogonal eigenvectors [$-2^{-0.5}$, $2^{-0.5}$], [$2^{-0.5}$, $2^{-0.5}$] independently on value of the coefficient b ($b \neq 0$). This pair of eigenvectors defines the second vector basis of the considered 2-dimensional space. In other words, the pairs of eigenvectors are determined only by basis units j_0 and j_1. These two pairs of eigenvector bases can be considered as a two-term vector alphabet of basis units of hyperbolic numbers in case of 2-dimensional space.

A similar situation is true for cases of other 2^n-dimensional hyperbolic numbers and eigenvectors of their matrix representations. For example, in the case of 4-dimensional hyperbolic numbers $ae_0 + b$*$e_1 + c$*$e_2 + d$*e_3, matrix representations of their basis units (see Fig. 2.5) have the following eigenvectors:

- The (4*4)-matrix [1, 0, 0, 0; 0, 1, 0, 0; 0, 0, 1, 0; 0, 0, 0, 1] representing the real unit e_0 has 4 eigenvectors [1, 0, 0, 0], [0, 1, 0, 0], [0, 0, 1, 0], [0, 0, 0, 1];
- The (4*4)-matrix [0, 1, 0 0; 1, 0, 0, 0; 0, 0, 0, 1; 0, 0, 1, 0] representing the first imaginary unit e_1 has 4 eigenvectors [$-2^{-0.5}$, $2^{-0.5}$, 0, 0], [0, 0, $-2^{-0.5}$, $2^{-0.5}$], [0, 0, $2^{-0.5}$, $2^{-0.5}$], [$2^{-0.5}$, $2^{-0.5}$, 0, 0];
- The (4*4)-matrix [0, 0, 1, 0; 0, 0, 0, 1; 1, 0, 0, 0; 0, 1, 0, 0] representing the second imaginary unit e_2 has 4 eigenvectors [$-2^{-0.5}$, 0, $2^{-0.5}$, 0], [0, $2^{-0.5}$, 0, $-2^{-0.5}$], [0, $2^{-0.5}$, 0, $2^{-0.5}$], [$-2^{-0.5}$, 0, $-2^{-0.5}$, 0];
- The (4*4)-matrix [0, 0, 0, 1; 0, 0, 1, 0; 0, 1, 0, 0; 1, 0, 0, 0] representing the third imaginary unit e_3 has 4 eigenvectors [0, $-2^{-0.5}$, $2^{-0.5}$, 0], [$2^{-0.5}$, 0, 0, $-2^{-0.5}$], [$2^{-0.5}$, 0, 0, $2^{-0.5}$], [0, $2^{-0.5}$, $2^{-0.5}$,0].

Correspondingly in the case of 4-dimensional hyperbolic numbers and their space, the 4-term eigenvector alphabet of their 4 basis units exists. In a general case of 2^n-dimensional hyperbolic numbers, the 2^n-term eigenvector alphabet of their 2^n basis units exists. Each member of such alphabet is a set of 2^n orthogonal vectors. The author briefly calls such alphabets of eigenvector bases of matrix representations of basis units of 2^n-dimensional hyperbolic numbers as «hyperbolic eigenvector alphabets» or simply «hyper-alphabets». Here the prefix "hyper" is the beginning of the word "hyperbolic" and its use is additionally justified by the fact that each member of such hyper-alphabet contains in itself 2^n eigenvectors, each of which can be considered – in special cases - as a member of another alphabet of the lower level.

Any transition from one such eigenvector basis into another (that is a transition of one member of such a hyper-alphabet into another) is carried out by means of an orthogonal matrix (orthogonal operator), that is, a real unitary matrix (previously, the structural connection of DNA alphabets with orthogonal matrices was shown by the author in [Petoukhov, 2018a]; unitary operators play a great role in quantum mechanics and quantum computing; for example, all calculations in quantum computers are based on unitary operators). Orthogonal operators preserve the space metric and define transformations of

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proper and improper rotations. Any sequence of basis units (or their sums) of 2^n-dimensional hyperbolic numbers corresponds to a certain sequence of eigenvector bases of these units, and also to a sequence of orthogonal matrices transforming successively these bases. Such algebraic sequences can be used for transmitting information. Taking into account some results of his previous published studies, the author supposes that genetic sequences are related with such algebraic sequences.

Moreover, the author puts forward the hypothesis that alphabets of eigenvectors of matrix representations of basis units of 2^n-dimensional hyperbolic numbers play a key role in transmitting biological information and that they can be considered as a foundation of coding information at different levels of biological organization. The corresponding languages using such alphabets define many inherited phenomenological structures in biology including molecular-genetic structures.

As known, the principle of transmitting information in the form of certain texts composed on the basis of certain "alphabets" is widely used in living organisms: genetic information is recorded in DNA molecules in the form of texts based on the DNA alphabet; music is a sequence of sound frequencies of one or another musical scale (that is, the "alphabet" of note sound frequencies of one octave); literary texts are written on the basis of literary alphabets, etc. The author believes that various alphabets and texts in these bioinformational fields can be effectively modeled and studied on the basis of the presented hidden algebraic alphabets as their joint algebraic foundation. This approach is connected with the theme of a «grammar of biology», which term was introduced by E.Chargaff in the title of his article on DNA peculiarities «Preface to a Grammar of Biology» [Chargaff, 1971] (see also the book [Yamagishi, 2017]).

Since alphabets are used as foundations of corresponding languages, each algebraic hyper-alphabet in 2^n-dimensional spaces with a concrete number n can be considered as a foundation of a corresponding algebraic language. From this point of view, many such algebraic languages using these hyper-alphabets exist in biology.

7 Quint ratios in DNA parameters and musical harmony

As known, thoughts about the key significance of musical harmony in the organization of the world exist from ancient time. For example, one can quote here a classical work of Chinese literature "Spring and Autumn" by Lu Bu We about the fundamental role of music and numbers 3 and 2 as numbers of Heaven and Earth: "*The origins of music lie far back in the past. Music arises from Measure and is rooted in the great Oneness. ... Music is founded on the harmony between Heaven and Earth*" (this citation is taken from the book [Hesse, 2002]. In Ancient China the ratio 3/2, traditionally termed as the quint ratio (or the pure perfect fifth), was used as the fundament of quint music scales. After Ancient Chinese, Pythagoreans also considered numbers 2 and 3 as the female and male numbers (or Yin and Yang numbers), which can give birth to new musical tones in their interconnection. Ancient Greeks attached an extraordinary significance to search of the quint 3:2 in natural systems because of their thoughts about musical harmony in the organization of the world. For example, Archimedes considered as the best result of his life a detection of the quint 3/2 between volumes and surfaces of a cylinder and a sphere entered in it.

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Science has been dealing with the physiological mechanisms of music perception for a long time [Weinberger, 2004]. There is no specialized center of music in the human brain, a sense of love for music can be considered dispersed throughout the body, similar to the dispersion of genetic DNA molecules throughout all of its cells. More than 30 thousand years ago, long before the advent of arithmetic, our ancestors already played stone flutes and bone harps. For example, the bone flute found in France is at least 32 thousand years old. The enjoyment of music is usually explained by the fact that it gives rise to emotions and feelings. Aristotle tried to understand how rhythms and melodies, being only sounds, resemble states of mind. Available data indicate that our affinity for music and musical creativity is biological in nature and the sense of musical harmony is based on innate mechanisms. Therefore, one should look for a connection between the genetic system and musical harmony.

For Europeans the idea of musical harmony is basically connected with the name Pythagoras. The Pythagorean musical scales, which are based on the quint ratio 3/2, played the main role in the Pythagorean's doctrine about a cosmic meaning of musical harmony. Fig. 7.1 shows the known interconnection of sound frequencies of notes of Pythagorean 7-stages scale (a heptatonic scale) on the basis of the ratio 3/2 when notes are spaced in the appropriate octaves.

fa (F)	do (C)	sol (G)	re (D^1)	la (A^1)	mi (E^2)	si (B^2)
87	130	196	293	440	660	990
$\mathbf{(3/2)^{-3}}$	$\mathbf{(3/2)^{-2}}$	$\mathbf{(3/2)^{-1}}$	$\mathbf{(3/2)^{0}}$	$\mathbf{(3/2)^{1}}$	$\mathbf{(3/2)^{2}}$	$\mathbf{(3/2)^{3}}$

Fig. 7.1. The quint sequence of the 7 notes of the Pythagorean musical scale is presented. The upper row shows the notes. The second row shows their frequencies. The third row shows the ratios between the frequencies of these notes to the frequency 293 Hz of the note re (D^1). The designation of notes is given on Helmholtz system. Values of frequencies are approximated to integers.

Pythagoras created the mathematical foundations of ancient Greek music, borrowing in a certian degree some ancient knowledge on musical harmony. His theory used the discovery that the frequency of a vibrating string is inversely proportional to its length and that musical consonances can be represented by the ratios of small integer numbers, first of all the octave ratio 2:1 and the quint ratio 3:2. These ideas became the basic fundamental ones of all music theory from antiquity to even modern times. For most Europeans from antiquity, quint scales in music are connected with this Pythagorean mathematical theory of musical harmony and with divisions of vibrating strings in the quint ratio 3:2.

In a general case, the Pythagorean scale is any scale, which can be constructed from only quint ratios 3:2 and octaves 2:1 [Sethares, 2005, p. 163]. One of known Pythagorean scales is a pentatonical scale, which is a five-stages music scale, all the sounds of which can be arranged in quint ratios. Its example is the set of the following 5 notes with their sound frequencies from Fig. 7.1: do(C)-sol(G)-re(D^1)-la(A^1)-mi(E^2) or respectedly 130-196-293-440-660 Hz. Other examples of Pythagorean scales are tetratonic and tritonic scales, which are correspondingly 4-stages and 3-stages music scales, all the sounds of which can be arranged by the quint ratio, for instance, 130-196-293-440 Hz for the tetratonic scale and 130-196-293 Hz for the tritonic scale.

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The historical fact is that these Pythagorean musical scales on the basis of the quint ratio were used by different civilisations around the world long before Pythagoras without knowledge of any mathematical laws [Apel, 1969; Day-O'Connell, 2007; Christidis, Arapo-poulou, Christi, 2007; Olsen, Sheehy, 1998; Todd Titon, 1996]. For example, the pentatonical scale is the foundation of traditional music of the Chinese, Vietnamese, Mongols, Turkic peoples (Bashkirs, Tatars, Chuvashes, etc.), the Inca Empire and the peoples of the South Andes in general. Pentatonics is also found in European musical folklore and in the oldest layers of the Russian folk song (especially in the so-called calendar ritual songs). Tetratonic music was noted as common in Polynesia and Melanesia. Tetratonic scales were known for example among the Plains Indians, the Arapaho, Blackfoot, Crow, Omaha, Kiowa, Pawnee, Sioux, some Plateau tribes, the Creek Indians, and in the Great Basin region among the Washo, Ute, Paiute, and Shoshone. In the Southwest, the Navajo people also largely used the pentatonic and tetratonic, occasionally also tritonic scales. Tetratonic, as well as tritonic scales, were commonly used by the tribal peoples of India, such as the Juang and Bhuyan of Orissa state [Sudhibhushan Bhattacharya, 1968]. Tetratonic scales are generally associated with prehistoric music [Baines, 1991].

G.Leibniz declared that music is arithmetic of soul, which computes without being aware of it. But what is there in living organisms that determines the special attraction of musical scales on the basis of the quint ratio 3/2 for representatives of various civilizations and epochs? A possible answer lies in the structural features of DNA molecules that are carriers of genetic information in humans and other living organisms. The author has paid attention to the fact that the parametric structure of DNA molecules is connected in many ways with the quint ratio 3/2 and with numbers 3 and 2 at various levels of their parametric organization [Petoukhov, 2008; Petoukhov, He, 2010]. Let us briefly say now about this relation between the musical harmony and structures of genetic molecules.

Molecules of heredity - DNA and RNA – contain sequences of 4 “letters” or nucleobases: adenine (A), cytosine (C), guanine (G), thymine (T) (or uracil U in RNA). Letters A-T(U) and C-G form complementary pairs with 2 and 3 hydrogen bonds in them, respectively. From the standpoint of its sequence of two and three hydrogen bonds, each DNA molecule is a long chain of numbers 2 and 3 of a type 32232332 ....

The genetic code encodes sequences of 20 amino acids in proteins by means of 64 triplets (three-letter words) that represent all possible combinations of these four letters (ATC, TTA, ...). Since A = T = 2, C = G = 3, each triplet has a numeric representation as a product of number of hydrogen bonds of its constituent letters. For example, the triplet ACT is represented by number 2*3*2 = 12. Each of 64 triplets is represented by one of such numbers of hydrogen bonds 2^3=8, 2^2*3=12, 2*3^2=18, 3^3=27, the pairwise relations between which are equal to the quint 3/2 in varying integer degrees (by analogy with music tetratonic scales), for example, 27/8 = $(3/2)^3$, 18/8 = $(3/2)^2$, etc.

Under considering pairs of adjacent triplets, then DNA molecule appears as a quint sequence of 7 kinds of numbers of hydrogen bonds with the following numeric representation: 2^6=64, 2^5*3=96, 2^4*3^2=144, 2^3*3^3=216, 2^2*3^4=324, 2*3^5=486, 3^6=729. Pairwise ratios in this series of numbers are equal to the quint 3/2 in the same powers as in the Pythagoras 7-stage scale in Fig. 7.1. If, for example, the frequency of 87 Hz of the note "F" is compared with the first number 64 of this series, then all other numbers of this series will correspond precisely to the other frequencies of the Pythagoras scale. Then any sequence of triplets (eg, insulin gene GGC-ATC-GTT-GAA-CAG-TGT- ...) can be associated uniquely

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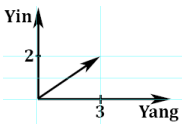
with a sequence of notes of Pythagoras 7-stages scale (figuratively speaking, we have "music of genes in the Pythagoras scale").

Accordingly, each DNA molecule as a chain of hydrogen bonds is characterized by its own sequences of the quint 3/2 in different integer degrees. By analogy with quint musical scales, depending on the chosen lengths of nucleobase fragments of DNA, we have – on the basis of considered hydrogen bonds - various systems for transmitting information signals with quint-power relations between signals.

The quint ratios are realized in DNA not only for the hydrogen bonds of complementary nucleobases, but also for several other parameters, such as sums of atoms in the rings of purines and pyrimidines (numbers 9 and 6 with their ratio 3/2), or sums of protons in the rings of complementary nitrogenous bases (numbers 60 and 40 with their ratio 3/2), and others. Chains of these parameters in DNA form their own sequences of quint ratios, which are similar to sequences of note frequencies in quint scales of music. In other words, Nature created DNA as a plexus of various sequences of quint ratios ("a quint polyphony of DNA"). The harmony of the parametric organization of the genetic system is akin to the musical harmony of the Pythagorean scales.

As it was reminded above, over the centuries from Ancient China to antiquity, the numbers 2 and 3 were considered respectively as female and male numbers (that is as Yin and Yang numbers) forming the important pair. The author proposes their consideration not as separate one-dimensional numbers but as two separate parts of two-dimensional number. Mathematics knows 3 main kinds of two-dimensional numbers: complex numbers, hyperbolic (or double) numbers and dual numbers [Kantor, Solodovnikov, 1989]. Taking into account a set of our results on relations of genetic system and inherited physiological phenomena with hyperbolic numbers, we choice namely hyperbolic numbers for a presentation of these historically known numbers 3 and 2 as two interrelated parts of single two-dimensional number $G_2 = 3+2j$, where j is imaginary unit with its features $j \neq \pm 1$, $j^2 = +1$; the index 2 refers 2-dimensionality of the number G_2. This hyperbolic number can be expressed as a point or a vector on a hyperbolic plane with Cartesian coordinates, in which the axis of abcissus is considered the axis of Yang-numbers, and the axis of ordinates is considered the axis of Yin-numbers. Fig. 7.2 shows this coordinate system and also the matrix form of presentation of hyperbolic numbers with its decomposition into 2 sparse matrices playing the role of real and imaginary basis units of hyperbolic numbers. This matrix [3, 2; 2, 3] is conditionally termed "quint matrix" since its components 3 and 2 give the ratio 3/2. (The same quint matrix [3, 2; 2, 3] appears under a consideration of DNA alphabet C, A, T, G and its three binary sub-alphabets [Petoukhov, 2008, Chapter 2; Petoukhov, He, 2010, Chapter 4]).



$$G_2 = \begin{vmatrix} 3, 2 \\ 2, 3 \end{vmatrix} = 3* \begin{vmatrix} 1, 0 \\ 0, 1 \end{vmatrix} + 2* \begin{vmatrix} 0, 1 \\ 1, 0 \end{vmatrix};$$

*	1	j_1
1	1	j_1
j_1	j_1	1

Fig. 7.2. The graphical and matrix presentation of 2-dimensional hyperbolic number $G_2 = 3 + 2j_1$ (by analogy with Fig. 2.4). The first sparse matrix [1, 0; 0, 1] is the identity matrix, the second sparse matrix [0, 1; 1, 0] presents imaginary unit j_1 having the property $[0, 1; 1, 0]^2 = [1, 0; 0, 1]$. The multiplication table of these sparse matrices, where 1 refers the matrix [1, 0; 0, 1], is also shown at right.

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8 Applications of matrix representations of 2^n-dimensional hyperbolic numbers in musicology

In the Introduction to this article, the important role of hypercomplex numbers in many fields of science has already been mentioned. This Section is devoted to the author's proposal to use in musicology 2^n-dimensional hyperbolic numbers and their matrix representations to study the laws of harmony of the development of themes in musical works (or in other words, the harmony of the plasticity of a musical work). As is known in musicology, the musical theme of a musical work is the basis of its development, the core of the formation of its form. Sometimes a theme is defined as any element, motive, or small musical construction, which is the basis for the further development of musical material. The structure of musical works has a clear logic of construction. Some masterpieces of world classics are literally calculated mathematically. It is no accident that in Ancient Greece, music was included in a number of mathematical sciences.

In musicology, to date, only one-dimensional numbers are used to express sound frequencies and durations of individual notes. The creative possibilities of the language of multidimensional numbers are just waiting for their use in musicology. Music acts on the listener as an operator, changing his state. And this operator's action is determined not by individual notes, but by harmony in the sequence of elements of a musical work ("harmony of plasticity" in music). How to mathematically explore this harmony of plasticity?

For this, the author proposes to use 2^n-dimensional hyperbolic numbers and their matrix representations, which are related with the alphabetic structures of genetic DNA molecules and many inherited physiological structures. The proposed use allows us to represent the sequence of elements of a musical work in the form of:

- a sequence of vectors (or points) of the vector metric space of 2^n-dimensional numbers;
- a sequence of corresponding matrix representations (or matrix operators) of 2^n-dimensional numbers.

Let us explain the scheme of this approach using a simplified example of a conditional musical fragment written on the basis of a musical scale having only three notes, for example, C (do^1), E (mi^1), G (sol^1) of the first octave (Fig. 8.1). Sound frequencies of these notes will be expressed in relative values as usual for the piano keyboard with its equal-tempered scale: 1, $2^{4/12}$, $2^{7/12}$. Durations of notes are traditionally given by the values 1, 2^{-1}, 2^{-2}, 2^{-3}, 2^{-4}, ...

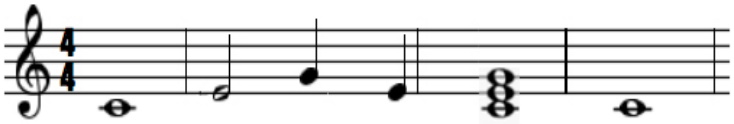

Fig. 8.1. A conditional musical fragment written on the basis of the musical scale having only three kinds of musical notes.

In our approach, for the vector analysis of this musical fragment, it is enough to use 4-dimensional vectors $\check{Z} = a_0\bar{e}_0 + a_1\bar{e}_1 + a_2\bar{e}_2 + a_3\bar{e}_3$ of 4-dimensional hyperbolic numbers. In

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the Cartesian coordinate system of the corresponding 4-dimensional space, we will consider $\bar{e}_0$, $\bar{e}_1$, $\bar{e}_2$, $\bar{e}_3$ as unit vectors of 4 coordinate axes. In this case, the note C with its relative frequency 1 is represented by the unit vector $\bar{e}_1$ of one coordinate axis, the note E with its frequency $2^{4/12}$ - by the vector $2^{4/12}\bar{e}_2$ of the second axis, the note G with its frequency $2^{7/12}$ - by the vector $2^{7/12}\bar{e}_3$ of the third axis. Durations 1, 2^{-1}, 2^{-2}, 2^{-3}, ... are represented by vectors of the fourth axis: $\bar{e}_0$, $2^{-1}\bar{e}_0$, $2^{-2}\bar{e}_0$, $2^{-3}\bar{e}_0$, etc.

In elements of musical works, the pitch of each note is not separable from its duration. In our approach, this symbiosis of "frequency + duration" of a musical element is represented by the sum of the named vectors. We also present chords as the sum of the vectors of their sound components and duration. Correspondingly four musical measures of the presented fragment (Fig. 8.1) are been recording as a sequence of vectors of a given 4-dimensional discrete space (Fig. 8.2):

$$\left| \bar{e}_0+\bar{e}_1 \right| 0,5\bar{e}_0+2^{4/12}\bar{e}_2 ; 0,25\bar{e}_0+2^{7/12}\bar{e}_3 ; 0,25\bar{e}_0+2^{4/12}\bar{e}_2 \left| \bar{e}_0+\bar{e}_1+2^{4/12}\bar{e}_2+2^{7/12}\bar{e}_3 \right| \bar{e}_0+\bar{e}_1 \right|$$

Fig. 8.2. The representation of the sequence of elements of the musical fragments from Fig. 8.1 as the sequence of their vectors.

But for any two vectors, there is a difference vector between them. Therefore, in the described approach, the sequence of musical elements appears additionally as a sequence of 4-dimensional difference vectors of transition from the vector of the previous musical element to the vector of the next musical element. Each such transition vector has a length and a conjugation angle with a subsequent transition vector. A metric analysis of their sequence allows you to study the harmony of the plasticity of a musical work, taking into account the symbiosis of its tonal and temporal organization. Musical works become the subject of metric vector analysis.

Such a vector analysis is possible not only for sequences of separate elements in musical works, but also for sequences of musical measures, periods, etc. This vector approach is suitable for musical works written in a wide variety of musical systems, for example, in 7-stage Pythagorean scale, 12-stages tempered musical scale and in any microchromatic scales. The difference is only in the choice of the corresponding 2^n-dimensional vectors for such vector analysis. For example, for a 7-stage system, it is sufficient to use the vectors of 8-dimensional hyperbolic numbers (seven coordinates are assigned to its 7 stages and one coordinate to durations); for a 12-stage system one can use vectors of 16-dimensional hyperbolic numbers (you assign 12 coordinates to its 12 stages and one coordinate to durations, taking zero values for other 3 coordinates).

In the case of using the described multi-dimensional numbers, cardinally new mathematical personages come into play in musicology: matrix operators, orthogonal bases of multidimensional spaces and orthogonal transformations of such bases related with hyper-alphabets described above in Section 6. These new personages allow significantly encreasing analytical possibilities in musicology by means of those mathematical tools, which are effectively used in many scientific and technology fields.

Now let us turn to using in musicology bisymmetric (2^n*2^n)-matrices, which represent 2^n-dimensional hyperbolic numbers (see above the Section 2). In this case, a musical work is considered as a sequence of matrix operators. For example, a 4-dimensional hyperbolic num-

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ber $a_0\bar{e}_0 + a_1\bar{e}_1 + a_2\bar{e}_2 + a_3\bar{e}_3$ is represented by the (4*4)-matrix, which is the sum of 4 sparse bisymmetric matrices representing 4 basic units e_0, e_1, e_2, e_3 (Fig. 8.3):

$$\begin{vmatrix} a_0 & a_1 & a_2 & a_3 \\ a_1 & a_0 & a_3 & a_2 \\ a_2 & a_3 & a_0 & a_1 \\ a_3 & a_2 & a_1 & a_0 \end{vmatrix} = a_0 \begin{vmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{vmatrix} + a_1 \begin{vmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{vmatrix} + a_2 \begin{vmatrix} 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{vmatrix} + a_3 \begin{vmatrix} 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{vmatrix}$$

Fig. 8.3. The decomposition of the matrix representation of 4-dimensional hyperbolic number $a_0\bar{e}_0 + a_1\bar{e}_1 + a_2\bar{e}_2 + a_3\bar{e}_3$.

Under analyzing this musical fragment, one can replace the vector representations of the basic units e_0, e_1, e_2, e_3 (in Fig. 8.2) with their matrix representations (from Fig. 8.3). In this case you pass to a representation of the musical fragment as a sequence of matrices (matrix operators). This introduces into musicology the ideology of matrix analysis from physics, where the action of the matrix operator on the state vector of a system determines a change in its state vector, etc.

Each of bisymmetric (4*4)-matrices, representing e_0, e_1, e_2, e_3 or their linear combinations, has a set of 4 orthogonal eigenvectors (a "hedgehog" set of vectors). Therefore, this musical fragment has a conditional artistic representation in the form of a sequence of "hedgehogs" carrying such 4 orthogonal vectors (Fig. 8.4):

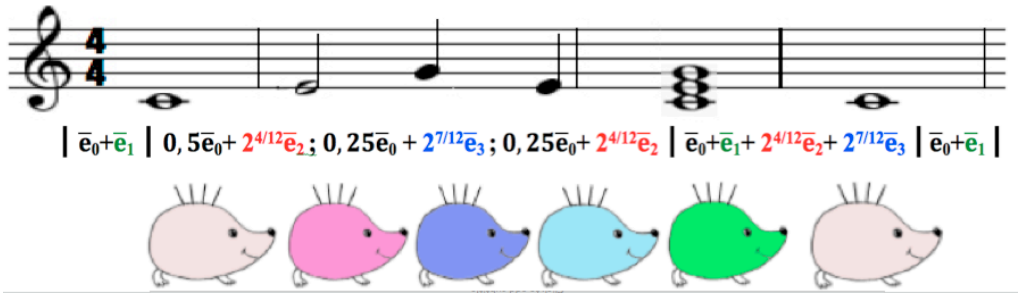

Fig. 8.4. The artistic image of the sequence of sets of 4 orthogonal eigenvectors of bisymmetric matrices, which represent elements of the musical fragment.

The transition from a set of orthogonal eigenvectors of a matrix representing some element of a given musical fragment to a set of orthogonal eigenvectors of a matrix representing a subsequent musical element is determined by a new matrix of corresponding orthogonal transformation. Therefore, a sequence of elements of a musical play corresponds to a sequence of matrices of orthogonal transformations, which transform the said sets of orthogonal eigenvectors into each other. The matrix of each of these orthogonal transformations, in turn, has its own set of orthogonal eigenvectors. Transitions between orthogonal sets of eigenvectors of neighboring matrices of the named sequence are again determined by matrices of some orthogonal transformations, which is accompanied by the appearance of a new - shortened - sequence of matrices of orthogonal transformations with their orthogonal sets of eigenvectors. As a result of repeating this procedure, for each new sequence of matrices of or-

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thogonal transformations that arises, a tree of orthogonal transformations arises (Fig. 8.5). Since orthogonal transformations represent proper and improper rotations in appropriate vector spaces, the development of a musical play from element to element can be artistically imaged as the spinning of dance couples in such multidimensional space.

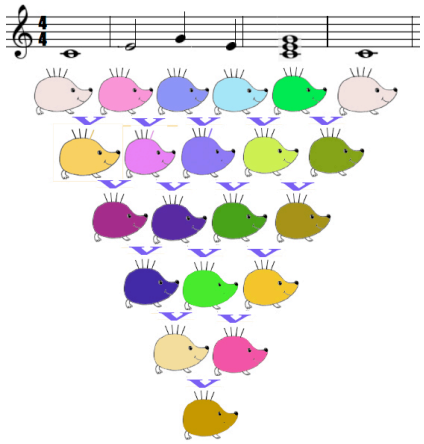

Fig. 8.5. The artistic image of the tree, whose levels show sequences of sets of 4 orthogonal eigenvectors of matrices of orthogonal transformations, which are hiddenly related with the sequence of elements of the musical fragment.

Apparently, ingenious composers intuitively feel the algebraic tonal-temporal harmony of music. Not without reason G.Leibniz argued that music is mathematics of soul, which computes without being aware of it. The deep interest to numerology by I.S. Bach is known, in connection with which some musicologists study the connection of his works with numerology.

A special place in the theme "Music and Mathematics" is occupied by the famous book "Bead Game" by H. Hesse. This book deeply speculates on time, when «*the analytical study of musical values had led to the reduction of musical events to physical and mathematical formulas*» and when there were invented «*the principles of a new language, a language of symbols and formulas, in which mathematics and music played an equal part, so that it became possible to combine astronomical and musical formulas, to reduce mathematics and music to a common denominator*». At its core, the "bead game" is the art of composing a metatext, a synthesis of all branches of art into one, universal art.

Described in this article searches of an adequate system of multidimensional numbers and matrix operators for the analysis and synthesis of musical works can be considered as a continuation of thoughts and beliefs of many musicians and thinkers about the connection between music and mathematics (with an author's addition of modern knowledge on algebraic features of the genetic coding in human and other living organisms). We believe that genetic DNA texts are those metatexts, in the image of which biological texts of various natures are built. This article jointly with the article [Petoukhov, 2019c] show the structural connections of genetic texts with 2^n-dimensional hyperbolic numbers. Taking all of these materials into account, the author proposes to look at music as a bead game with its basis on hyperbolic numbers and corresponding matrix operators.

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9 Advantages of matrix representations of hyperbolic numbers

The matrix forms of presentation of 2^n-dimensional hyperbolic numbers deserve a special attention since they have the following useful properties:

1. This presentation form is based on symmetric matrices, which are closely related with the theory of resonances of oscillatory systems, having many degrees of freedom, [Petoukhov, 2015, 2016]. Symmetrical matrices are related with the theory of resonance of L. Pauling whose book [Pauling, 1940] about this theory in structural chemistry is the most quoted among scientific books of the XX century. 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. Pauling claimed that living organisms are chemical in nature, and resonances in their molecules should be very essential for biological phenomena. 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 was historically the first form of quantum mechanics, which retains its value to this day.
2. These symmetric matrices are Hermitian (self-adjoint) matrices, which play an important role in quantum mechanics. By this reason they can be used in development of applications of ideas and methods of quantum mechanics and quantum informatics in the field of bioinformatics and algebraic biology. In this connection some of author's works [Petoukhov, 2018a,b, 2019a,b; Petoukhov, Petukhova, Svirin, 2019] are devoted to using formalisms of quantum mechanics and quantum informatics in bioinformatics and algebraic biology including analysis of long genetic and and literary texts. For example, in long DNA sequences of nucleobases, where complementary nucleobases C and G (A and T) are linked by 3 (2) hydrogen bonds, 2^n-dimensional hyperbolic numbers $[\%3, \%2; \%2, \%3]^{(n)}$ (where %3 and %2 denote percentages of numbers 3 and 2 of hydrogen bonds in the analyzed DNA sequence; n = 2, 3, 4, 5) effectively models percentages of monoplets, doublets, triplets, tetraplets and pentaplets of these numbers 3 and 2 of hydrogen bonds [Petoukhov, 2018].
3. These symmetric matrices can be interpreted as metric tensors, which are main invariants in Riemanian geometry and which can be used in the theory of morpho-resonance morphogenesis [Petoukhov, 2008, 2015, 2016];
4. These symmetric matrices are related with hyperbolic rotations [ch x, sh x; sh x, ch x], which are particular cases of hyperbolic numbers and are connected with the theory of biological phyllotaxis laws [Bodnar, 1992, 1994; Stakhov, 2009], with problems of locomotion control [Smolyaninov, 2000], with the main psychophysical law of Weber-Fechner (see above and also in [Petoukhov, 2016]), with Lorenz transformations in the special theory of relativity;
5. These bisymmeric matrices are related with doubly stochastic matrices (under an appropriate normalization of bisymmetric matrices), whose using for genetics is described below;

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6. These symmetric matrices are related with the theory of solitons of sine-Gordon equation [Petoukhov, 1999, 2008; Petoukhov, He, 2009]. Such solitons are the only relativistic type of solitons; they were put forward for the role of the fundamental type of solitons of living matter in the book [Petoukhov, 1999].

Symmetric matrices possess a wonderful property to express resonances [Bellman, 1960; Balonin, 2000]. 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 = λ*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 termed its eigenvectors, and the scale factors λ_i with them are termed its eigenvalues or, briefly, spectrum A. 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 and eigenvectors of the matrix A, which are defined by the matrix equation A*s = λ*s, the "characteristic equation" of the matrix A is analyzed: det(A − E) = 0, where E – the identity matrix (see more in [Petoukhov, 2016]). Matrices, which are relevant to the various problems of the theory of oscillations, are usually symmetric real matrices [Gladwell, 2004]. Such matrices have real eigenvalues and their eigenvectors are orthogonal.

Symmetric matrices representing hyperbolic numbers are simultaneously metric tensors by their structure. Metric tensors are main invariants of Riemanian geometry, which can be used for modelling inherited curvilinear forms of biological bodies. By definition, the metric tensor in the *n*-dimensional affine space with the scalar multiplication introduced is defined by the nondegenerate matrix $||g_{ij}||$ under the condition of symmetry $g_{ij} = g_{ji}$ [Rashevskij, 1964], which is satisfied by the structure of bisymmetric matrices of hyperbolic numbers. The coordinates g_{ij} of the metric tensor are the pairwise scalar products of vectors of the frame, on which it is built. If we extract the square root from a bisymmetric matrix, we get a square matrix whose columns are vectors of this frame. It is interesting that the extraction of the square root from quint matrices of 2^n-dimensional hyperbolic numbers $[3, 2; 2, 3]^{(n)}$, which has integer components, get square matrices of 2^n-dimensional hyperbolic numbers $[\varphi, \varphi^{-1}; \varphi^{-1}, \varphi]^{(n)}$ whose components are irrational numbers of the golden section $\varphi = (1+5^{0.5})/2 = 1{,}618\ldots$ in integer powers; the golden section φ is famous in the aesthetics of proportions and described by many authors in a series of inherited physiological systems [Petoukhov, 2008; Petoukhov, He, 2010]. It means that metric tensors, having forms of quint matrices of hyperbolic numbers, are built on a frame of "golden" vectors, all components of which are equal to the golden sections in integer powers.

10 2^n-dimensional hyperbolic numbers and phenomenologic rules of percentages in genetics

The author revealed that in some cases it is possible to use 2^n-dimensional hyperbolic numbers and their matrix representations for modeling some phenomenological rules in biology, first of all, in genetics. In this cases the tensor family of symmetric matrices $[\%S, \%W; \%W, \%S]^{(n)}$ is under consideration, where %S and %W refer to percentages of biological realisation of some events denoted by symbols S and W (%W+%S=100%).

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This tensor family contains matrix representations of 2-dimensional hyperbolic numbers %S + %W*j_1; of 4-dimensional hyperbolic numbers %S*%S + %S*%W*j_1 + %W*%S*j_2 + %W*%W*j_3; of 8-dimensional hyperbolic numbers, etc. Expressions like as %S*%S, %S*%W, %W*%W can be considered as percentages of realisation of doublets SS, SW, WW in chains of these events. Let us show some concrete phenomenologic data.

Any long DNA sequence contains many millions of nucleotides A, C, G, T. For example a DNA filament of the first chromosome of the human genome contains about 250 millions of these letters. In DNA double helixes, nitrogenous bases C-G and A-T form complementary pairs by means of 3 and 2 hydrogen bonds (it can be denoted as C=G=3 and A=T=2). Correspondingly, any DNA sequence contains a long chain of numbers 2 and 3 of hydrogen bonds, for example, 33223223233… . We term such number chains of hydrogen bonds as "hydrogen bond sequences" (briefly, "hydrogen texts"). The author analysed the properties of such long hydrogen bond sequences for many different organisms (here the term "long" means DNA sequences containing ≥ 100000 letters).

Studying such binary "hydrogen texts" 33223223233… of a wide number of various genomes, the author discovered that percentages (or frequencies) of hydrogen monoplets (3, 2), doublets (33, 32, 23, 22), triplets (333, 332, 323, 322, 233, 232, 223, 222), tetraplets and pentaplets in them are subordinated to hidden rules: percentages of monoplets (values %3 and %2) are strongly interrelated with percentages of other H-*n*-plets (*n* = 2, 3, 4, 5). These interrelations are effectively described by a tensor family of matrices $[\%3, \%2; \%2, \%3]^{(n)}$ representing 2^n-dimensional hyperbolic numbers:

- %3 + %2*j (when *n*=1);
- %3*%3 +%3*%2*e_1+%2*%3*e_2+%2*%2*e_3 (when *n*=2);
- etc.

Fig. 10.1 shows one example of matrices from this tensor family: the second tensor power of the percentage matrix $[\%3, \%2; \%2, \%3]^{(2)}$, which represents 4-dimensional hyperbolic number %3*%3 +%3*%2*e_1+%2*%3*e_2+%2*%2*e_3.

$$\begin{vmatrix} \%3, \%2 \\ \%2, \%3 \end{vmatrix}^{(2)} = \begin{vmatrix} \%3*\%3, \%3*\%2, \%2*\%3, \%2*\%2 \\ \%3*\%2, \%3*\%3, \%2*\%2, \%2*\%3 \\ \%2*\%3, \%2*\%2, \%3*\%3, \%3*\%2 \\ \%2*\%2, \%2*\%3, \%3*\%2, \%3*\%3 \end{vmatrix}$$

Fig. 10.1. The second tensor power of the percentage matrix [%3, %2; %2, %3] represents 4-dimensional hyperbolic number %3*%3*e_0+%3*%2*e_1+%2*%3*e_2+%2*%2*e_3.

As it turned out, coefficients of these hyperbolic numbers effectively model percentages of corresponding n-plets in long DNA sequences: for example, the value %3*%2 models the percentage of doublets 32, and the value %2*%3*%3 models the percentage of triplets 233. Knowing only percentages of monoplets %3 and %2, you can predict percentages of dozens of hydrogen *n*-plets in long DNA.

For an illustration of this statement, Fig. 10.2 shows - in a graphical form - an example of phenomenological values of probabilities of all members of alphabets of hydrogen *n*-plets (*n* = 1, 2, 3, 4, 5) in the case of the DNA sequence of the first chromosome of the plant *Arabidopsis thaliana*, which contains 30427671 nucleotide pairs. Simultaneously, Fig.

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10.2 shows model values of these percentages as components of 2^n-dimensional hyperbolic numbers $[q, p; p, q]^{(n)}$, where q=0,35873552 and p=0,64126448, n = 1, 2, 3, 4, 5.

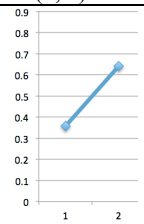
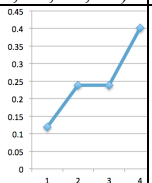
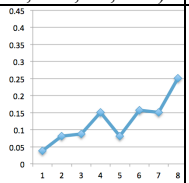
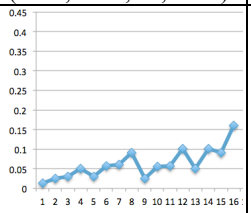
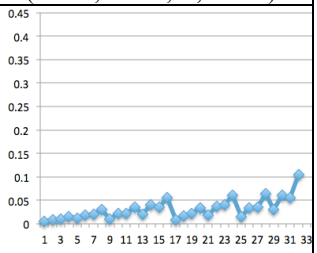
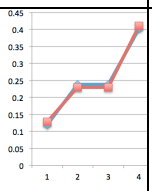
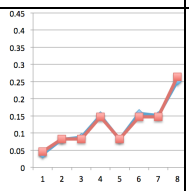
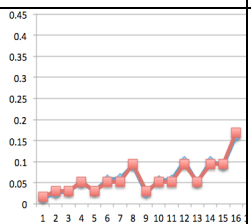
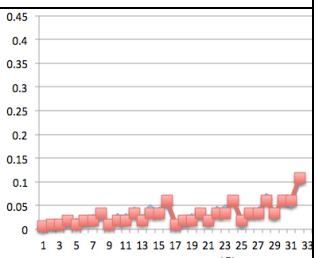
Percentages of 2 monoplets (3, 2)	Percentages of 4 doublets (33, 32, 23, 22)	Percentages of 8 triplets (333, 332, …, 222)	Percentages of 16 tetraplets (3333, 3332, …, 2222)	Percentages of 32 pentaplets (33333, 33332,…, 22222)
 q=0,35873552 p=0,64126448				
q=0,35873552 p=0,64126448	 $[q, p; p, q]^{(2)}$	 $[q, p; p, q]^{(3)}$	 $[q, p; p, q]^{(4)}$	 $[q, p; p, q]^{(5)}$

Fig. 10.2. The graphic representation of percentages of all kinds of hydrogen n-plets (n = 1, 2, 3, 4, 5) in the DNA sequence of the first chromosome of the plant *Arabidopsis thaliana* (initial data relating to this chromosome were accessed from https://www.ncbi.nlm.nih.gov/nuccore/NC_003070.9). Blue points in the graphs show phenomenological percentages of n-plets of numbers of hydrogen bonds, while red points show model values of these probabilities as components of 2^n-dimensional hyperbolic numbers $[q, p; p, q]^{(n)}$, where q and p are percentages of hydrogen bonds 3 and 2 in this DNA.

Fig. 10.3 shows phenomenological and model values of percentages of all members of hydrogen n-plet alphabets (n = 1, 2, 3, 4) for the same DNA sequence as in Fig. 10.2. It can be seen that these model values reproduce phenomenological values with the level of accuracy, which one can see in Fig. 10.2.

Percentages of hydrogen monoplets 3 and 2
Reality: q = [3] = 0,3587; p = [2] = 0,6413
Probabilities of hydrogen doublets (4 kinds of doublets: 33, 32, 23, 22)
Reality: [33] = 0,1198; [32] = 0,2390; [23] = 0,2389; [22] = 0,4023.
Model: [33] = 0,1287; [32] = 0,2300; [23] = 0,2300; [22] = 0,4112.
Percentages of hydrogen triplets (8 kinds of triplets: 333, 332, 323, 322, 233, 232, 223, 222)
Reality: [333]= 0,0385; [332]= 0,0812; [323]= 0,0880; [322]= 0,1507; [233]= 0,0812; [232]= 0,1577; [223]= 0,1514; [222]= 0,2512.
Model: [333]=0,0462; [332]=0,0825; [323]=0,0825; [322]=0,1475; [233]=0,0825; [232]=0,1475; [223]=0,1475; [222]=0,2637.

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Percentages of hydrogen tetraplets (16 kinds of tetraplets: 3333, 3332, 3323, 3322, 3233, 3232, 3223, 3222, 2333, 2332, 2323, 2322, 2233, 2232, 2223, 2222)
Reality: [3333]=0,0132; [3332]=0,0253; [3323]=0,0310; [3322]=0,0502; [3233]=0,0311; [3232]=0,0570; [3223]=0,0601; [3222]=0,0906; [2333]=0,0253; [2332]=0,0560; [2323]=0,0570; [2322]=0,1007; [2233]=0,0502; [2232]=0,1008; [2223]=0,0907; [2222]=0,1607.
Model: [3333]=0,0166; [3332]=0,0296; [3323]=0,0296; [3322]=0,0529; [3233]=0,0296; [3232]=0,0529; [3223]=0,0529; [3222]=0,0946; [2333]=0,0296; [2332]=0,0529; [2323]=0,0529; [2322]=0,0946; [2233]=0,0529; [2232]=0,0946; [2223]=0,0946; [2222]=0,1691.

Fig. 10.3. Phenomenological values (in blue color) and model values (in red color) of percentages of all kinds of hydrogen n-plets (n = 1, 2, 3, 4) in the DNA sequence of the first chromosome of *Arabidopsis thaliana* (appropriate graphs are shown in Fig. 10.2; initial data relating to this chromosome were accessed from https://www.ncbi.nlm.nih.gov/nuccore/NC_003070.9). Numbers in square brackets refer to percentages of corresponding hydrogen n-plets (for example, the symbol [323] refers to the percentage of the hydrogen triplet 323 in the hydrogen sequence of this DNA like 322-232-233-…). All values are rounded to the fourth decimal place.

Similar results have been obtained in our analysis of the plant, *Arabidopsis thaliana*; nematode, *Caenorhabditis elegans*; fruit fly, *Drosophila melanogaster*; house mouse, *Mus musculus;* and Homo Sapiens, drawing on nuclear chromosome data and DNA sequence data obtained from GenBank.

The author has also calculated percentages of all kinds of n-plets (n = 1, 2, 3, 4, 5) in 19 genomes of bacteria and archaea from the full list in the article [Rapoport, Trifonov, 2012, p. 2]: "*Aquifex aeolicus, Acidobacteria bacterium, Bradyrhizobium japonicum, Bacillus subtilis, Chlamydia trachomatis, Chromobacterium violaceum, Dehalococcoides ethenogenes, Escherichia coli, Flavobacterium psychrophilum, Gloeobacter violaceus, Helicobacter pilory, Methanosarcina acetivorans, Nanoarchaeum equitans, Syntrophus aciditrophicus, Streptomyces coelicolor, Sulfolobus solfataricus, Treponema denticola, Thermotoga maritima and Thermus thermophiles*". The calculated sets of these percentages were also modelled on the basis of sets of coordinates of appropriate 2^n-dimensional hyperbolic numbers $[q, p; p, q]^{(n)}$. These results confirm that the proposed model approach on the basis of 2^n-dimensional hyperbolic numbers $[q, p; p, q]^{(n)}$ can be used to obtain idealized models of percentages of all kinds of n-plets in actual long DNA sequences (n = 1, 2, 3, 4, … is much less than the length of such sequences).

The proposed application of 2^n-dimensional hyperbolic numbers allows the prediction of percentages of all kinds of considered hydrogen n-plets in long DNA sequences with a high level of accuracy, using knowledge of percentages of only two numbers - 3 and 2 – of hydrogen bonds in the DNA sequence.

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11 2^n-dimensional hyperbolic numbers and phenomenologic rules of percentages in long literary texts

Impressive recent discoveries in genetics have borrowed terminology from linguistics and the theory of communications. As experts in molecular genetics note, "*the more we understand laws of coding of the genetic information, the more strongly we are surprised by their similarity to principles of linguistics of human and computer languages*" [Ratner, 2002, p. 203].

Leading experts in the field of structural linguistics have long believed that languages of human dialogue were formed as a continuation of genetic language or, are, at least, closely connected with genetic language. Analogies between systems of genetic and linguistic information are of wide and important scientific interest, which this article briefly illustrates. Some relevant concepts will be referred to by R. Jakobson [1987, 1999], one of the most famous lingusitics experts and author of an in-depth theory of binary lingustic oppositions. Jointly with F. Jacob, Nobel Prize winner in molecular genetics, and with other linguistic specialists holding the same views, Jakobson proposed that genetic language is the structural basis of linguistic languages [Jacob et al., 1968; Jakobson, 1985]. In particular, according to Jakobson, all relations among linguistic phonemes are decomposed into a series of binary oppositions of elementary differential attributes (or traits). By analogy, the set of four letters of the genetic alphabet contains the three binary sub-alphabets, which allow creating new mathematical models in molecular genetics [Petoukhov, 2017, 2018a]. As Jakobson wrote, the genetic code system is the basic simulator, which underlies all verbal codes of human languages. "*The heredity in itself is the fundamental form of communications ... Perhaps, the bases of language structures, which are imposed on molecular communications, have been constructed by its structural principles directly*" [Jakobson, 1985, p. 396]. These questions had arisen to Jakobson as consequence of his long-term research into the connections between linguistics, biology and physics. Such connections were considered at a united seminar of physicists and linguists, organized by Niels Bohr and Roman Jakobson, jointly, at the Massachusetts Institute of Technology.

"*Jakobson reveals distinctly a binary opposition of sound attributes as underlying each system of phonemes... The subject of phonology has changed by him: the phonology considered phonemes (as the main subject) earlier, but now Jakobson has offered that distinctive attributes should be considered as "quantums" (or elementary units of language)… Jakobson was interested especially in the general analogies of language structures with the genetic code, and he considered these analogies as indubitable*" [Ivanov, 1985]. We are reminded also of the title of the monograph "On the Yin and Yang nature of language" [Bailey, 1982], which is characteristic for the theme of binary oppositions in linguistics.

F. Jacob, Nobel Prize winner in molecular genetics, also considered the relationship between genetics and linguistic languages in connection with the principle of binary oppositions, systematically described in the Ancient Chinese book "I-Ching". He wrote: « *C'est peut-être I Ching qu'il faudrait étudier pour saisir les relations entre hérédité et langage*» (In English: *To understand the relationship between genetics and language, perhaps it would be necessary to study the Ancient Chinese "I Ching"*) [Jacob, 1974, p. 205].

This connection between linguistics and the genetic code interests many researchers, and some even perceive linguistic language as a living organism. In his book, "Linguistic Genetics", Makovsky says: "*A look at language as a living organism, subject to the natural laws of*

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nature,, ascends to a deep antiquity … Research of a nature, of disposition and of reasons of isomorphism between genetic and linguistic regularities is one of the most important fundamental problems for linguistics of our time" [Makovsky, 1992].

In this Section the author describes the structural analogies between long DNA-'texts' and long literary works in Russian. The represented analysis of long literary Russian texts uses binary-oppositional phonetic features of the Russian alphabet, whose importances were accented by R.Jakobson and which have similarities with binary-oppositional features of genetic lanquage.

The DNA alphabet of nucleobases A, C, G and T has the binary-oppositional structure in accordance with their molecular traits (Fig. 11.1 left): it contains the sub-alphabet of purines (A, G), each of which has two rings in its molecular structure, and the sub-alphabet of pyrimidines (T, C), each of which has only one ring. Each of these sub-alphabets possesses its own binary-oppositional structure since it contains two sub-sub-alphabets defined by 2 or 3 hydrogen bonds: in the sub-alphabet of purines, adenine A has 2 hydrogen bonds and guanine G has 3 hydrogen bonds; in the sub-alphabet of pyrimidines, cytosine C has 3 hydrogen bonds and thymine T has 2 hydrogen bonds (Fig. 11. 1 right).

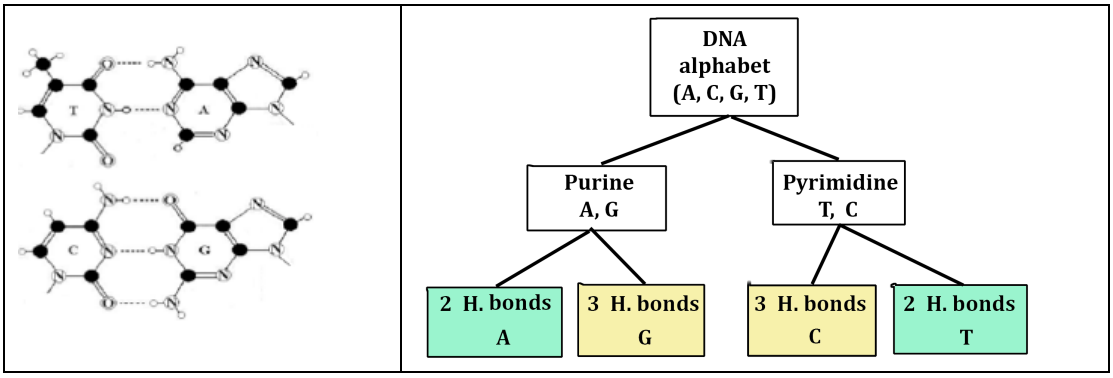

Fig. 11.1. Left: the DNA alphabet of 4 nucleobases A, C, G and T. Right: the scheme of binary-oppositional structure of this DNA alphabet.

The Russian alphabet has also a binary-oppositional phonetic structure since it has two binary-oppositional sub-alphabets: the sub-alphabet of vowels and the sub-alphabet of consonants. Each of these sub-alphabets also has its own binary-oppositional structure: the sub-alphabet of vowels consists of the sub-sub-alphabet of long vowels and the sub-sub-alphabet of short (or iotated) vowels; the sub-alphabet of consonants consists of the sub-sub-alphabet of voiced consonants and the sub-sub-alphabet of deaf consonants (Fig. 11.2 right). The soft sign "ь" and the hard sign "ъ" in the Russian alphabet do not convey any sound and therefore they are not taken into account in its phonologic structure.

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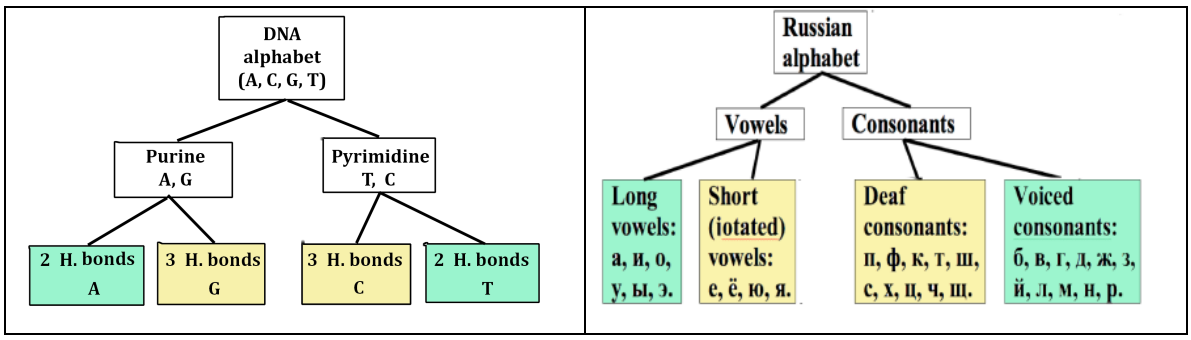

Fig. 11.2. The similarity of binary-oppositional structures of the DNA alphabet (left) and the alphabet of Russian lanquage (right).

For analyzing long literary Russian texts, let us introduce two corresponding classes of equivalency for letters of the Russian alphabet (in Fig. 11.2 the first class is marked by yellow and the second class is marked by green):

1. The first class of equivalency combines all short (iotated) vowels and all deaf consonants: е, ё, ю, я, п, ф, к, т, ш, с, х, ц, ч, щ. We denote all the 14 members of this class by the common symbol 0;
2. The second class of equivalency combines all long vowels and all voiced consonants: а, и, о, у, ы, э, б, в, г, д, ж, з, й, л, м, н, р. We denote all the 17 members of this class by the common symbol 1.

Leaving only these letters in the literary text, and replacing each letter with the symbol of its equivalence class 0 or 1, we obtain the representation of the text by a binary sequence of the type 100101100....

In such binary representation of long literary texts, let us denote percentages of letters from classes of equivalency 0 and 1 by symbols %0 and %1 correspondingly. Then consider the bisymmetric matrix of percentages [%0, %1; %1, %0], representing 2-dimensional hyperbolic number, and the matrix tensor family $[\%0, \%1; \%1, \%0]^{(n)}$, representing 2^n-dimensional hyperbolic numbers:

- $\%0*e_0 + \%1*e_1$ (if $n = 1$);
- $\%0*\%0*e_0 + \%0*\%1*e_1 + \%1*\%0*e_2 + \%1*\%1*e_3$ (if $n = 2$),
- etc.

The author studied percentages %0 and %1 of letters of these two classes in long literary texts by L.N.Tolstoy, A.S.Pushkin, F.M.Dostoevsky, etc. More precisely, for each fixed n, the author analyzed percentage of each type of n-plets inside the mentioned binary representation of any long Russian language literary text (or a long literary text of any other language translated into Russian). Under a fixed value n, each of these percentages is equal to the ratio: “the total quantity of a corresponding type of n-plets” divided by “the total quantity of these binary n-plets”. For example, in the text of the work "Anna Karenina", by Leo Tolstoy, in its binary representation there are 654523 doublets 00, 01, 10 and 11. This number includes 75895 doublets 00, 142504 doublets 01, 142547 doublets 10 and 293577 doublets 11. Correspondingly, the percentage of doublets 00 is equal to 75895/654523 = 0,115954672;

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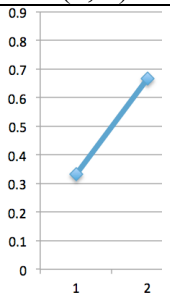
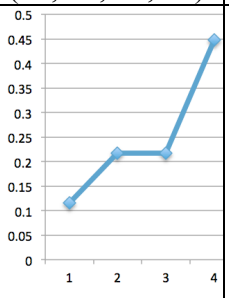
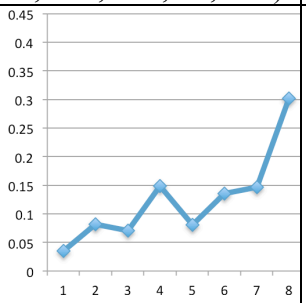
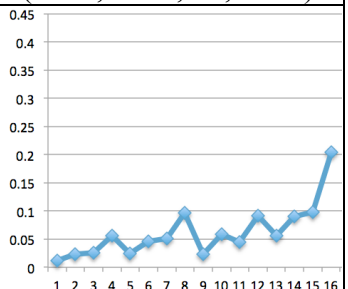
the percentage of doublets 01 is equal to 142504/654523 = 0,217721914; the percentage of doublets 10 is equal to 142547/654523 = 0,21778761; the percentage of doublets 11 is equal to 293577/654523 = 0,448535804 (such values of percentages are shown below rounded to four decimal places).

By analogy with binary sequences of hydrogen bonds 32232223… in long DNA, it turned out - in the case of these literary texts - that knowing only percentages of monoplets %0 and %1 in such binary representation of a long Russian text, one can predict percentages of dozens of types of *n*-plets in it. Coordinates of 2^n-hyperbolic numbers $[\%0,\%1;\ \%1,\%0]^{(n)}$ effectively model percentages of corresponding types of *n*-plets in long Russian texts: for example, the product of values %1*%0*%1 models the percentage of binary triplets 101, etc.

Figs. 11.3 and 11.4 represent results – in graphical and tabular forms - of the analysis of the novel «Anna Karenina» of Leo Tolstoy by the above described approach. Significant correspondences can be seen between phenomenologic values of percentages (blue points in graphs in Fig. 11.3) of all considered types of *n*-plets, and model values (red points in graphs), represented by coordinates of 2^n-dimensional hyperbolic numbers $[\%0,\ \%1;\ \%1,\ \%0]^{(n)}$, $n = 2, 3, 4$. These graphs reveal that the model points of red color are almost exactly superimposed on the phenomenologic points of blue color. Fig. 11.4 shows the proximity of the numerical phenomenological and model values of the studied percentages. All values are rounded to four decimal places. Therefore, knowing only two percentages %0 and %1 of monoplets 0 and 1 in the binary *n*-plet representation of this well known novel, percentages of all other considered types of *n*-plets can be predicted. We presume that a similar model correspondence also holds true for $n = 5, 6,$ ... (if *n* is much less than the length of the considered literary text) but this should be studied in future research.

L.N. Tolstoy «Anna Karenina» (1309047 letters)			
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3337092 %1= 0,6662908			

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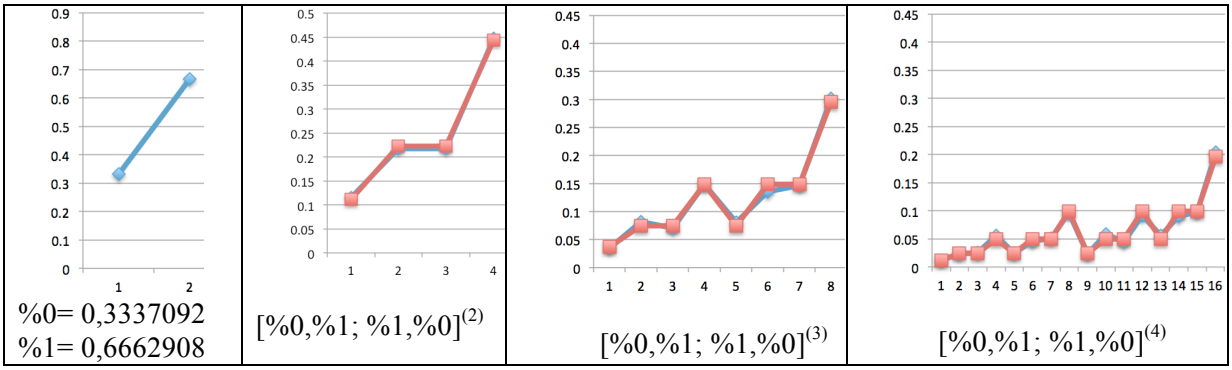

Fig. 11.3. Graphical analysis results of the novel "Anna Karenina" by Leo Tolstoy (the original literary text was accessed from http://samolit.com/books/62/). Percentages of all the types of binary *n*-plets (n = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the percentages of hydrogen *n*-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0,\%1; \%1,\%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (n) refers to tensor powers.

L.N. Tolstoy «Anna Karenina» (1309047 letters)	
Percentages of types of monoplets	
Reality:	%0 (or 0_P)= 0,3337; %1 (or 1_P) = 0,6663
Percentages of types of binary doublets	
Reality:	0_P0_P=0,1160; 0_P1_P=0,2177; 1_P0_P=0,2178; 1_P1_P=0,4485.
Model:	0_P0_P=0,1114; 0_P1_P=0,2223; 1_P0_P=0,2223; 1_P1_P=0,4439.
Percentages of types of binary triplets	
Reality:	$0_P0_P0_P$=0,0348; $0_P0_P1_P$=0,0818; $0_P1_P0_P$=0,0708; $0_P1_P1_P$=0,1481; $1_P0_P0_P$=0,0808; $1_P0_P1_P$=0,1353; $1_P1_P0_P$=0,1465; $1_P1_P1_P$=0,3019.
Model:	$0_P0_P0_P$=0,0372; $0_P0_P1_P$=0,0742; $0_P1_P0_P$=0,0742; $0_P1_P1_P$=0,1481; $1_P0_P0_P$=0,0742; $1_P0_P1_P$=0,1481; $1_P1_P0_P$=0,1481; $1_P1_P1_P$=0,2958.
Percentages of types of binary tetraplets	
Reality:	$0_P0_P0_P0_P$=0,0114; $0_P0_P0_P1_P$=0,0232; $0_P0_P1_P0_P$=0,0257; $0_P0_P1_P1_P$=0,0559; $0_P1_P0_P0_P$=0,0247; $0_P1_P0_P1_P$=0,0460; $0_P1_P1_P0_P$=0,0505; $0_P1_P1_P1_P$=0,0970; $1_P0_P0_P0_P$=0,0231; $1_P0_P0_P1_P$=0,0582; $1_P0_P1_P0_P$=0,0446; $1_P0_P1_P1_P$=0,0914; $1_P1_P0_P0_P$=0,0565; $1_P1_P0_P1_P$=0,0899; $1_P1_P1_P0_P$=0,0975; $1_P1_P1_P1_P$=0,2045.
Model:	$0_P0_P0_P0_P$=0,0124; $0_P0_P0_P1_P$=0,0248; $0_P0_P1_P0_P$=0,0248; $0_P0_P1_P1_P$=0,0494; $0_P1_P0_P0_P$=0,0248; $0_P1_P0_P1_P$=0,0494; $0_P1_P1_P0_P$=0,0494; $0_P1_P1_P1_P$=0,0987; $1_P0_P0_P0_P$=0,0248; $1_P0_P0_P1_P$=0,0494; $1_P0_P1_P0_P$=0,0494; $1_P0_P1_P1_P$=0,0987; $1_P1_P0_P0_P$=0,0494; $1_P1_P0_P1_P$=0,0987; $1_P1_P1_P0_P$=0,0987; $1_P1_P1_P1_P$=0,1971.

Fig. 11.4. The numeric representation of the analysis of the novel "Anna Karenina" by Leo Tolstoy (the original literary text was accessed from http://samolit.com/books/62/). Percent-

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ages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded to four decimal places. Blue numbers correspond to phenomenologic values of the percentages for cases named in tabular sections, while red numbers correspond to model values of these percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers. Denotations 0_p and 1_p are used as equivalents of denotations %0 and %1.

Below the author shows some results received by similar analysis of famous Russian literary works: L.N. Tolstoy «War and Peace»; F.M. Dostoevsky «Crime and Punishment» and «Idiot»; A.S. Pushkin «Evgenij Onegin» and «Dubrovsky»; the Russian Bible. All these results are similar to those described for the novel «Anna Karenina» (Figs. 11.3 and 11.4): they confirm that percentages of binary *n*-plets (*n* = 1, 2, 3, 4) are, to some degree, interrelated to each other and that this interrelation can be effectively modeled on the basis of 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where *n* = 1, 2, 3, 4. The computer program for the analysis of literary texts was created by our graduate student V.I. Svirin.

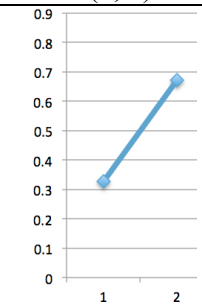
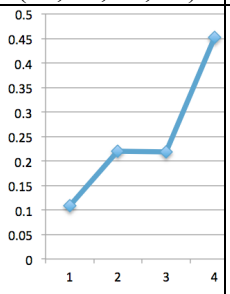
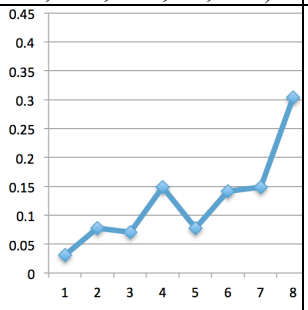
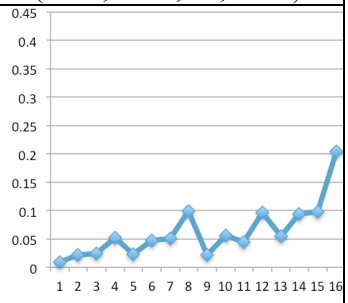
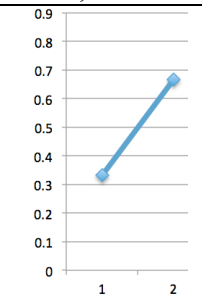
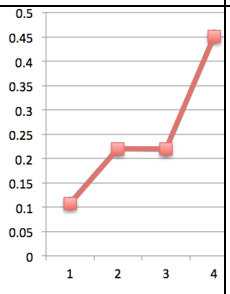
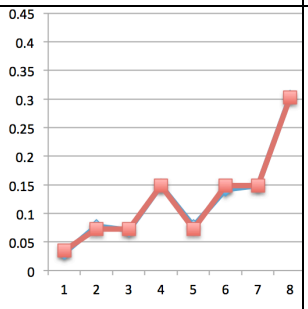
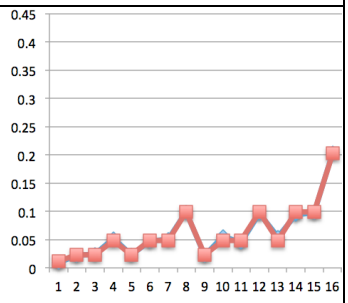
L.N. Tolstoy «War and Peace», Book I (1068479 letters)			
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,32830126 %1= 0,67169874			
 %0= 0,32830126 %1= 0,67169874	 $[\%0,\%1; \%1,\%0]^{(2)}$	 $[\%0,\%1; \%1,\%0]^{(3)}$	 $[\%0,\%1; \%1,\%0]^{(4)}$

Fig. 11.5. Graphical analysis results of the novel "War and Peace" (Book 1) by Leo Tolstoy (the original literary text was accessed from http://samolit.com/books/64/). Percentages

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of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the percentages of hydrogen *n*-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers.

L.N. Tolstoy «War and Peace», Book I (1068479 letters)	
Percentages of types of binary monoplets	
Reality:	%0 (or 0_P) = 0,3283; %1 (or 1_P) = 0,6717
Percentages of types of binary doublets	
Reality:	0_P0_P=0,1088; 0_P1_P=0,2200; 1_P0_P=0,2190; 1_P1_P=0,4522.
Model:	0_P0_P=0,1078; 0_P1_P=0,2205; 1_P0_P=0,2205; 1_P1_P=0,4512.
Percentages of types of binary triplets	
Reality:	$0_P0_P0_P$=0,0314; $0_P0_P1_P$=0,0774; $0_P1_P0_P$=0,0705; $0_P1_P1_P$=0,1484; $1_P0_P0_P$=0,0778; $1_P0_P1_P$=0,1419; $1_P1_P0_P$=0,1490; $1_P1_P1_P$=0,3036.
Model:	$0_P0_P0_P$=0,0354; $0_P0_P1_P$=0,0724; $0_P1_P0_P$=0,0724; $0_P1_P1_P$=0,1481; $1_P0_P0_P$=0,0724; $1_P0_P1_P$=0,1481; $1_P1_P0_P$=0,1481; $1_P1_P1_P$=0,3031.
Percentages of types of binary tetraplets	
Reality:	$0_P0_P0_P0_P$=0,0096; $0_P0_P0_P1_P$=0,0220; $0_P0_P1_P0_P$=0,0250; $0_P0_P1_P1_P$=0,0521; $0_P1_P0_P0_P$=0,0234; $0_P1_P0_P1_P$=0,0474; $0_P1_P1_P0_P$=0,0504; $0_P1_P1_P1_P$=0,0988; $1_P0_P0_P0_P$=0,0214; $1_P0_P0_P1_P$=0,0562; $1_P0_P1_P0_P$=0,0451; $1_P0_P1_P1_P$=0,0966; $1_P1_P0_P0_P$=0,0546; $1_P1_P0_P1_P$=0,0943; $1_P1_P1_P0_P$=0,0984; $1_P1_P1_P1_P$=0,2049.
Model:	$0_P0_P0_P0_P$=0,0116; $0_P0_P0_P1_P$=0,0238; $0_P0_P1_P0_P$=0,0238; $0_P0_P1_P1_P$=0,0486; $0_P1_P0_P0_P$=0,0238; $0_P1_P0_P1_P$=0,0486; $0_P1_P1_P0_P$=0,0486; $0_P1_P1_P1_P$=0,0995; $1_P0_P0_P0_P$=0,0238; $1_P0_P0_P1_P$=0,0486; $1_P0_P1_P0_P$=0,0486; $1_P0_P1_P1_P$=0,0995; $1_P1_P0_P0_P$=0,0486; $1_P1_P0_P1_P$=0,0995; $1_P1_P1_P0_P$=0,0995; $1_P1_P1_P1_P$=0,2036.

Fig. 11.6. Numeric analysis results of the novel "War and Peace" (Book 1) by Leo Tolstoy (the original literary text was accessed from http://samolit.com/books/64/). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded to four decimal places. Blue numbers correspond to phenomenologic values of percentages for cases named in tabular sections, while red numbers correspond to model values of these percentages calculated as coordinates of 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers. Denotations 0_p and 1_p are used as equivalents of denotations %0 and %1.

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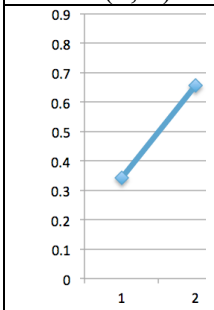
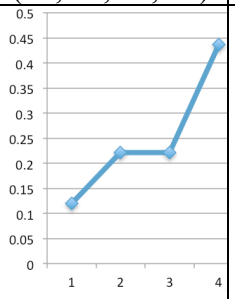
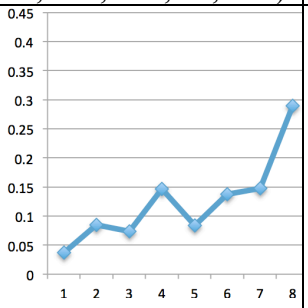
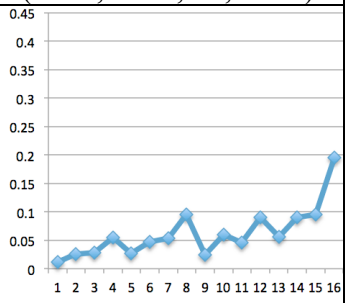
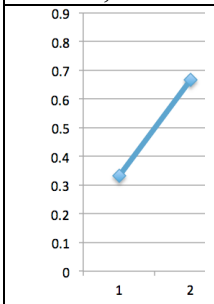
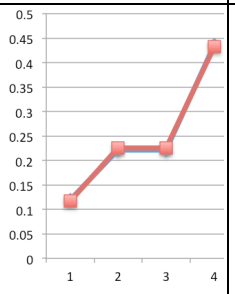
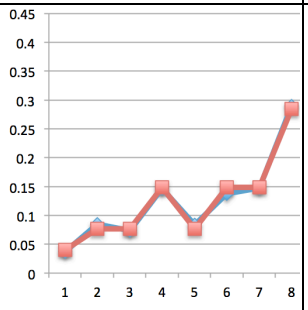
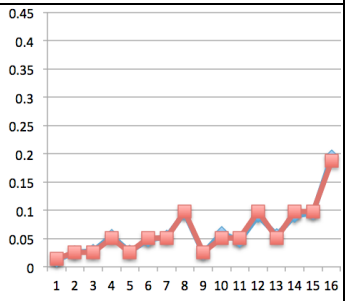
F.M. Dostoevsky «Crime and Punishment» (818099 letters)			
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3420845 %1= 0,6579155			
 %0= 0,3420845 %1= 0,6579155	 $[\%0,\%1;\ \%1,\%0]^{(2)}$	 $[\%0,\%1;\ \%1,\%0]^{(3)}$	 $[\%0,\%1;\ \%1,\%0]^{(4)}$

Fig. 11.7. Graphical analysis results of the novel “Crime and Punishment” by F.M. Dostoevsky (the original literary text was accessed from http://samolit.com/books/57/). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the percentages of hydrogen *n*-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (n) refers to tensor powers.

F.M. Dostoevsky «Crime and Punishment» (818099 letters)				
Percentages of types of binary monoplets				
Reality:	%0 (or 0_P) = 0,3421;	%1 (or 1_P) = 0,6579		
Percentages of members in the alphabet of binary doublets				
Reality:	0_P0_P = 0,1203;	0_P1_P = 0,2219;	1_P0_P = 0,2216;	1_P1_P = 0,4362.
Model:	0_P0_P = 0,1170;	0_P1_P = 0,2251;	1_P0_P = 0,2251;	1_P1_P = 0,4329.

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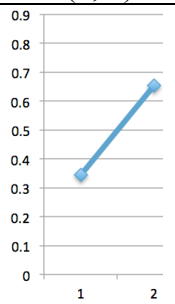
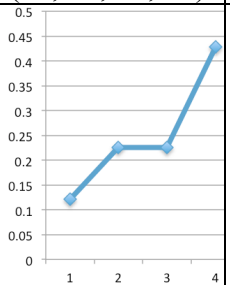
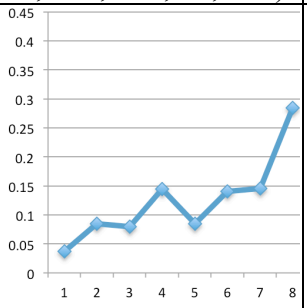
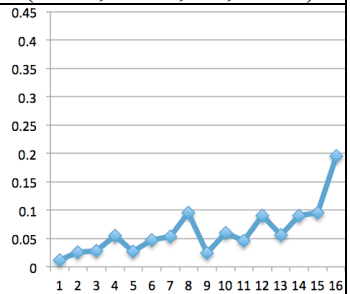
Percentages of types of binary triplets	
Reality:	$0_P0_P0_P=0{,}0370$; $0_P0_P1_P=0{,}0843$; $0_P1_P0_P=0{,}0738$; $0_P1_P1_P=0{,}1464$; $1_P0_P0_P=0{,}0838$; $1_P0_P1_P=0{,}1377$; $1_P1_P0_P=0{,}1472$; $1_P1_P1_P=0{,}2897$.
Model:	$0_P0_P0_P=0{,}0400$; $0_P0_P1_P=0{,}0770$; $0_P1_P0_P=0{,}0770$; $0_P1_P1_P=0{,}1481$; $1_P0_P0_P=0{,}0760$; $1_P0_P1_P=0{,}1481$; $1_P1_P0_P=0{,}1481$; $1_P1_P1_P=0{,}2848$.
Percentages of types of binary tetraplets	
Reality:	$0_P0_P0_P0_P=0{,}0119$; $0_P0_P0_P1_P=0{,}0258$; $0_P0_P1_P0_P=0{,}0284$; $0_P0_P1_P1_P=0{,}0551$; $0_P1_P0_P0_P=0{,}0265$; $0_P1_P0_P1_P=0{,}0467$; $0_P1_P1_P0_P=0{,}0535$; $0_P1_P1_P1_P=0{,}0954$; $1_P0_P0_P0_P=0{,}0249$; $1_P0_P0_P1_P=0{,}0594$; $1_P0_P1_P0_P=0{,}0458$; $1_P0_P1_P1_P=0{,}0900$; $1_P1_P0_P0_P=0{,}0560$; $1_P1_P0_P1_P=0{,}0898$; $1_P1_P1_P0_P=0{,}0952$; $1_P1_P1_P1_P=0{,}1954$.
Model:	$0_P0_P0_P0_P=0{,}0137$; $0_P0_P0_P1_P=0{,}0263$; $0_P0_P1_P0_P=0{,}0263$; $0_P0_P1_P1_P=0{,}0507$; $0_P1_P0_P0_P=0{,}0263$; $0_P1_P0_P1_P=0{,}0507$; $0_P1_P1_P0_P=0{,}0507$; $0_P1_P1_P1_P=0{,}0974$; $1_P0_P0_P0_P=0{,}0263$; $1_P0_P0_P1_P=0{,}0507$; $1_P0_P1_P0_P=0{,}0507$; $1_P0_P1_P1_P=0{,}0974$; $1_P1_P0_P0_P=0{,}0507$; $1_P1_P0_P1_P=0{,}0974$; $1_P1_P1_P0_P=0{,}0974$; $1_P1_P1_P1_P=0{,}1874$.

Fig. 11.8. Numeric analysis results of the novel "Crime and Punishment" by F.M. Dostoevsky (the original literary text was accessed from http://samolit.com/books/57/). Percentages of all the types of binary n-plets (n = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded to four decimal places. Blue numbers correspond to phenomenologic values of percentages for cases named in tabular sections, while red numbers correspond to model values of these percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (n) refers to tensor powers. Denotations 0_p and 1_p are used as equivalents of denotations %0 and %1.

F.M. Dostoevsky «Idiot» (1001129 letters)			
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3459674 %1= 0,6540326			

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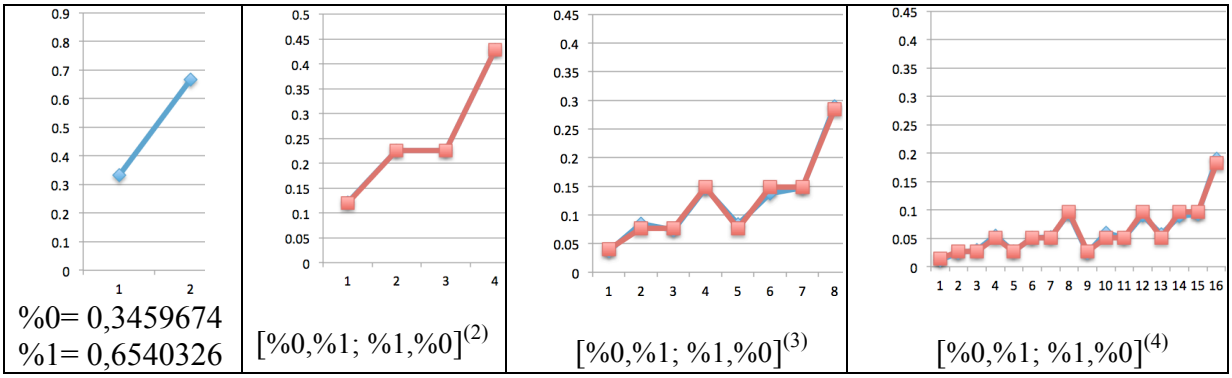

Fig. 11.9. Graphical analysis results of the novel "Idiot" by F.M. Dostoevsky (the original literary text was accessed from http://samolit.com/books/56/). Percentages of all the types of binary n-plets (n = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the percentages of hydrogen n-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0,\%1;\ \%1,\%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (n) refers to tensor powers.

F.M. Dostoevsky «Idiot» (1001129 letters)
Percentages of types of binary monoplets
Reality: %0 (or 0_P) = 0,3460; %1 (or 1_P) = 0,6540
Percentages of types of binary doublets
Reality: 0_P0_P=0,1208; 0_P1_P=0,2251; 1_P0_P=0,2252; 1_P1_P=0,4289.
Model: 0_P0_P=0,1197; 0_P1_P=0,2263; 1_P0_P=0,2263; 1_P1_P=0,4278.
Percentages of types of binary triplets
Reality: $0_P0_P0_P$=0,0367; $0_P0_P1_P$=0,0845; $0_P1_P0_P$=0,0792; $0_P1_P1_P$=0,1449; $1_P0_P0_P$=0,0847; $1_P0_P1_P$=0,1405; $1_P1_P0_P$=0,1405; $1_P1_P1_P$=0,2839.
Model: $0_P0_P0_P$=0,0414; $0_P0_P1_P$=0,0783; $0_P1_P0_P$=0,0783; $0_P1_P1_P$=0,1480; $1_P0_P0_P$=0,0783; $1_P0_P1_P$=0,1480; $1_P1_P0_P$=0,1480; $1_P1_P1_P$=0,2798.
Percentages of types of binary tetraplets
Reality: $0_P0_P0_P0_P$=0,0118; $0_P0_P0_P1_P$=0,0251; $0_P0_P1_P0_P$=0,0290; $0_P0_P1_P1_P$=0,0545; $0_P1_P0_P0_P$=0,0276; $0_P1_P0_P1_P$=0,0517; $0_P1_P1_P0_P$=0,0519; $0_P1_P1_P1_P$=0,0941; $1_P0_P0_P0_P$=0,0249; $1_P0_P0_P1_P$=0,0597; $1_P0_P1_P0_P$=0,0505; $1_P0_P1_P1_P$=0,0909; $1_P1_P0_P0_P$=0,0570; $1_P1_P0_P1_P$=0,0885; $1_P1_P1_P0_P$=0,0931; $1_P1_P1_P1_P$=0,1899.
Model: $0_P0_P0_P0_P$=0,0143; $0_P0_P0_P1_P$=0,0271; $0_P0_P1_P0_P$=0,0271; $0_P0_P1_P1_P$=0,0512; $0_P1_P0_P0_P$=0,0271; $0_P1_P0_P1_P$=0,0512; $0_P1_P1_P0_P$=0,0512; $0_P1_P1_P1_P$=0,0968; $1_P0_P0_P0_P$=0,0271; $1_P0_P0_P1_P$=0,0512; $1_P0_P1_P0_P$=0,0512; $1_P0_P1_P1_P$=0,0968; $1_P1_P0_P0_P$=0,0512; $1_P1_P0_P1_P$=0,0968; $1_P1_P1_P0_P$=0,0968; $1_P1_P1_P1_P$=0,1830.

Fig. 11.10. Numeric analysis results of the novel "Idiot" by F.M. Dostoevsky (the original literary text was accessed from http://samolit.com/books/56/). Percentages of all the types of

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binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded to four decimal places. Blue numbers correspond to phenomenologic values of the percentages for cases named in tabular sections, while red numbers correspond to model values of these percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers. Denotations 0_p and 1_p are used as equivalents of denotations %0 and %1.

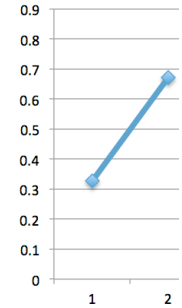
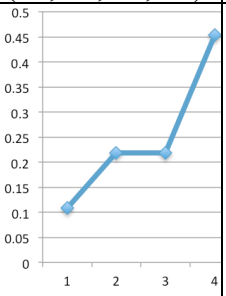
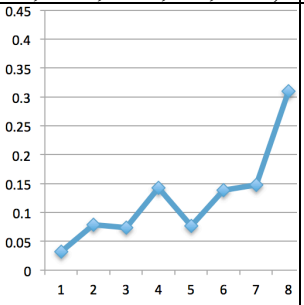
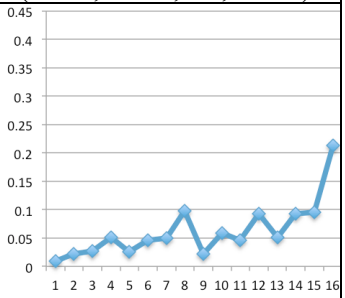
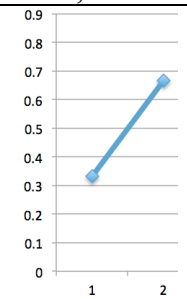
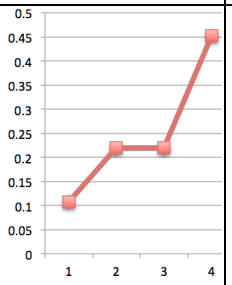
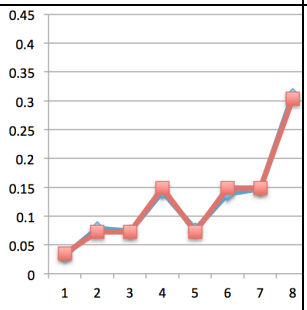
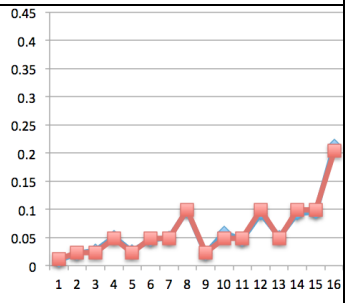
A.S. Pushkin «Evgenij Onegin» (107146 letters)			
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3277771 %1= 0,6722229			
 %0= 0,3277771 %1= 0,6722229	 $[\%0,\%1; \%1,\%0]^{(2)}$	 $[\%0,\%1; \%1,\%0]^{(3)}$	 $[\%0,\%1; \%1,\%0]^{(4)}$

Fig. 11.11. Graphical analysis results of the novel "Evgenij Onegin" by A.S. Pushkin (the original literary text was accessed from http://tululu.org/b57798/). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the percentages of hydrogen *n*-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers.

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A.S. Pushkin «Evgenij Onegin» (107146 letters)				
Percentages of types of binary monoplets				
Reality:	%0 (or 0_P) = 0,3278;	%1 (or 1_P) = 0,6722		
Percentages of members in the alphabet of binary doublets				
Reality:	0_P0_P = 0,1090;	0_P1_P = 0,2189;	1_P0_P = 0,2187;	1_P1_P = 0,4534.
Model:	0_P0_P = 0,1074;	0_P1_P = 0,2203;	1_P0_P = 0,2203;	1_P1_P = 0,4519.
Percentages of types of binary triplets				
Reality:	$0_P0_P0_P$=0,0316;	$0_P0_P1_P$=0,0789;	$0_P1_P0_P$=0,0738;	$0_P1_P1_P$=0,1428;
	$1_P0_P0_P$=0,0769;	$1_P0_P1_P$=0,1389;	$1_P1_P0_P$=0,1476;	$1_P1_P1_P$=0,3095.
Model:	$0_P0_P0_P$=0,0352;	$0_P0_P1_P$=0,0722;	$0_P1_P0_P$=0,0722;	$0_P1_P1_P$=0,1481;
	$1_P0_P0_P$=0,0722;	$1_P0_P1_P$=0,1481;	$1_P1_P0_P$=0,1481;	$1_P1_P1_P$=0,3038.
Percentages of types of binary tetraplets				
Reality:	$0_P0_P0_P0_P$=0,0098;	$0_P0_P0_P1_P$=0,0223;	$0_P0_P1_P0_P$=0,0272;	$0_P0_P1_P1_P$=0,0509;
	$0_P1_P0_P0_P$=0,0251;	$0_P1_P0_P1_P$=0,0457;	$0_P1_P1_P0_P$=0,0500;	$0_P1_P1_P1_P$=0,0974;
	$1_P0_P0_P0_P$=0,0217;	$1_P0_P0_P1_P$=0,0588;	$1_P0_P1_P0_P$=0,0457;	$1_P0_P1_P1_P$=0,0930;
	$1_P1_P0_P0_P$=0,0513;	$1_P1_P0_P1_P$=0,0928;	$1_P1_P1_P0_P$=0,0953;	$1_P1_P1_P1_P$=0,2131.
Model:	$0_P0_P0_P0_P$=0,0115;	$0_P0_P0_P1_P$=0,0237;	$0_P0_P1_P0_P$=0,0237;	$0_P0_P1_P1_P$=0,0485;
	$0_P1_P0_P0_P$=0,0237;	$0_P1_P0_P1_P$=0,0485;	$0_P1_P1_P0_P$=0,0485;	$0_P1_P1_P1_P$=0,0996;
	$1_P0_P0_P0_P$=0,0237;	$1_P0_P0_P1_P$=0,0485;	$1_P0_P1_P0_P$=0,0485;	$1_P0_P1_P1_P$=0,0996 ;
	$1_P1_P0_P0_P$=0,0485;	$1_P1_P0_P1_P$=0,0996;	$1_P1_P1_P0_P$=0,0996;	$1_P1_P1_P1_P$=0,2042.

Fig. 11.12. Numeric analysis results of the novel "Evgenij Onegin" by A.S. Pushkin (the original literary text was accessed from http://tululu.org/b57798/). Percentages of all the types of binary n-plets (n = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded to four decimal places. Blue numbers correspond to phenomenologic values of the percentages for cases named in tabular sections, while red numbers correspond to model values of these percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (n) refers to tensor powers. Denotations 0_p and 1_p are used as equivalents of denotations %0 and %1.

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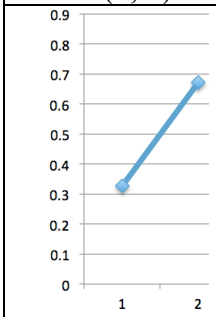
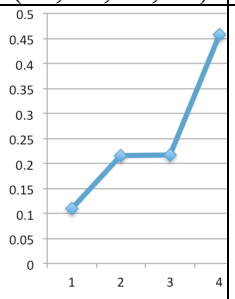
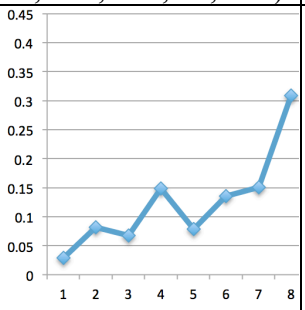
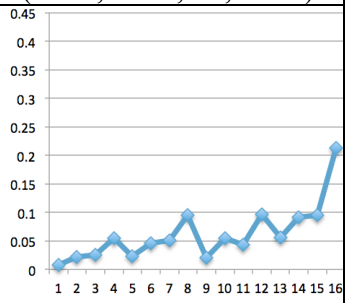
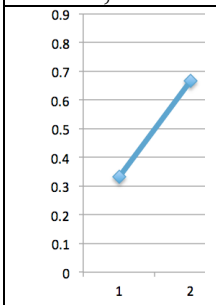
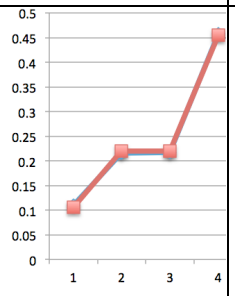
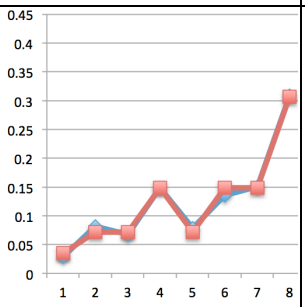
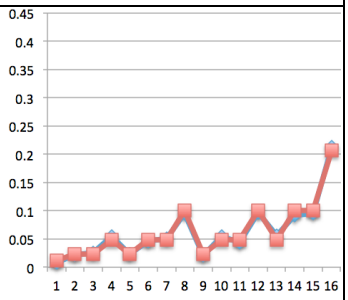
A.S. Pushkin «Dubrovsky» (106891 letters)			
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3259021 %1= 0,6740979			
 %0= 0,3259021 %1= 0,6740979	 $[\%0,\%1;\ \%1,\%0]^{(2)}$	 $[\%0,\%1;\ \%1,\%0]^{(3)}$	 $[\%0,\%1;\ \%1,\%0]^{(4)}$

Fig. 11.13. Graphical analysis results of the novel "Dubrovsky" by A.S. Pushkin (the original literary text was accessed from http://samolit.com/books/61/). Percentages of all the types of binary n-plets (n = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the percentages of hydrogen n-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (n) refers to tensor powers.

A.S. Pushkin «Dubrovsky» (106891 letters)
Percentages of types of binary monoplets
Reality: %0 (or 0_P) = 0,3259; %1 (or 1_P) = 0,6741
Percentages of types of binary doublets
Reality: 0_P0_P = 0,1100; 0_P1_P = 0,2152; 1_P0_P = 0,2166; 1_P1_P = 0,4582.
Model: 0_P0_P = 0,1062; 0_P1_P = 0,2197; 1_P0_P = 0,2197; 1_P1_P = 0,4544.
Percentages of types of binary triplets

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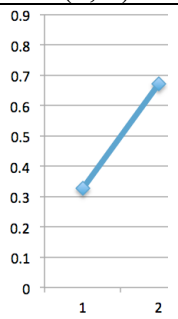
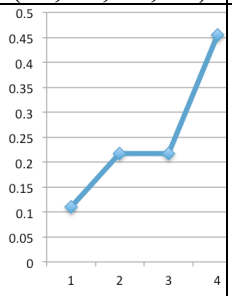
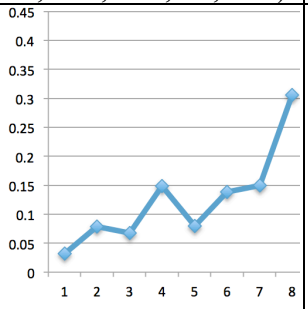
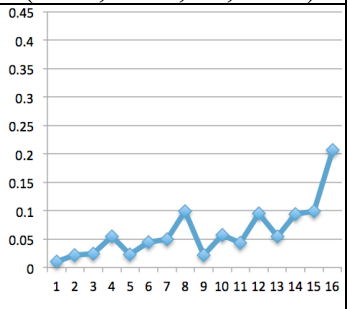
Reality:	$0_P0_P0_P=0,0295$; $0_P0_P1_P=0,0816$; $0_P1_P0_P=0,0671$; $0_P1_P1_P=0,1491$; $1_P0_P0_P=0,0784$; $1_P0_P1_P=0,1358$; $1_P1_P0_P=0,1503$; $1_P1_P1_P=0,3083$.
Model:	$0_P0_P0_P=0,0346$; $0_P0_P1_P=0,0716$; $0_P1_P0_P=0,0716$; $0_P1_P1_P=0,1481$; $1_P0_P0_P=0,0716$; $1_P0_P1_P=0,1481$; $1_P1_P0_P=0,1481$; $1_P1_P1_P=0,3063$.
Percentages of types of binary tetraplets	
Reality:	$0_P0_P0_P0_P=0,0081$; $0_P0_P0_P1_P=0,0223$; $0_P0_P1_P0_P=0,0257$; $0_P0_P1_P1_P=0,0549$; $0_P1_P0_P0_P=0,0234$; $0_P1_P0_P1_P=0,0459$; $0_P1_P1_P0_P=0,0506$; $0_P1_P1_P1_P=0,0952$; $1_P0_P0_P0_P=0,0211$; $1_P0_P0_P1_P=0,0553$; $1_P0_P1_P0_P=0,0437$; $1_P0_P1_P1_P=0,0971$; $1_P1_P0_P0_P=0,0564$; $1_P1_P0_P1_P=0,0916$; $1_P1_P1_P0_P=0,0959$; $1_P1_P1_P1_P=0,2127$.
Model:	$0_P0_P0_P0_P=0,0113$; $0_P0_P0_P1_P=0,0233$; $0_P0_P1_P0_P=0,0233$; $0_P0_P1_P1_P=0,0483$; $0_P1_P0_P0_P=0,0233$; $0_P1_P0_P1_P=0,0483$; $0_P1_P1_P0_P=0,0483$; $0_P1_P1_P1_P=0,0998$; $1_P0_P0_P0_P=0,0233$; $1_P0_P0_P1_P=0,0483$; $1_P0_P1_P0_P=0,0483$; $1_P0_P1_P1_P=0,0998$; $1_P1_P0_P0_P=0,0483$; $1_P1_P0_P1_P=0,0998$; $1_P1_P1_P0_P=0,0998$; $1_P1_P1_P1_P=0,2065$.

Fig. 11.14. Numeric analysis results of the novel "Dubrovsky" by A.S. Pushkin (the original literary text was accessed from http://samolit.com/books/61/). Percentages of all the types of binary n-plets (n = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded to four decimal places. Blue numbers correspond to phenomenologic values of the percentages for cases named in tabular sections, while red numbers correspond to model values of these percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (n) refers to tensor powers. Denotations 0_p and 1_p are used as equivalents of denotations %0 and %1.

Russian Bible (3122489 letters)			
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3279771 %1= 0,6720229			

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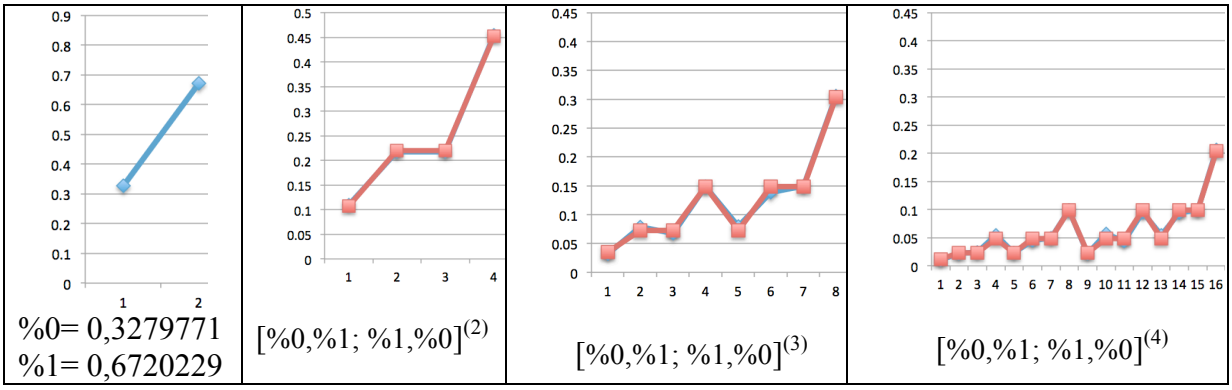

Fig. 11.15. Graphical analysis results of the Russian Bible (the original literary text was accessed from http://petoukhov.com/bible.zip). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the percentages of hydrogen *n*-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers.

Russian Bible (3122489 letters)
Percentages of types of binary monoplets
Reality: %0 (or 0_P) = 0,3280; %1 (or 1_P) = 0,6720
Percentages of types of binary doublets
Reality: 0_P0_P = 0,1107; 0_P1_P = 0,2171; 1_P0_P = 0,2174; 1_P1_P = 0,4548.
Model: 0_P0_P = 0,1076; 0_P1_P = 0,2204; 1_P0_P = 0,2204; 1_P1_P = 0,4516.
Percentages of types of binary triplets
Reality: $0_P0_P0_P$ = 0,0318; $0_P0_P1_P$ = 0,0789; $0_P1_P0_P$ = 0,0678; $0_P1_P1_P$ = 0,1484; $1_P0_P0_P$ = 0,0794; $1_P0_P1_P$ = 0,1386; $1_P1_P0_P$ = 0,1493; $1_P1_P1_P$ = 0,3058.
Model: $0_P0_P0_P$=0,0353; $0_P0_P1_P$=0,0723; $0_P1_P0_P$=0,0723; $0_P1_P1_P$=0,1481; $1_P0_P0_P$=0,0723; $1_P0_P1_P$=0,1481; $1_P1_P0_P$=0,1481; $1_P1_P1_P$=0,3035.
Percentages of types of binary tetraplets
Reality: $0_P0_P0_P0_P$=0,0099; $0_P0_P0_P1_P$=0,0222; $0_P0_P1_P0_P$=0,0245; $0_P0_P1_P1_P$=0,0543; $0_P1_P0_P0_P$=0,0232; $0_P1_P0_P1_P$=0,0448; $0_P1_P1_P0_P$=0,0493; $0_P1_P1_P1_P$=0,0995; $1_P0_P0_P0_P$=0,0222; $1_P0_P0_P1_P$=0,0568; $1_P0_P1_P0_P$=0,0438; $1_P0_P1_P1_P$=0,0948; $1_P1_P0_P0_P$=0,0552; $1_P1_P0_P1_P$=0,0937; $1_P1_P1_P0_P$=0,0997; $1_P1_P1_P1_P$=0,2063.
Model: $0_P0_P0_P0_P$=0,0116; $0_P0_P0_P1_P$=0,0237; $0_P0_P1_P0_P$=0,0237; $0_P0_P1_P1_P$=0,0486; $0_P1_P0_P0_P$=0,0237; $0_P1_P0_P1_P$=0,0486; $0_P1_P1_P0_P$=0,0486; $0_P1_P1_P1_P$=0,0995; $1_P0_P0_P0_P$=0,0237; $1_P0_P0_P1_P$=0,0486; $1_P0_P1_P0_P$=0,0486; $1_P0_P1_P1_P$=0,0995; $1_P1_P0_P0_P$=0,0486; $1_P1_P0_P1_P$=0,0995; $1_P1_P1_P0_P$=0,0995; $1_P1_P1_P1_P$=0,2040.

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Fig. 11.16. Numeric analysis results of the Russian Bible (the original literary text was accessed from http://petoukhov.com/bible.zip). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded to four decimal places. Blue numbers correspond to phenomenologic values of the percentages for cases named in tabular sections, while red numbers correspond to model values of these percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers. Denotations 0_p and 1_p are used as equivalents of denotations %0 and %1.

Presented results show that the described properties of long Russian literary texts reflect, first of all, the deep specifics of Russian language and not the particular literary style of a particular writer. It can be assumed that any long literary text in a foreign language, translated into Russian, will demonstrate similar properties. It will be interesting to study if there are similar patterns in the texts of other languages with differing alphabets and differing phonetic features.

Presented results reveal such analogies between long genetic texts and and long Russian literary texts, which are related with their binary-oppositional structures, percentage features of texts and 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$.

12 Doubly stochastic matrices and tensor families of hyperbolic numbers

A square matrix is called doubly stochastic if all entries of the matrix are nonnegative and the sum of the elements in each row and each column is unity [Prasolov, 1994]. In previous Sections 10 and 11 we studied phenomenologic long binary sequences like as 01101001… . We simulated phenomenologic percentages (or frequencies) of their doublets 00, 01, 10, 11, of their triplets 000, 001, 010,…110, 111 and of their other *n*-plets by means of coordinates of 2^n-dimensional hyperbolic numbers $[p, q; q, p]^{(n)}$, where *p* refers precentages %0 of monoplets 0, and *q* refers percentages %1 of monoplets 1 (in binary sequences, the sum of percentages of monoplets 0 and 1 is equal to unity: $p + q = 1$).

It is easy to check that each matrix of this tensor family $[p, q; q, p]^{(n)}$ (Fig. 12.1) is doubly stochastic matrix since it is nonegative and the sum of its entries in each row and each column is unity. For example, the sum of entries in each row and in each column in the (4*4)-matrix $M^{(2)}$ is equal to unity: pp + pq + qp + qq = p(p + q) + q(p + q)= p + q =1.

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$$M=\begin{vmatrix} p, q \\ q, p \end{vmatrix} \quad M^{(2)}=\begin{vmatrix} pp, pq, qp, qq \\ pq, pp, qq, qp \\ qp, qq, pp, pq \\ qq, qp, pq, pp \end{vmatrix} \quad M^{(3)}=\begin{vmatrix} ppp, ppq, pqp, pqq, qpp, qpq, qqp, qqq \\ ppq, ppp, pqq, pqp, qpq, qpp, qqq, qqp \\ pqp, pqq, ppp, ppq, qqp, qqq, qpp, qpq \\ pqq, pqp, ppq, ppp, qqq, qqp, qpq, qpp \\ qpp, qpq, qqp, qqq, ppp, ppq, pqp, pqq \\ qpq, qpp, qqq, qqp, ppq, ppp, pqq, pqp \\ qqp, qqq, qpp, qpq, pqp, pqq, ppp, ppq \\ qqq, qqp, qpq, qpp, pqq, pqp, ppq, ppp \end{vmatrix}$$

Fig. 12.1. Three first members of the tensor family $[p, q; q, p]^{(n)}$ of bisymmetric doubly stochastic matrices for percentages p and q (where p+q=1) are shown.

The revealed connections of bisymmetric doubly stochastic matrices with structures of long genetic and literary texts (described in Sections 10 and 11) are interesting since doubly stochastic matrices have essential applications in many scientific fields: linear programming and planing, theory of games and optimization, forming of coalitions, models for oncology study, economy, etc. Some algebraic simulations of genetic and biologic materials in this article can be also considered as models on basis of bisymmetric doubly stochastic matrices. In addition, the Hardy-Weinberg law, which is called in biologic literature as the basis of mathematical constructions in population genetics and contemporary evolutionary theory, is simulated on the basis of the tensor family $[p, q; q, p]^{(n)}$ of bisymmetric doubly stochastic matrices where $p + q = 1$ [Petoukhov, 2018, doi: 10.20944/preprints201804.0131.v2]. On the way of further applications of doubly stochastic matrices for analysis of biologic structures, many interesting studies and results are possible, which are related, in particular, with using the Darwinian concept of natural selection. The author plans to publish a few of such results some later.

13 Regarding Punnett squares for the trait inheritance in Mendelian genetics

According to Mendel's law of independent assortment of inherited traits, 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.

In genetics from 1906 year, Punnett squares represent Mendel's laws of inheritance of traits under poly-hybrid crosses. In Punnet squares, combinations of dominant and recessive alleles of genes from parent reproductive cells – gametes – are represented (Fig. 13.1).

		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

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Fig. 13.1. 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».

Punnett squares have strong analogies with square «tables of tensor inheritance» of eigenvalues of original matrices (or «parental» matrices), which were introduced in [Petoukhov, 2016]. Let us say on this in more details in relation to bisymmetric matrices and their tensor (or Kronecker) product.

As known, doubly stochastic matrices and bisymmetric matrix representations of 2^n-hyperbolic numbers have real eigenvalues. The operation of the tensor product of any two square matrices V and W have the following property: the eigenvalues of matrix V⊗W are equal to a product of c_i*d_j, where c_i and d_j are eigenvalues of the matrices V and W. This feature of the tensor inheritance of eigenvalues of the original matrices (or "parental" matrices) V and W in the result of their tensor product can be conveniently represented in the form of "tables of inheritance". Fig. 13.2 shows the example of two simplest cases, conventionally referred to as monohybrid and dihybrid cases of a tensor hybridization of two bisymmetric matrices (for example, two doubly stochastic matrices or two matrices representing 2-dimensional hyperbolic numbers). In the first case, the tensor product of two bisymmetric (2*2)-matrices V and W, which have the same spectrum of real eigenvalues A and a, gives the (4*4)-matrix Q=V⊗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 spectrum of real eigenvalues AB, Ab, aB, ab, gives (16*16)-matrix with 16 eigenvalues, represented in the tabular form.

		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

Fig. 13.2. Examples of tables of inheritance of eigenvalues under the tensor product in cases of bisymmetric (2*2)-matrices and (4*4)-matrices.

This formal analogy - between Punnett squares of combinations of alleles and tables of tensor inheritance of eigenvalues of the considered bisymmetric matrices - 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 considered bisymmetric matrices.

14 Fractal-like multi-dimensional configurational spaces of hyperbolic types

This Section is devoted to the use of 2^n-dimensional hyperbolic numbers for modeling heritable fractal-like biostructures, which are developing step by step in ontogenesis of biological bodies.

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Living bodies in a course of their ontogenesis from the embryonic state to the mature state gradually increase the number of body parts. Accordingly, the number of parameters, characterizing the developing body, increases. This leads to appropriate phased increasing a dimensionality of a configurational space of parameters of the body. In many cases of such ontogenetic development one can see the following iterative process: body structural elements, which exist at a previous stage of ontogenesis, produce - at the next step of ontogenesis - new elements with similar structures (Fig. 14.1). In the result, after some repetitions of this ontogenetic procedure, complex fractal-like structure of the multi-level body appears. A multidimensional configurational space of parameters of such body has a fractal-like system of its different subspaces having similar patterns of parametric states. One of many examples of such phased producing a fractal-like structure of multi-level body is ontogenetic producing new and new dichotomic branches in some plants (Fig. 14.1, left).

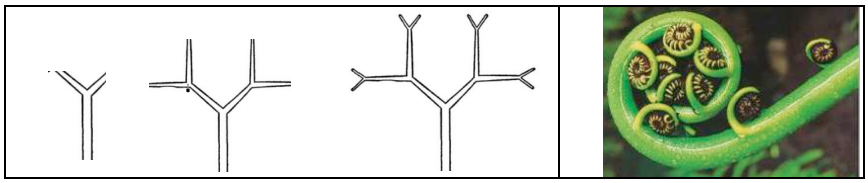

Fig. 14.1. Illustrations for the phased ontogenetic development of fractal-like biological structures (from https://studbooks.net/2365314/tehnika/istoriya_poyavleniya_razvitiya).

Regarding the theme of fractal-like structures in biological bodies, one can note a great number of publications is devoted to algorithmic creation of fractal-like geometric figures in spaces of a fixed (!) dimensionality, first of all, in 2-dimensional complex plane. There are also known works devoted to constructions of fractal geometric patterns on the plane of hyperbolic (or double) numbers [Pavlov, Panchelyuga, Panchelyuga, 2009a,b].

In contrast to these works, the author proposes an approach to model an algorithmic reproduction of patterns, which are similar each other, not in a space of a fixed dimensionality but in different subspaces of multidimensional configurational spaces of parameters of multi-level bodies under their phased ontogenetic development. Due to similarity of parametric structures in its different subspaces, each of considered configurational spaces becomes a fractal-like space in the whole.

The author notes the following possibility of modelling such multi-step ontogenetic development of biological objects and their configurational spaces, which receive new and new parameters and dimensionalities step by step. Let us take the matrix representation of hyperbolic number $[f_1(t), f_2(t); f_2(t), f_1(t)]$ whose components $f_1(t)$ and $f_2(t)$ are functions of time. Fig. 14.2 shows that if this (2*2)-matrix is tensor multiplied on the left by a hyperbolic number [1, 1; 1, 1], which acts as a generator of additional dimensionalities of the configurational space, the result is (4*4)-matrix representing 4-dimensional hyperbolic number $f_1(t)*e_0 + f_2(t)*e_1 + f_1(t)*e_2 + f_2(t)*e_3$. This 4-dimensional configurational space repeats in its subspaces (namely the first plane on the basis vectors e_0 and e_1, and the second plane on the basis vectors e_2 and e_3) the same functions $f_1(t)$ and $f_2(t)$, which were in the initial 2-dimensional space.

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$$\begin{vmatrix} 1 & 1 \\ 1 & 1 \end{vmatrix} \otimes \begin{vmatrix} f_1(t), f_2(t) \\ f_2(t), f_1(t) \end{vmatrix} = \begin{vmatrix} f_1(t), f_2(t), f_1(t), f_2(t) \\ f_2(t), f_1(t), f_2(t), f_1(t) \\ f_1(t), f_2(t), f_1(t), f_2(t) \\ f_2(t), f_1(t), f_2(t), f_1(t) \end{vmatrix} = f_1(t)*e_0 + f_2(t)*e_1 + f_1(t)*e_2 + f_2(t)*e_3$$

Fig. 14.2. An initial step of a generation of a fractal-like 2^n-dimensional space whose subspaces have identical contents. Here e_0, e_1, e_2 and e_3 are basis units from Fig. 2.5.

Repeating the required number of times this operation of the tensor multiplication on the left using the generator [1, 1; 1, 1], we obtain a hierarchical tree of 2^n-dimensional hyperbolic numbers and their corresponding 2^n-dimensional configurational spaces for algorithmic modelling multi-step onthogenesis of a fractal-like morphogenetic construction. Different levels of this tree have subspaces with the same functions $f_1(t)$ and $f_2(t)$, which were in the initial 2-dimensional space; in this sense one can speech about a fractal-like structure of this hierarchy of multi-dimensional configurational spaces of parameters.

We briefly note that the noted generator [1, 1; 1, 1] (Fig. 14.2) can be used in a more complicated form if its components are some functions of time $g_i(t)$, for example [$g_1(t)$, $g_2(t)$; $g_2(t)$, $g_1(t)$]. For modeling biological cyclic processes based on such fractal-like sets of subspaces, the case, in which the functions $f_1(t)$, $f_2(t)$, $g_1(t)$ and $g_2(t)$ are cyclic functions of time, is especially interesting.

15 Pythagoras and the importance of the concept of number

The notion of “number” is the main notion of mathematics and mathematical natural sciences. Pythagoras has formulated the famous idea: “*Numbers rule the world*” or “*All things are numbers*”. This Pythagorean slogan arose not because that the number can express a quantity of objects. Pythagoras was engaged in figured numbers associated with geometric figures: triangular, square, 5-angled, 12-angled, etc. Seeing that different numbers can dictate different geometric shapes, he came up with the idea that numbers have an internal structure and able to organize the outside world according to their properties. In view of this idea, natural phenomena should be explained by means of systems of numbers; the systems of numbers play a role of the beginning for uniting all things and for expressing the harmony of nature [Kline, 1980]. For the Pythagoreans, the number expressed the "essence" of everything, and therefore the phenomena should be explained only with the help of numbers; it was numerical relations that served as the unifying principle of all things and expressed the harmony and order of nature.

Many prominent scientists and thinkers were supporters of this Pythagorean standpoint or of one similar to it. As W. Heisenberg noted, modern physics, where matrices are used as a higher form of numbers, is moving along the same path along which the Pythagoreans walked [Heisenberg, 1958]. Not without reason B. Russell noted that he did not know any other person who could exert such influence on the thinking of people as Pythagoras [Russell,

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1945]. Taking this into account, one can believe that there is no more fundamental scientific idea in the world than this idea about a basic meaning of numbers.

Our research results and the proposed approach can be considered as a further development of this fundamental idea of Pythagoras in connection with the structural organization of the genetic system and inherited biological phenomena.

16 The hypothesis of an analogue of the Weber-Fechner law related to the transmission of information along single nerve fibres

In Section 5 above, the connection of hyperbolic rotations with the basic psychophysical Weber-Fechner law, which has a logarithmic character, was shown. This law is equally applicable to the perception of sensory information through a variety of sensory channels and it can be considered as the law of not only the nervous system, but "*the law of protoplasm*" in accordance with known data [Schulz, 1916]. In the nervous system, sensory information associated with this logarithmic law is transmitted through single nerve fibers in the form of special series of spikes (nervous impulses). It can be assumed that the transmission of information through single nerve fibers is itself associated with some analogue of the Weber-Fechner logarithmic law. This Section contains the author's thoughts on this topic.

As known, the magnitude of the action potential set up in any single nerve fibre is independent of the strength of the exciting stimulus, provided the latter is adequate. An electrical stimulus below threshold strength fails to elicit a propagated spike potential. If it is of threshold strength or over, a spike (a nervous impulse or an action potential) of maximum magnitude is set up. Either the single fibre does not respond with spike production, or it responds to the utmost of its ability under the conditions at the moment. This property of single nerve fibres is termed the all-or-none law (see, for *example,* [Kalat, 2016]). After generating each spike, each neuron has a refractory period t_0, when it is incapable of generating a new spike.

Electrical spikes in brain neurons are produced by using a flow of Na^+ and K^+ ions, which is provided by so called Na^+/K^+ pump [Hodgkin and Huxley, 1952]. It should be noted that the generation of each nervous spike is connected with the same numbers 3 and 2, which were mentioned above many times: the Na^+/K^+ pump uses the energy of one ATP molecule to exchange 3 intracellular Na^+ ions for 2 extracellular K^+ ions [Glitsch, 2001]. Some publications claim that functional features of the Na^+/K^+ pump can be used for brain computations [Forrest, 2014]. In pevious Sections, we have interpreted numbers 3 and 2 as two different parts of the single hyperbolic number $3+2j_1$ (Fig. 2.4, etc). Meeting now this pair of numbers 3 and 2 in generating nervous spikes, one can think that the hyperbolic number $3+2j_1$ plays a certain role in brain computations on the basis of such spike generatings. (The author here expresses special thanks to Professor Matthew He from USA, who told him 2 years ago on publications about these numbers 3 and 2 when generating spikes in neurons).

In the sequence of spikes running along the nerve fiber, the time intervals «t» between adjacent spikes are - in a general case - not equal to each other, but can differ significantly. These changes of the time intervals between spikes carry information transmitted over the

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nerve fiber. Taking into account all the data on the Weber-Fechner law described above, the author hypothesizes on the existence of the following analogue of the Wever-Fechner law in nervous systems:

- in single nerve fibers, the information significance (or the intensity of information perception) of a interpulse interval for the nervous system is a logarithmic function of the duration of this interval in accordance with the following equation:

$$p = k*\ln(t/t_0) \qquad (15.1)$$

where «p» is the information significance of the interpulse interval for the nervous system, «t» is a duration of the interpulse interval, «t_0» is a refractory period (time threshold) of the neuron, ln – natural logarithm, k – a weight factor. Fig. 16.1 compares formulations of the Weber-Fechner law and its supposed analoque for neurons.

The Weber-Fechner law for sensory perceptions	The supposed analoque of the Veber-Fechner law for time sequences of spikes in single nerve fibers
$p = k*\ln(x/x_0)$	$p = k*\ln(t/t_0)$
p - the intensity of perception	p - the information significance of the interpulse interval for the nervous system
x – stimulus intensity	t - a duration of the interpulse interval
x_0 - threshold stimulus	t_0 - is a refractory period (time threshold)
ln – natural logarithm	ln – natural logarithm
k – a weight factor	k – a weight factor

Fig. 16.1. Comparing formulations of the Weber-Fechner law and its supposed analoque for neurons.

From the standpoint of proposed approach to transmitting information along single nerve fibers, these information processes are also related with hyperbolic numbers and with hyperbolic rotations as their particular cases.

17 Some concluding remarks

The development of modern mathematical natural sciences is based on the use of certain mathematical tools. Mathematical tools of theoretical research can be compared with glasses for a visually impaired person: adequate glasses provide a person with a clear and beautiful picture of reality, which he had previously seen as blurred and hidden by fog. Darwin once wrote: "*I have deeply regretted that I did not proceed far enough at least to understand something of the great leading principles of mathematics; for men thus endowed seem to have an extra sense*" (this quotation is taken from [May, 2004]).

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This article attracts attention of researches to an important role of hyperbolic numbers and their matrix representations in algebraic modelling structural features of genetic phenomena (see also [Petoukhov, 2019 c]). The author puts forward the hypothesis that hyper-alphabets of eigenvectors of matrix representations of basis units of 2^n-dimensional hyperbolic numbers play a key role in transmitting biological information and that they can be considered as one of foundations of coding information at different levels of biological organization. He believes that corresponding languages using such hyper-alphabets define many inherited phenomenological structures in biology including molecular genetic structures. In particular, using these hyper-alphabets gives new algebraic tools to study phenomenologic rules in genetics, long literary texts (at least, in Russian language) and also harmony of musical pieces. The proposed algebraic approach is connected with the theme of a grammar of biology mentioned above.

In the author's opinion, the proposed kind of mathematics is beautiful and it can be used for further developing of algebraic biology and informatics in accordance with the famous statement by P. Dirac, who taught that a creation of a physical theory must begin with the beautiful mathematical theory: "*If this theory is really beautiful, then it necessarily will appear as a fine model of important physical phenomena. It is necessary to search for these phenomena to develop applications of the beautiful mathematical theory and to interpret them as predictions of new laws of physics*" (this quotation is taken from [Arnold, 2007]). According to Dirac, all new physics, including relativistic and quantum, are developing in this way. One can suppose that this statement is also true for mathematical biology.

Appendix I. Dyadic groups of binary numbers, modulo-2 addition and matrices of dyadic shifts

This article has repeatedly used a special decomposition of bisymmetric (2^n*2^n)-matrices, which represented them as a sum of 2^n sparse matrices, defining multiplication tables of corresponing algebras (Figs. 2.3, 2.4, 7.2, 8.3). Just these sparce matrices represented the basic units of hyperbolic numbers. This Appendix explains what this special kind of decomposition is.

Bisymmetric matrix representations of 2^n-dimensional hyperbolic numbers have the peculiarity that the set of numbers of the first row of the matrix is completely repeated in each subsequent row with some permutation or "shift". This permutation is called the dyadic shift and is associated with the well-known operation of modulo-2 addition described below. Matrices constructed by this principle are called dyadic shift matrices. Matrix representations of 2^n-dimensional hyperbolic numbers are constructed by analogy with dyadic shift matrices. Decompositions of such matrices provide that each of appearing sparse matrices contains only one identical non-zero number in each row (Figs. 2.3, 2.4, 7.2, 8.3).

Modulo-2 addition is utilized broadly in the theory of discrete signal processing as a 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:

$$0 + 0 = 0,\ 0 + 1 = 1,\ 1 + 0 = 1,\ 1 + 1 = 0 \qquad \text{(A1)}$$

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For example, modulo-2 addition of two binary numbers 110 and 101, which are equal to 6 and 5 respectively in decimal notation, gives the result 110⊕101 = 011, which is equal to 3 in decimal notation (⊕is the symbol for modulo-2 addition). The set of binary numbers

$$000, 001, 010, 011, 100, 101, 110, 111 \qquad \text{(A2)}$$

forms a dyadic group with 8 members, in which modulo-2 addition serves as the group operation [Harmuth, 1989]. By analogy dyadic groups of binary numbers with 2^n members can be presented. The distance in this symmetry group is known as the Hamming distance. Since the Hamming distance satisfies the conditions of a metric group, the dyadic group is a metric group. The modulo-2 addition of any two binary numbers from (A2) always gives a new number from the same series. The number 000 serves as the unit element of this group: for example, 010⊕000 = 010. The reverse element for any number in this group is the number itself: for example, 010⊕010 = 000. Each member from (A2) possesses its inverse-symmetrical partner (or a mating number), which arises if the binary symbol of the member is transformed by the inverse replacements 0→1 and 1→0. For example, binary numbers 010 and 101 give an example of such pair of mating numbers.

The series (A2) is transformed by modulo-2 addition with the binary number 001 into a new series (A3) of the same numbers:

$$001, 000, 011, 010, 101, 100, 111, 110 \qquad \text{(A3)}$$

Such changes in the initial binary sequence, produced by modulo-2 addition of its members with any binary numbers (A2), are termed dyadic shifts [Ahmed and Rao, 1975; Harmuth, 1989]. If any system of elements demonstrates its connection with dyadic shifts, it indicates that the structural organization of its system is related to the logic of modulo-2 addition. The article shows additionally that the structural organization of genetic systems is related to logic of modulo-2 addition.

By means of dyadic groups, a special family of (2^n*2^n)-matrices can be constructed which are termed “matrices of dyadic shifts” and which are used widely in technology of discrete signal processing [Ahmed, Rao, 1975; Harmuth, 1977, §1.2.6]. Fig. A1 shows examples of bisymmetric matrices of dyadic shifts. In these matrices their rows and columns are numerated by means of binary numbers of an appropriate dyadic group. All matrix cells are numerated by means of binary numbers of the same dyadic group in such way that a binary numeration of each cell is a result of modulo-2 addition of binary numerations of its column and its row. For example, the cell from the column 110 and the row 101 obtains the binary numeration 011 by means of such addition. Such numerations of matrix cells are termed “dyadic-shift numerations” (or simply “dyadic numeration”).

	0	1
0	0	1
1	1	0

	00 (0)	01 (1)	10 (2)	11 (3)
00 (0)	00 (0)	01 (1)	10 (2)	11 (3)
01 (1)	01 (1)	00 (0)	11 (3)	10 (2)
10 (2)	10 (2)	11 (3)	00 (0)	01 (1)
11 (3)	11 (3)	10 (2)	01 (1)	00 (0)

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	000 (0)	001 (1)	010 (2)	011 (3)	100 (4)	101 (5)	110 (6)	111 (7)
000 (0)	000 (0)	001 (1)	010 (2)	011 (3)	100 (4)	101 (5)	110 (6)	111 (7)
001 (1)	001 (1)	000 (0)	011 (3)	010 (2)	101 (5)	100 (4)	111 (7)	110 (6)
010 (2)	010 (2)	011 (3)	000 (0)	001 (1)	110 (6)	111 (7)	100 (4)	101 (5)
011 (3)	011 (3)	010 (2)	001 (1)	000 (0)	111 (7)	110 (6)	101 (5)	100 (4)
100 (4)	100 (4)	101 (5)	110 (6)	111 (7)	000 (0)	001 (1)	010 (2)	011 (3)
101 (5)	101 (5)	100 (4)	111 (7)	110 (6)	001 (1)	000 (0)	011 (3)	010 (2)
110 (6)	110 (6)	111 (7)	100 (4)	101 (5)	010 (2)	011 (3)	000 (0)	001 (1)
111 (7)	111 (7)	110 (6)	101 (5)	100 (4)	011 (3)	010 (2)	001 (1)	000 (0)

Fig. A1. The examples of matrices of dyadic shifts. Parentheses contain expressions of the numbers in decimal notation.

Appendix II. Matrix representations of basis units of 32-dimensional hyperbolic numbers

The Appendix contains matrix representations of basis units e_0, e_1, e_2, …, e_{31} of 32-dimensional hyperbolic numbers $a_0e_0+a_1e_1+a_2e_2+….+a_{31}e_{31}$. Each of these matrices is a permutation matrix having in each row and in each column onle one entry 1, all other matrix cells contain zero. Each of matrices is a matric of dyadic shifts described above in the Appendix I.

e_0 (the unit matrix):

1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

e_1 :

0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0

e_2 :

0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0

e_3 :

0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0

e_4 :

0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	**1**

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0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

e_5 :

0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0

e_6 :

0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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e_7 :

0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0

e_8 :

0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_9 :

0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0

e_{10} :

0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0

e_{11} :

0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{12} :

0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{13} :

0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{14} :

0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{15} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

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e_{16} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{17} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{18} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{19} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{20} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{21} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{22} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{23} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{24} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{25} :

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{26} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{27} :

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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e_{28} :

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{29} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e_{30} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0

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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

e_{31} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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References

Ahmed, N.U., Rao, K.R. *Orthogonal transforms for digital signal processing*. Springer-Verlag New York, Inc. (1975).

Apel W. *Harvard Dictionary of Music*. Cambridge, Massachusetts: Harvard University Press (1969). ISBN 978-0-674-37501-7.

Arnold V. A complexity of the finite sequences of zeros and units and geometry of the finite functional spaces. Lecture at the session of the Moscow Mathematical Society, (May 13, 2007), http://elementy.ru/lib/430178/430281.

Bailey Ch.-J.N. (1982). On the Ying and Yang Nature of Language. Ann Arbor: Karoma.

Baines A. *Woodwind Instruments and Their History*. New York: Courier Dover Publications (1991), ISBN 978-0-486-26885-9].

Ballonoff P. Some Properties of Transforms in Cultural Theory. - Int J Theor Phy, 49, pp. 2998–3004 (2010), DOI 10.1007/s10773-010-0438-7.

Balonin N.A. New course on the theory of motion control (Novyi kurs teorii upravleniia dvizheniem). Saint Petersburg State University, Saint Petersburg (2000) (in Russian).

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

Bellman R. *Introduction to Matrix Analysis*. N-Y: Mcgraw-Hill Book Comp. (1960)]

Bodnar O.Ya. Geometry of phyllotaxis. *Reports of the Academy of Sciences of Ukraine*, №9, pp. 9-15 (1992).

Bodnar O.Ya. *Golden Ratio and Non-Euclidean Geometry in Nature and Art*. Lviv: Publishing House "Sweet" (1994).

Chargaff E. Preface to a Grammar of Biology: A hundred years of nucleic acid research. – Science, 172, 637-642 (1971).

Christidis A.-F., Arapopoulou M., Christi M. *A History of Ancient Greek: From the Beginnings to Late Antiquity*. Cambridge: Cambridge University Press (2007). ISBN 978-0-521-83307-3.

Gladwell G.M.L. Inverse Problems in Vibration. London, Kluwer Academic Publishers, (2004).

Collins Concise Dictionary, 4th edition, HarperCollins, Glasgow (1999). ISBN 0 00 472257 4.

Day-O'Connell J. *Pentatonicism from the Eighteenth Century to Debussy*. Rochester: University Rochester Press (2007). ISBN 978-1-58046-248-8.

Fimmel E., Danielli A., Strüngmann L. On dichotomic classes and bijections of the genetic code. *J. Theor. Biol*., 336, 221–230. https://doi.org/10.1016/j.jtbi.2013.07.027 (2013).

Forrest M.D. The sodium-potassium pump is an information processing element in brain computation. *Frontiers in Physiology*, 5, article 472 (2014).

doi: 10.3389/fphys.2014.00472, PMCID: PMC4274886, PMID: 25566080, https://sci-hub.se/10.3389/fphys.2014.00472 .

Frey-Wissling A., Muhlethaler K. *Ultrastructural plant cytology, with an Introduction to molecular biology*. Amsterdam, New York, Elsevier Pub. Co. (1965).

Glitsch H. G. Electrophysiology of the sodium-potassium-ATPase in cardiac cells. *Physiol. Rev*. 81, pp. 1791–2826 (2001).

Gsponer A., Hurni J.-P. Quaternions in mathematical physics (2): Analytical bibliography, http://arxiv.org/abs/math-ph/0511092, 3th version from 6 July 2008.

Harkin A.A., Harkin J.B. Geometry of Generalized Complex Numbers. *Mathematics Magazine*, v. 77(2), p. 118-29 (2004).

Harmuth, **H**. **F**. *Sequency theory. Foundations and applications*. N.-Y.: Academic Press. (1977).

Harmuth, H. **F**. *Information theory applied to space-time physics*. Washington: The Catholic University of America, DC (1989)

Heisenberg W. *Physics and philosophy*. New York: Harper & Row, 1958.

Hesse H. *The Glass Bead Game*. St Martins Press (2002), ISBN 0312278497, 9780312278496]).

Hodgkin A. L., Huxley A. F. A quantitative description of membrane current and its application to conduction and excitation in nerve. *J. Physiol*. (Lond.) 117, pp. 500–544 (1952).

Ivanov Viach.Vs. Linguistic way of Roman Jakobson. – In: Jakobson R.O. *Selected*

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

works. M., Progress (1985, in Russian).

Jacob F. (1974). Le modele linguistique en biologie. *Critique, Mars*, *30*(322), pp.197-205.

Jacob F., Jakobson R., Levi-Strauss C., Heritier P.L. (1968). Vivre et parler. – *Lettre francaises*, p. 1221-1222, Feb. 1968.

Jakobson R.O. (1985). Selected works. M., Progress (1985, in Russian).

Jakobson R. (1987). *Language in Literature.* Cambridge: MIT Press (1987).

Jakobson R.O. (1999). *Texts, Documents, Studies*. Moscow: RGGU (1999, in Russian).

Jean R. *Phyllotaxis. A systemic study in plant morphogenesis*. Cambridge Univ. Press (2006).

Kalat J.W. *Biological psychology* (12 ed.). (2016). Australia. ISBN 9781305105409. OCLC 898154491

Kantor I.L., Solodovnikov A.S. *Hypercomplex numbers*. Berlin, New York: Springer-Verlag (1989). ISBN 978-0-387-96980-0.

Klein F. Elementary Mathematics from an Advanced Standpoint: Arithmetic, Algebra, Analysis. London: Dover Publications (2004).

Kline M. *Mathematics: The Loss of Certainty*. Oxford University Press (1982).

Makovsky M.M. Linguistic genetics. M., Nauka (1992, in Russian).

May R.M. Uses and Abuses of Mathematics in Biology. *Science*, v. 303, pp. 790-793 (6 February 2004).

McCulloch W.S. Embodiments of mind. Cambridge (Mass.), MIT Press, 1965, 438 p.

Nielsen M.A., Chuang I.L. *Quantum Computation and Quantum Information*. New York: Cambridge University Press. https://doi.org/10.1017/CBO9780511976667 (2010).

Olsen D.A., Sheehy D.E. (Eds.) *The Garland Encyclopedia of World Music*, Volume 2: South America, Mexico, Central America, and the Caribbean. New York: Taylor & Francis. (1998). ISBN 0824060407.

Pauling L. *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. (1940).

Pavlov D.G., Panchelyuga M.S., Panchelyuga V.A. On the form of the analogue of the Julia set at zero value of the parameter on the plane of the double variable. *Hypercomplex numbers in geometry and physics*, v. 6, N 1 (11), pp. 146-151 (2009a).

Pavlov D.G., Panchelyuga M.S., Panchelyuga V.A. On the form of analogues of the Julia set on the plane of a double variable. *Hypercomplex numbers in geometry and physics*, v. 6, N 2 (12), pp. 161-175 (2009b).

Petoukhov S.V. *Biomechanics, bionics and symmetry*. Moscow, Nauka (1981)

Petoukhov S.V. *Biosolitons*. Moscow: GP Kimrskaya tipographia, 288p. (1999).

Petoukhov S.V. *Matrix genetics, algebrases of genetic code, noise immunity*. Moscow, RCD, 316 p. (2008) (in Russian).

Petoukhov S.V. Matrix genetics and algebraic properties of the multi-level system of genetic alphabets. *Neuroquantology*, v. 9, №4, p. 60-81 (2011).

Petoukhov S.V. The concept of resonances in genetics ("resonant bioinformatics"). Selected proceedings of the VII International Congress "Weak and Super-Weak Fields and Radia tions in Biology and Medicine", 7. 09.2015, St. Petersburg, pp.1-41 (2015).

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

http://www.biophys.ru/lib/sci/resonance/460-resonance-00001.

Petoukhov S.V. The system-resonance approach in modeling genetic structures. *Biosystems*, v. 139, p. 1-11 (January 2016).

Petoukhov S.V. Genetic coding and united-hypercomplex systems in the models of algebraic biology. *Biosystems*, v. 158, August 2017, pp. 31–46 (2017).

Petoukhov S.V. The Genetic Coding System and Unitary Matrices. Preprints 2018, 2018040131 (doi: 10.20944/preprints201804.0131.v2), submitted 27.09.2018. http://www.preprints.org/manuscript/201804.0131/v2 (2018a).

Petoukhov S.V. Structural Connections between Long Genetic and Literary Texts. *Preprints* **2018**, 2018120142, online 15 02 2019. (DOI: 10.20944/preprints201812.0142.v2) (2018b). https://www.preprints.org/manuscript/201812.0142/v2

Petoukhov S.V. Nucleotide Epi-Chains and New Nucleotide Probability Rules in Long DNA Sequences. *Preprints* **2019**, 2019040011 (doi: 10.20944/preprints201904.0011.v2) (2019a). https://www.preprints.org/manuscript/201904.0011/v2.

Petoukhov S.V. Connections Between Long Genetic and Literary Texts. The Quantum-Algorithmic Modelling. In: Hu Z., Petoukhov S., Dychka I., He M. (eds) *Advances in Computer Science for Engineering and Education II*. pp 534-543, ICCSEEA 2019. Advances in Intelligent Systems and Computing, vol. 938. Springer, Cham. Online publication on 29 March 2019. (2019b). https://link.springer.com/chapter/10.1007/978-3-030- 16621-2_50#citeas .

Petoukhov S.V. Hyperbolic Numbers in Modeling Genetic Phenomena. *Preprints* 2019, 2019080284, 36 pages (2019c). (doi: 10.20944/preprints201908.0284.v2). https://www.preprints.org/manuscript/201908.0284/v2 .

Petoukhov S.V., He M. *Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications*. IGI Global, USA (2010). http://petoukhov.com/Petoukhov,%20He%20-%202010%20-%20Symmetrical%20Analysis%20Techniques%20for%20Genetic%20Systems%20and%20Bioinformatics.pdf.

Petoukhov S.V., Petukhova E.S., Svirin V.I. Symmetries of DNA alphabets and quantum informational formalisms. *Symmetry: Culture and Science*, Vol. 30, No. 2, 161-179 (2019), https://doi.org/10.26830/symmetry_2019_2_161

Prasolov V.V. Problems and Theorems in Linear Algebra (Translations of Mathematical Monographs, Vol. 134). American Mathematical Society, 225 pages, 1994. ISBN-10: 0821802364; ISBN-13: 978-0821802366

Rapoport A.E., Trifonov E.N. Compensatory nature of Chargaff's second parity rule. *Journal of Biomolecular Structure and Dynamics*, November, 1-13, (2012), DOI:10.1080/07391102.2012.736757

Ratner V.A. *Genetics, Molecular Cybernetics*. Novosibirsk: Nauka, 2002 (in Russian).

Rashevskij P.K. *Tensor analysis and Riemannian geometry*. Moscow, Nauka (1964).

Russell B. A *history of western philosophy*. New York: Touchstone (1945).

Sethares W.A. Tuning, Timbre, Spectrum, Scale. London, Springer, p.163 (2005). ISBN 1-85233-797-4.

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 16 January 2020 doi:10.20944/preprints201908.0284.v3

Shervatov V.G. *Hyperbolic functions*. Moscow, GITTL (1954).

Shults E. The organism as a creativity. In the book "*Questions of theory and psychology of creativity" ("Voprosy teorii i psikhologii tvorchestva")*, Russia, Kharkov, vol.7, pp. 108-190 (1916) (in Russian)].

Smolyaninov V.V. Spatio-temporal problems of locomotion control. Uspekhi Fizicheskikh Nauk, v. 170, N 10, pp. 1063–1128 (2000), DOI: https://doi.org/10.3367/UFNr.0170.200010b.1063.

Stakhov A.P. *The Mathematics of Harmony. From Euclid to Contemporary Mathematics and Computer Science*. New Jersey, World Scientific (2009).

Stambuk N. Circular coding properties of gene and protein sequences. *Croat. Chem. Acta*, 72, pp. 999-1008 (1999).

Sudhibhushan Bhattacharya. *Ethno-musicology and India*. Indian Publications, p. 54 (1968). Retrieved 22 June 2012.

Todd Titon J.T. *Worlds of Music: An Introduction to the Music of the World's Peoples*, Shorter Version. Boston: Cengage Learning (1996). ISBN 9780028726120.

Vernadsky V.I. *The chemical structure of the biosphere and its environment*. Moscow, Nauka (1965) (in Russian).

Weinberger N.M. Music and brain. *Sci. Amer.,* 291 (5), pp. 88-95 (2004).

Yamagishi M.E.B. Mathematical Grammar of Biology. – Switzerland, Springer International Publishing AG (2017). ISBN 978-3-319-62689-5.

Zharov V.E. *Spherical astronomy*. Friazino: RFFI (2002).