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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 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 psychophysical 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. A general hyperbolic rule regarding the oligomer cooperative organization of different genomes is described jointly with its quantum-information model. Besides, the

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hypothesis about some analog 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 the 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 the next generations. G. Mendel, in his experiments with plant hybrids, found that the transmission of traits during the crossing of organisms occurs by 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 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 [McFadden, Al-Khalili, 2018]. For this reason, the author focuses on studying the system of genetic alphabets and the genetic code in the

form of mathematical matrices constructed on binary-oppositional features of DNA alphabets.

In 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 encode 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. The genetic coding of information has noise immunity, which allows the transfer of genetic information from ancestors to descendants along the generation chain through 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 other sciences. It is about unraveling the bioinformatical patents of living matter.

This article draws special attention to structural analogies of the molecular system of genetic coding with one of the 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, the theory of games and optimizations, etc. and interesting for their application in algebraic biology.

The main task of mathematical natural sciences is the creation of mathematical models of natural systems. The 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 the development of theories and calculations in problems of heat, light, sounds, fluctuations, elasticity, gravitation, mag-

netism, 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 particular to works by O. Bodnar who noted that ontogenetic transformations of phyllotaxis lattices in plants can be formally modeled 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 the geometry of living bodies has structural relations with Minkovsky geometry. Another evidence in favor of structural relations 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".

All physiological systems must be argued with a genetic coding system to be genetically encoded for their survival and inheritance into the 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 known data about ratios of musical harmony in the parametric organization of DNA molecules, new algebraic approaches are proposed for analyzing the 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

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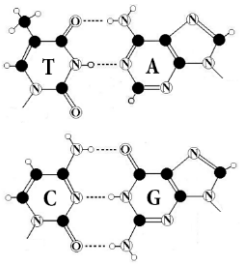
thymine T. They form a DNA alphabet of 4 monoplets. Besides, DNA alphabets of 16 doublets and 64 triplets also exist. It is known [Fimmel, Danielli, Strüngmann, 2013; Petoukhov, 2008; Petoukhov, He, 2010; Stambuk, 1999] that these four nucleobases A, C, G, and T are interrelated due to their symmetrical 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 onds	$\mathbf{0}_3$	$\mathbf{1}_3$	$\mathbf{0}_3$	$\mathbf{1}_3$

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 based on 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 through 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 posi-

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tion 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 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 a 4-bit binary number $0_20_10_20_1$, the doublet CA – as a 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 a 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 enumerated by binary symbols in line with the following principle. Entries of each column are enumerated 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-purine-purine” and so this column is correspondingly enumerated 011). By contrast, entries of each of rows are enumerated 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.

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

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two matrices, each of the 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

	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

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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 the tables is constructed in line with the principle of binary numeration of its column and rows based on 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

9	6	6	4
6	9	4	6

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2	3

6	4	9	6
4	6	6	9

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 the 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

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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 the 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 synonymical 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):

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

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 $a*\mathbf{1}+b*\mathbf{j}$ 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]:

$$\begin{vmatrix} \cosh & x, \end{vmatrix}$$

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

Symmetric matrices that represent hyperbolic numbers have real eigenvalues and orthogonal eigenvectors (which distinguishes them from non-symmetric 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 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}

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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 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 III 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

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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 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:

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

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$(F_{n+1}/F_n) \rightarrow (F_{n+2}/F_{n+1})$: 2/1 → 3/2 → 5/3 → 8/5 → 13/8 → 21/13 →… (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, …. (3.4)

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

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:

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

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

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

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

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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 $(u^2 - v^2)^{0.5}$:

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

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:

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

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:

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

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

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

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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 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

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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 multiresonance 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:

$3e_0+2e_1+1e_2+1e_3$; $5e_0+3e_1+2e_2+1e_3$; $8e_0+5e_1+3e_2+2e_3$; $13e_0+8e_1+5e_2+3e_3$; … (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):

$1e_0+1e_1+3e_2+7e_3$; $1e_0+3e_1+5e_2+11e_3$; $2e_0+4e_1+8e_2+18e_3$; $3e_0+7e_1+13e_2+29e_3$;… (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

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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 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):

$-8e_0-4e_1+4e_2+12e_3$; $-12e_0-8e_1+4e_2+20e_3$; $-20e_0-12e_1+8e_2+32e_3$; $-32e_0-20e_1+12e_2+32e_3$;.. (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.

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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):

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

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]

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 num-

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ber 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).

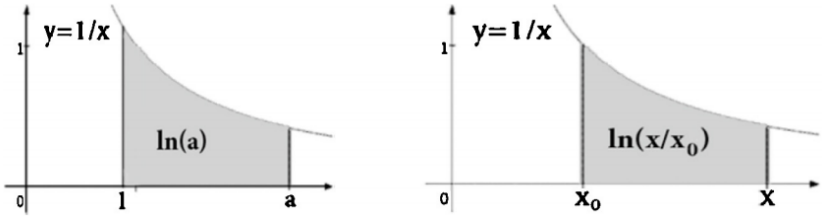

Fig. 5.1. Natural logarithm as the area under the hyperbola y = 1/x. Left: ln(a) is equal to the area under the hyperbola from 1 to a. Right: $\ln(x/x_0)$ is equal to the area under the hyperbola from x_0 to x.

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 most pleasant forms, human persons come to the preference of the

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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 [φ, φ^{-1}; φ^{-1}, φ]. 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],

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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).

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

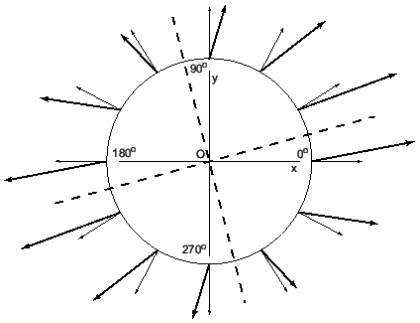

Fig. 6.1. Illustration of actions of the matrix A on vectors [x, y] (from [Zharov, 2002])

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 +

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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

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

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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.

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

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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.

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, Arapopoulou, 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 com-

binations 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 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.

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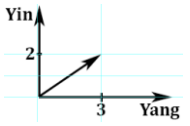
As it was reminded above, over the centuries from Ancient China to antiquity, the numbers 2 and 3 were considered respectively as female and male numbers (that is as Yin and Yang numbers) forming the important pair. The author proposes their consideration not as separate one-dimensional numbers but as 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

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(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}, ...

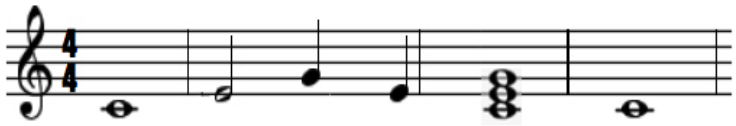

Fig. 8.1. A conditional musical fragment written on the basis of the musical scale having only three kinds of musical notes.

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 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):

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

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

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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 number $a_0\bar{e}_0 + a_1\bar{e}_1 + a_2\bar{e}_2 + a_3\bar{e}_3$ 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):

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

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):

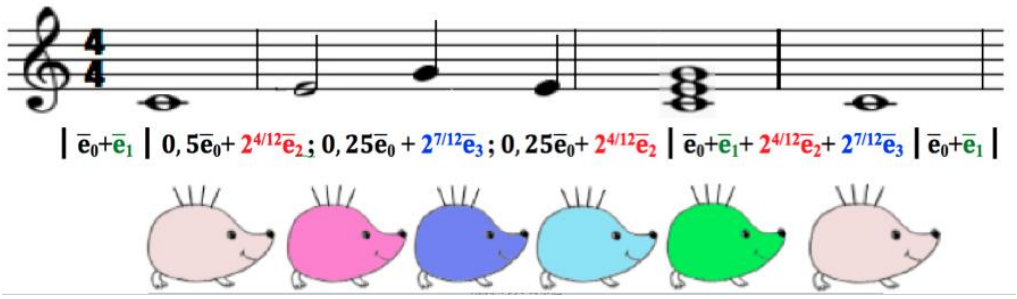

Fig. 8.4. The artistic image of the sequence of sets of 4 orthogonal eigenvectors of
bisymmetric matrices, which represent elements of the musical fragment.

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 trans-

formation. 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 orthogonal 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.

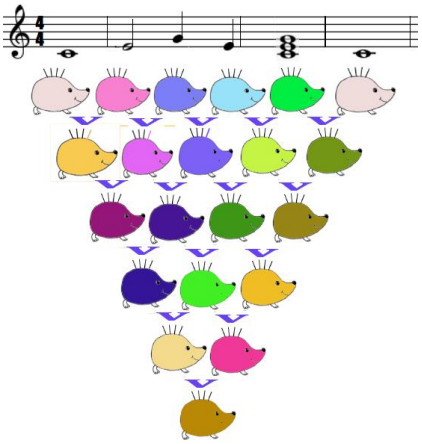

Fig. 8.5. The artistic image of the tree, whose levels show sequences of sets of
4 orthogonal eigenvectors of matrices of orthogonal transformations, which are
hiddenly related with the sequence of elements of the musical fragment.

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.

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

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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;
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.

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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%).

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

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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

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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. 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.

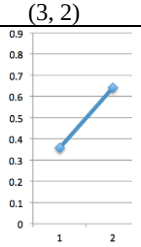
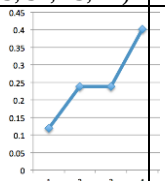
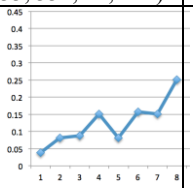
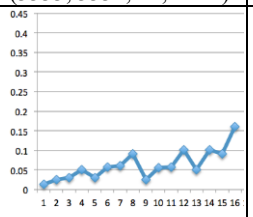
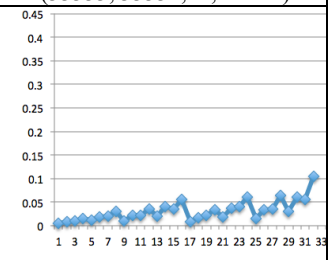
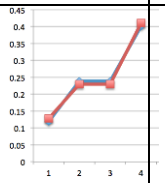
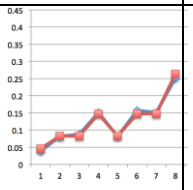
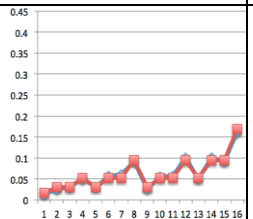
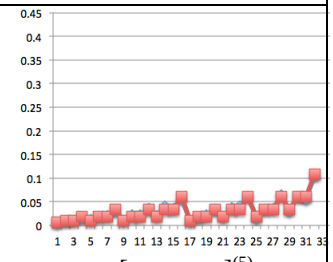
Percentages of 2 monoplets (3, 2)	Percentages of 4 doublets (33, 32, 23, 22)	Percentages of 8 triplets (333, 332, …, 222)	Percentages of 16 tetraplets (3333, 3332, …, 2222)	Percentages of 32 pentaplets (33333, 33332,…, 22222)
 q=0,35873552 p=0,64126448				
q=0,35873552 p=0,64126448	 $[q, p; p, q]^{(2)}$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

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 chro-

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mosome 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.
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;

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[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*-

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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.

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 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 ac-

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cented 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).

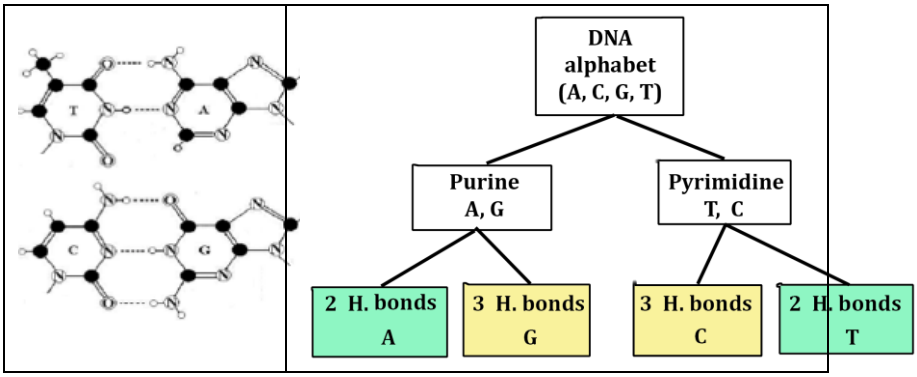

Fig. 11.1. Left: the DNA alphabet of 4 nucleobases A, C, G and T. Right: the scheme of
binary-oppositional structure of this DNA alphabet.

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.

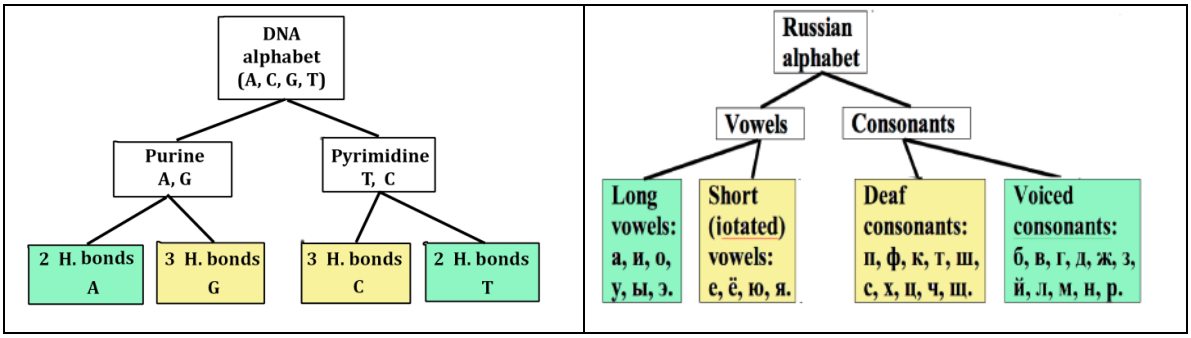

Fig. 11.2. The similarity of binary-oppositional structures of the DNA alphabet (left) and the alphabet of Russian lanquage (right).

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:

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- $\%0*e_0 + \%1*e_1$ (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; 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

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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.

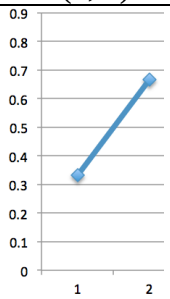
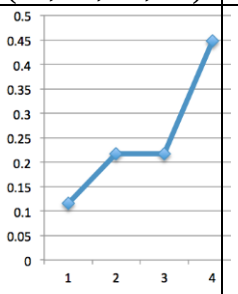
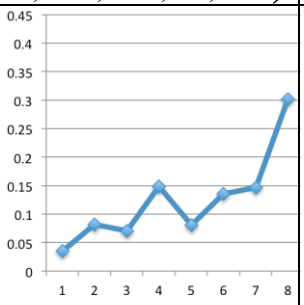
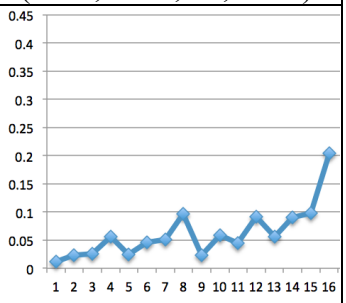
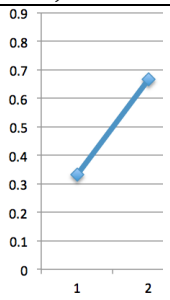
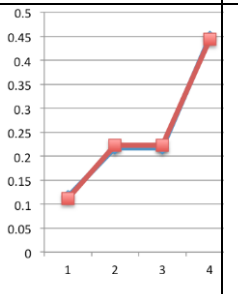
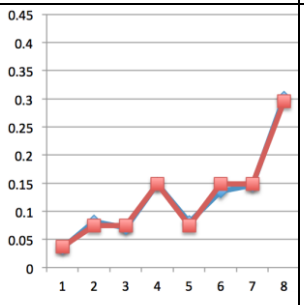
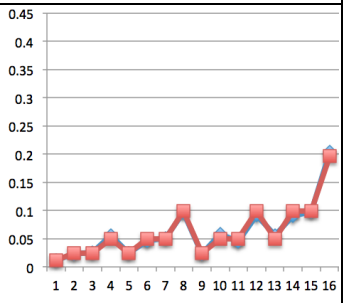
<table>
<tr><th colspan="4">L.N. Tolstoy «Anna Karenina» (1309047 letters)</th></tr>
<tr><th>Percentages of
2 monoplets
(0, 1)</th><th>Percentages of
4 doublets
(00, 01, 10, 11)</th><th>Percentages of
8 triplets
(000, 001, 010, …, 111)</th><th>Percentages of
16 tetraplets
(0000, 0001, …, 1111)</th></tr>
<tr><td> 
%0= 0,3337092
%1= 0,6662908</td><td>  </td><td>  </td><td>  </td></tr>
<tr><td> 
%0= 0,3337092
%1= 0,6662908</td><td> 
[%0,%1; %1,%0](2)</td><td> 
[%0,%1; %1,%0](3)</td><td> 
[%0,%1; %1,%0](4)</td></tr>
</table>

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

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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;

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$0_P1_P1_P1_P$=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/). 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.

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)

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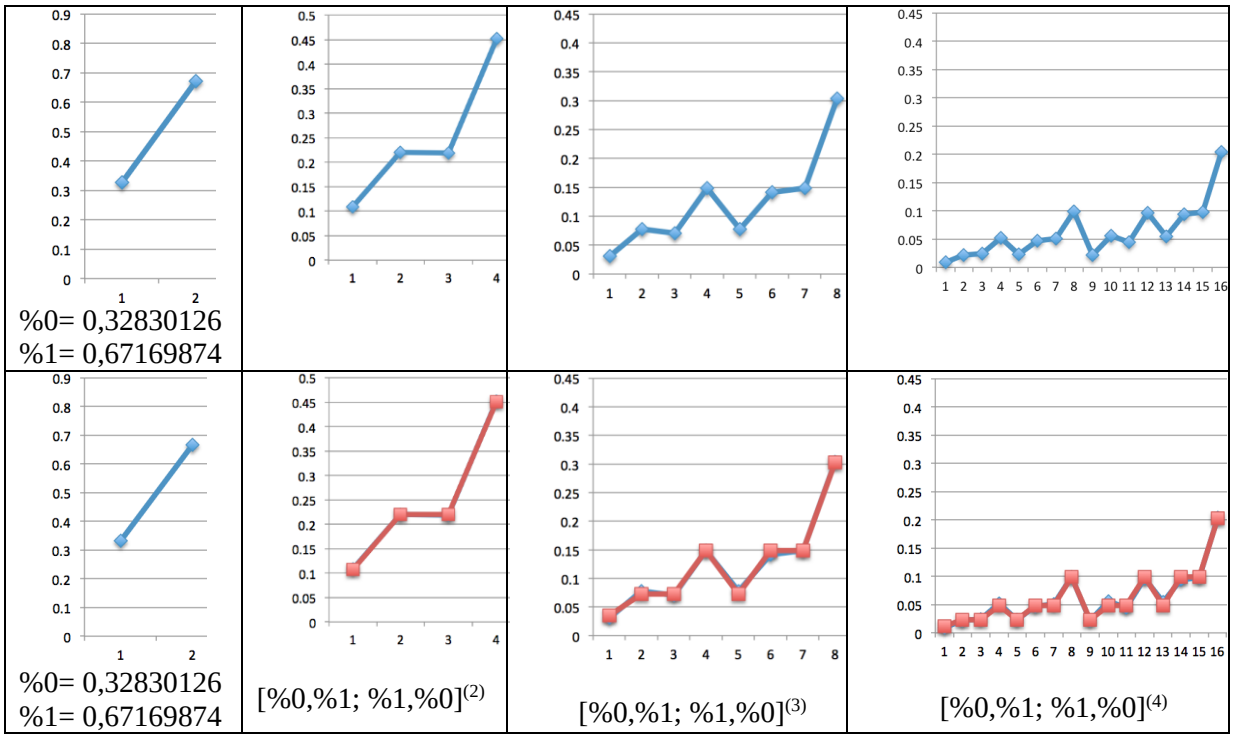

Fig. 11.5. Graphical analysis results of the novel "War and Peace" (Book 1) by Leo Tolstoy (the original literary text was accessed from http://samolit.com/books/64/). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points 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;

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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 hyper-

bolic 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.

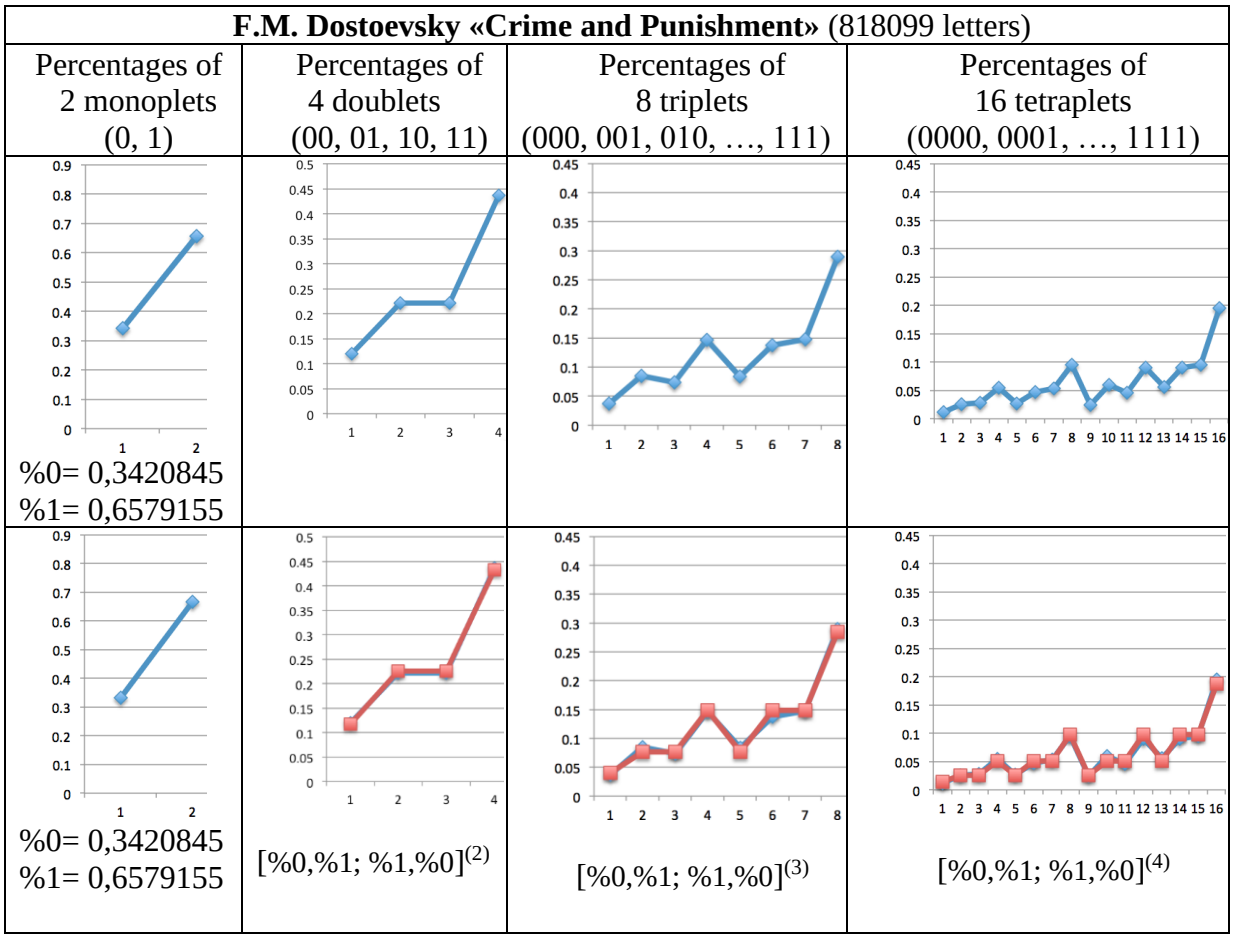

Fig. 11.7. Graphical analysis results of the novel "Crime and Punishment" by F.M. Dostoevsky (the original literary text was accessed from http://samolit.com/books/57/). Percentages of all the types of binary n-plets (n = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond to phenomenologic values of the

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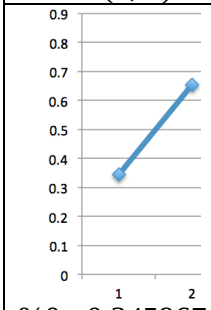
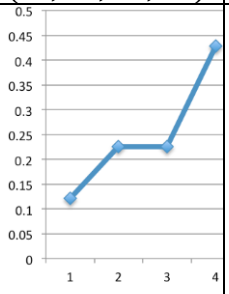
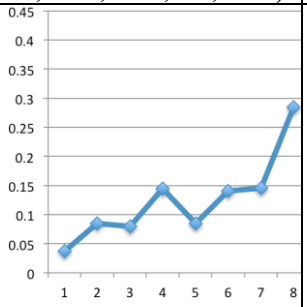
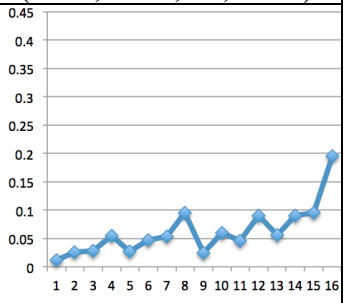
percentages of hydrogen *n*-plets, while red points correspond to model values of the percentages calculated as coordinates of the 2^n-dimensional hyperbolic numbers $[\%0, \%1; \%1, \%0]^{(n)}$, where %0 and %1 are percentages of monoplets 0 and 1; (*n*) refers to tensor powers.

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.
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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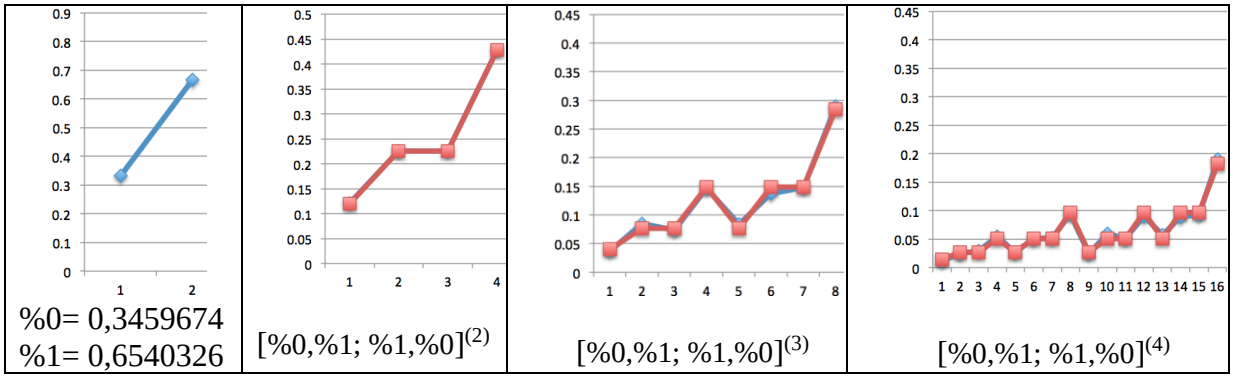

Fig. 11.9. Graphical analysis results of the novel "Idiot" by F.M. Dostoevsky (the original literary text was accessed from http://samolit.com/books/56/). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond 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;

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$0_P1_P1_P$=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 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)

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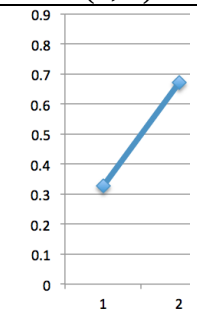
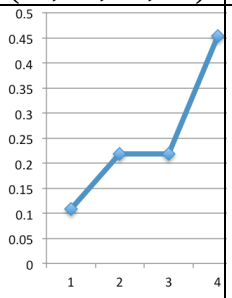
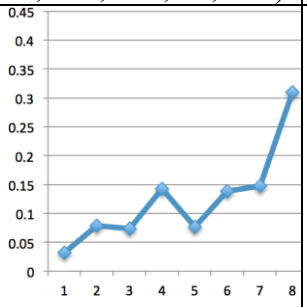
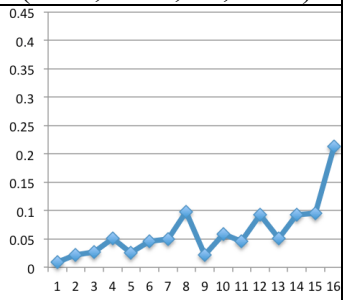
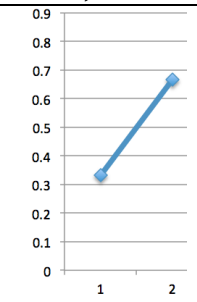
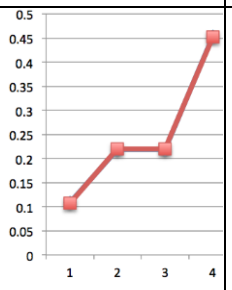
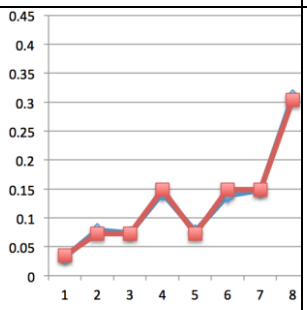
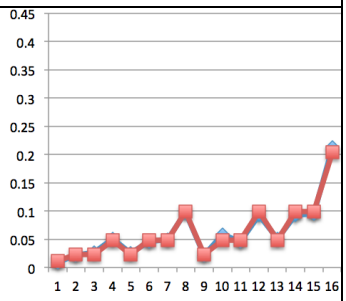
Percentages of 2 monoplets (0, 1)	Percentages of 4 doublets (00, 01, 10, 11)	Percentages of 8 triplets (000, 001, 010, …, 111)	Percentages of 16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3277771 %1= 0,6722229			
 %0= 0,3277771 %1= 0,6722229	 [%0,%1; %1,%0](2)	 [%0,%1; %1,%0](3)	 [%0,%1; %1,%0](4)

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.

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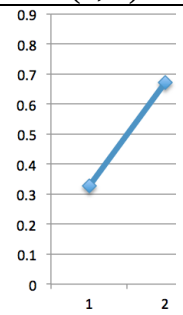
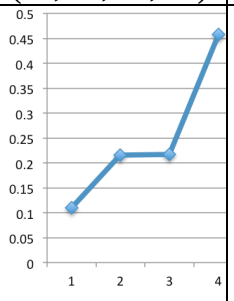
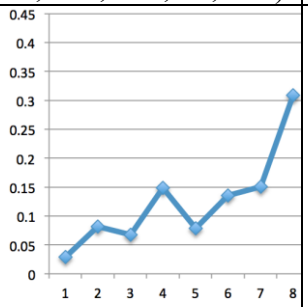
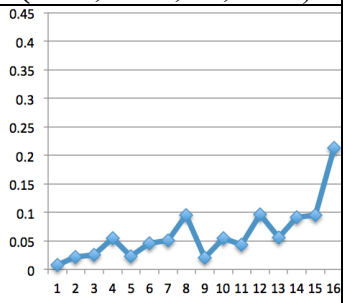
Fig. 11.12. Numeric analysis results of the novel "Evgenij Onegin" by A.S. Pushkin (the original literary text was accessed from http://tululu.org/b57798/). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representation of this novel are shown. All values are rounded 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.

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			

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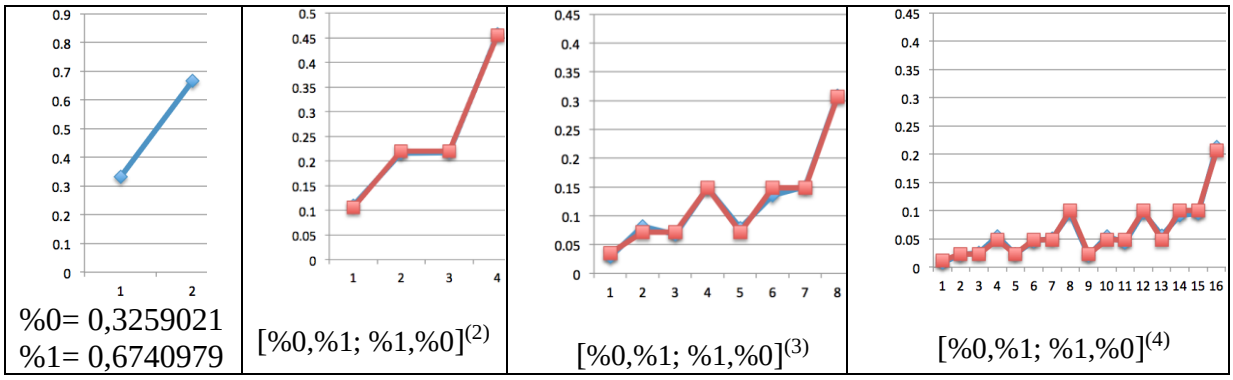

Fig. 11.13. Graphical analysis results of the novel "Dubrovsky" by A.S. Pushkin (the original literary text was accessed from http://samolit.com/books/61/). Percentages of all the types of binary *n*-plets (*n* = 1, 2, 3, 4) from the binary representations of this novel are shown. Blue points correspond 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
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;

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$1_P1_P1_P$=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	Percentages of	Percentages of	Percentages of

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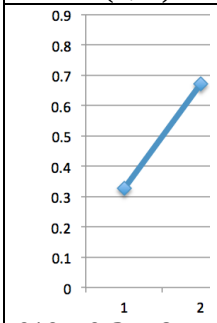
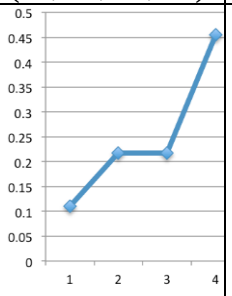
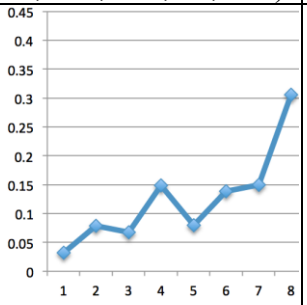
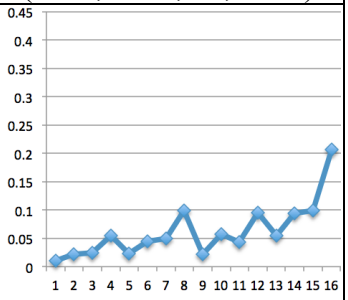
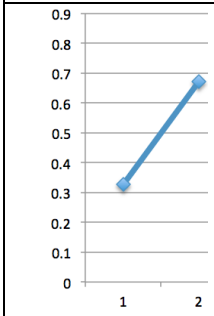
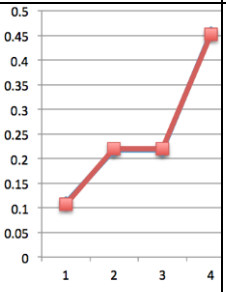
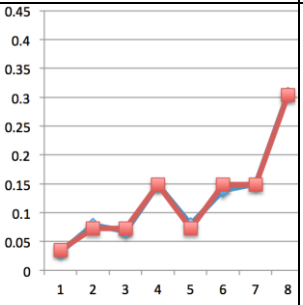
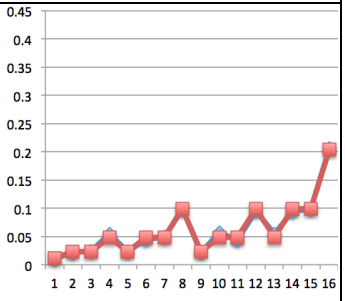
2 monoplets (0, 1)	4 doublets (00, 01, 10, 11)	8 triplets (000, 001, 010, …, 111)	16 tetraplets (0000, 0001, …, 1111)
 %0= 0,3279771 %1= 0,6720229			
 %0= 0,3279771 %1= 0,6720229	 [%0,%1; %1,%0](2)	 [%0,%1; %1,%0](3)	 [%0,%1; %1,%0](4)

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

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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.

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

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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.

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

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

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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

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.

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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.

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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.

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).

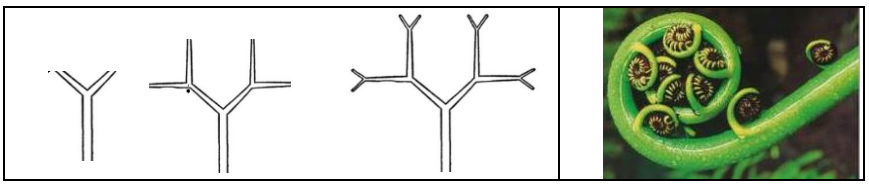

Fig. 14.1. Illustrations for the phased ontogenetic development of fractal-like biological structures (from https://studbooks.net/2365314/tehnika/istoriya_poyavleniya_razvitiya).

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

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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.

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

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

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of people as Pythagoras [Russell, 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.

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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 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:

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

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,

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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 Weber-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 The hyperbolic rule in the oligomer cooperative organization of genomes.

The traditional term “oligomer” refers to a molecular complex of chemical that consists of a few repeating units. Nucleotides A, T, C, and G serve as such repeating units in DNA oligomers, which can have different lengths and which can be also called n-plets, where *n* refers to the oligomer length. Each of nucleotide sequences in eukaryotic and prokaryotic genomes can be considered as a sequence of monomers (like as A-C-A-T-G-T-…), or a sequence of doublets (like as AC-

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AT-GT-GG-…), or a sequence of triplets (like as ACA-TGT-GGA-…), etc. Regarding the quantitative analysis of DNA sequences, researches usually study quantities and percentages (or probability, or frequencies) of separate kinds of *n*-plets. For example, the well-known second Chargaff rule concerns percentages of separate kinds of nucleotides A, T, C and G in long single-stranded DNA. In contrast to such studies, the author suggested analyzing - in DNA and RNA sequences – characterizations of their cooperative forms of organization such as the total amounts of those oligomers of the same length, which belong to the same equivalence class, defined by some their general trait [Petoukhov, 2018c; Petoukhov, Petukhova, Svirin, 2019]. Below this approach is explained.

Let us return for a moment to the tensor family of genetic matrices $[C, A; T, G]^{(n)}$, whose first three members are shown in Fig. 2.2. One can see in such (2^n*2^n)-matrices that each of their $(2^{n-1}*2^{n-1})$-quadrants contains only those $4^{(n-1)}$ oligomers (or *n*-plets), which begin with the same nucleotide C, A, T, or G. One can denote such quadrant sets of *n*-plets as classes (or cooperative groupings) of C_1-oligomers, A_1-oligomers, T_1-oligomers, and G_1-oligomers correspondingly (their index 1 indicates that this nucleotide occupies the first position in oligomers). For example, the class of A_1-doublets contains 4 members (AA, AT, AC, and AG); the class of A_1-triplets contains 16 members (AAA, ATA, ACA, AGA, AAT, ATT, ACT, AGT, AAC, ATC, ACC, AGC, AAG, ATG, ACG, and AGG), etc. The same is true for the classes of T_1-oligomers, C_1-oligomers, G_1-oligomers.

Do these genetic (2^n*2^n)-matrices from their tensor family have anything to do with the quantitative characterizations of DNA sequences in eukaryotic and prokaryotic genomes? The results obtained by the author give a positive answer to this question, discovering the existence of those quantitative rules in DNA sequences that are associated with these genetic matrices and complete sets of *n*-plets in their separate quadrants. These rules of genomic DNA sequences concern - in each of them - the total amounts of *n*-plets from appropriate classes of C_1-oligomers, A_1-oligomers, T_1-oligomers, or G_1-oligomers. In other words, they concern total amounts of DNA oligomers (or *n*-plets) having the fixed length *n* and beginning with the same nucleotide A, T, C, or G.

Below a few results of the study of the total amounts of *n*-plets from such cooperative groupings in eukaryotic and prokaryotic ge-

nomes are briefly presented. The author's method for such a study is called the oligomeric sum method (abbreviation, OS-method). The totality of data obtained by analyzing a nucleotide sequence by the OS-method is called its OS-representation or its OS-portrait.

In this representation the following denotations are used:

- S_A, S_T, S_C, and S_G refer to quantities of monomers A, T, C, and G in the analyzed nucleotide sequence correspondingly;
- $\Sigma_{A,n,1}$, $\Sigma_{T,n,1}$, $\Sigma_{C,n,1}$, and $\Sigma_{G,n,1}$ refer to total amounts of all n-plets having the letter A, T, C, and G in their first position correspondingly.

One can remind here that genomic sequences on the GenBank sites usually contain some letters N, indicating that there can be any nucleotide in this place (https://www.ncbi.nlm.nih.gov/books/NBK21136/). By this reason, the total amount of all monomers A, T, C, G (that is the sum $S_A + S_T + S_C + S_G$), calculated for the sequence from the GenBank data, is slightly less than the complete length of the DNA sequence, which is indicated in the GenBank. But practically this is not essential for the results of the application of the OS-method to analyze genomic sequences.

Let us consider for instance the human chromosome № 1 whose DNA sequence contains about 250 million nucleotides. The initial data on the DNA sequences of this chromosome was taken from the GenBank: https://www.ncbi.nlm.nih.gov/nuccore/NC_000001.11. The application of the OS-method to the analysis of the human chromosome №1 includes the following steps, which are typical also for cases of other DNA and RNA sequences:

- Firstly, one should calculate phenomenological quantities of monomers A, T, C, and G in the considered nucleotide sequence. In the case of the human chromosome № 1, the following quantities are calculated: $S_A = 67070277$, $S_T = 67244164$, $S_C = 48055043$, $S_G = 48111528$;
- Secondly, one should calculate the total amounts $\Sigma_{A,n,1}$, $\Sigma_{T,n,1}$, $\Sigma_{C,n,1}$, and $\Sigma_{G,n,1}$ of n-plets in classes of A_1-oligomers, T_1-oligomers, C_1-oligomers, and G_1-oligomers under $n = 1, 2, 3, \ldots$ (for analysis of human chromosomes and various eukaryotic and prokaryotic genomes, the author usually takes $n = 1, 2, 3, \ldots, 19, 20$ or, in special cases, $n = 1, 2, 3, \ldots, 99, 100$).

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For human chromosome № 1, phenomenological values of the total amounts of *n*-plets from the class C_1-oligomers are shown in the graphical form for $n = 1, 2, 3, \ldots, 20$ in Fig.17.1, left (in blue). Here the abscissa axis represents the values of *n*, and the ordinate axis represents the values of the total amounts $\Sigma_{A,n,1}$ of *n*-plets, having the nucleotide A in their first position.

The first amazing result is that all 20 phenomenological points [*n*, $\Sigma_{A,n,1}$] lie - with a high level of accuracy - along the hyperbola $H_{A,1} = S_A/n = 67070277/n$ shown in red in Fig. 17.1,middle. Deviations of phenomenological quantities $\Sigma_{A,n,1}$ from model values S_A/n lie in the range -0.030%÷0.024%, that is, they comprise only hundredths of a percent.

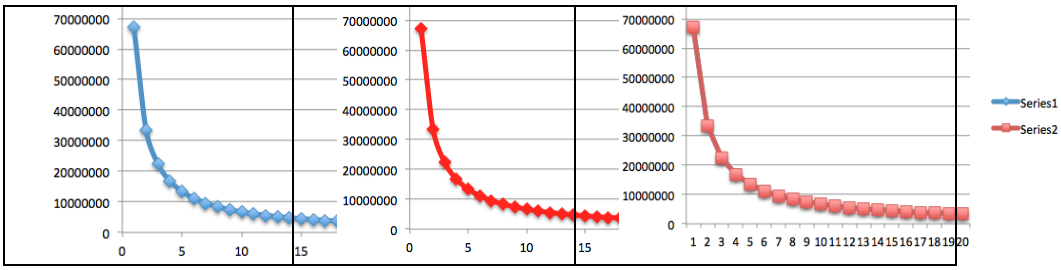

Fig. 17.1. The case of the human chromosome №1. In all 3 graphs, the abscissa axis represents the values of $n = 1, 2, 3, \ldots, 20$. **Left**: the set of phenomenological values $\Sigma_{A,n,1}$ of the total amount of n-plets having the nucleotide A in their first position. The ordinate axis represents the values of the total amounts $\Sigma_{A,n,1}$ of such *n*-plets. **Middle**: the modeling hyperbola with points $H_{A,1} = S_A/n$; the ordinate axis represents its values $S_A/n = 67070277/n$. **Right**: this modeling points $H_{A,1} = S_A/n$ (in red) almost completely closes the points of phenomenological quantities $\Sigma_{A,n,1}$ (in blue) since both kinds of points practically coincide.

One should remind that the total quantities of different kinds of *n*-plets, belong to the class of A_1-oligomers, under fixed *n* is equal to $2^{2(n-1)}$. For example, if $n = 20$ then you have a huge number 2^{38} different kinds of 20-plets of the class of A_1-oligomers. Of course, not all kinds of the mentioned 20-plets are represented in the human chromosome №1, but the total quantity of those 20-plets, which exist in this chromosome, is practically equal to $S_A/20$ with a high level of accuracy shown below.

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Similar results were obtained when studying in this chromosome the total amounts of *n*-plets having in their first position the nucleotide T (Fig. 17.2, at left), and the nucleotide C (Fig. 17.2, at middle), and the nucleotide G (Fig. 17.2, at right). The sets of phenomenological values of the total amounts $\Sigma_{T,n,1}$, $\Sigma_{C,n,1}$, and $\Sigma_{G,n,1}$ of *n*-plets are also modeled effectively by appropriate hyperbolas $H_{T,1}$, $H_{C,1}$, $H_{G,1}$ (17.1), which differ from each other only by their numerators S_T, S_C, and S_G:

$H_{T,1}=S_T/n=67244164/n$, $H_{C,1}=S_C/n=48055043/n$, $H_{G,1}=S_G/n=48111528/n$ (17.1)

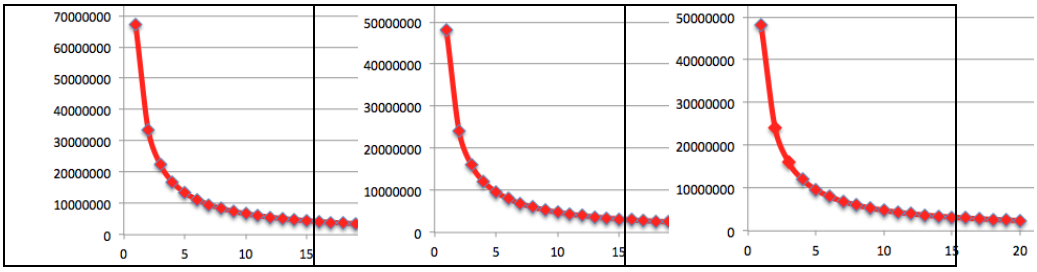

Fig. **17.2**. Additional graph data to the OS-representation of the human chromosome №1. Model values $H_{T,1}(n)$, $H_{C,1}(n)$, and $H_{G,1}(n)$ (in red) from expressions (17.1) practically coincide phenomenological values $\Sigma_{T,n,1}$, $\Sigma_{C,n,1}$, and $\Sigma_{G,n,1}$ of the total amount of n-plets having in their first position the nucleotide T (at left), the nucleotide C (at middle), and the nucleotide G (at the right graph). The numerical data on this coincidence is shown below.

Fig. 17.3 shows real (that is phenomenological) and model values for the OS-portrait of the human chromosome №1. The model values to the total amounts of *n*-plets (n = 1, 2, 3,…, 20), having in their first position a certain nucleotide (A, T, C, or G), are calculated correspondingly through the points of the hyperbolas $H_{A,1} = S_A/n = 67070277/n$, $H_{T,1}=S_T/n=67244164/n$, $H_{C,1}=S_C/n=48055043/n$, and $H_{G,1}=S_G/n=48111528/n$. Deviations Δ% of phenomenological quantities from model values are also shown in percent (model value is taken as 100%). One can see that these deviations are much lesser than 0,2% in all cases.

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N	1	2	3	4	5	6	7	8	9	10
A										
Real	67070277	33537501	22360413	16768845	13413532	11179286	9584038	8383461	7453552	6706672
Model	67070277	33535139	22356759	16767569	13414055	11178380	9581468	8383785	7452253	6707028
Δ%A	0.000	-0.007	-0.016	-0.008	0.004	-0.008	-0.027	0.004	-0.017	0.005
T										
Real	67244164	33620498	22412993	16808862	13445360	11207274	9606748	8405040	7470145	6724359
Model	67244164	33622082	22414721	16811041	13448833	11207361	9606309	8405521	7471574	6724416
Δ%T	0.000	0.005	0.008	0.013	0.026	0.001	-0.005	0.006	0.019	0.001
C										
Real	48055043	24024903	16012711	12013624	9612227	8005708	6865944	6008215	5336968	4803919
Model	48055043	24027522	16018348	12013761	9611009	8009174	6865006	6006880	5339449	4805504
Δ%C	0.000	0.011	0.035	0.001	-0.013	0.043	-0.014	-0.022	0.046	0.033
G										
Real	48111528	24057606	16040889	12028924	9625086	8021235	6869132	6013412	5348337	4813156
Model	48111528	24055764	16037176	12027882	9622306	8018588	6873075	6013941	5345725	4811153
Δ%G	0.000	-0.008	-0.023	-0.009	-0.029	-0.033	0.057	0.009	-0.049	-0.042

n	11	12	13	14	15	16	17	18	19	20
A										
Real	6095821	5588773	5160139	4792078	4472245	4192017	3946422	3726860	3531067	3354107
Model	6097298	5589190	5159252	4790734	4471352	4191892	3945310	3726127	3530015	3353514
Δ%A	0.024	0.007	-0.017	-0.028	-0.020	-0.003	-0.028	-0.020	-0.030	-0.018
T										
Real	6111970	5601854	5173904	4801395	4479492	4202773	3954021	3735327	3535288	3360459
Model	6113106	5603680	5172628	4803155	4482944	4202760	3955539	3735787	3539167	3362208
Δ%T	0.019	0.033	-0.025	0.037	0.077	0.000	0.038	0.012	0.110	0.052
C										
Real	4370502	4002753	3694018	3433636	3202830	3003511	2826568	2668499	2531448	2402186
Model	4368640	4004587	3696542	3432503	3203670	3003440	2826767	2669725	2529213	2402752
Δ%C	-0.043	0.046	0.068	-0.033	0.026	-0.002	0.007	0.046	-0.088	0.024
G										
Real	4374518	4013372	3701250	3435824	3210839	3006763	2830698	2673815	2532772	2407301
Model	4373775	4009294	3700887	3436538	3207435	3006971	2830090	2672863	2532186	2405576
Δ%G	-0.017	-0.102	-0.010	0.021	-0.106	0.007	-0.021	-0.036	-0.023	-0.072

Fig. 17.3. Real and model values to the OS-representation of the human chromosome №1. The real total amounts of *n*-plets (*n* = 1, 2, …, 20) having in their first position a certain nucleotide (A, T, C, or G) are shown (in blue) jointly with their model values (in red). Deviations Δ% of real quantities from model values are also shown in percent (model value is taken as 100%).

The described modeling hyperbolas $H_{A,1} = S_A/n$, $H_{T,1} = S_T/n$, $H_{C,1} = S_C/n$, and $H_{G,1} = S_G/n$ serve as mathematical standards for the phenom-

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enological rule. These hyperbolas differ from each other only in the magnitude of their numerators, and therefore they can be specified by the general expression (17.2):

$$H_{N,1}(n) = S_N/n, \quad (17.2)$$

where N refers to any of nucleotides A, T, C, or G; S_N refers to the number of corresponding monomers A, T, C, or G in the analyzed nucleotide sequence. If you know the total quantity

S_N of the monomer N, you can predict - with a high level of accuracy - the total amounts of *n*-plets belonging to the class N_1-oligomers by using the general expression (17.2). This phenomenological fact testifies in favor of the cooperative entity of the nucleotide sequence in the human chromosome №1.

Obviously, by the corresponding compression of the ordinate axis in these cartesian coordinate systems (that is by appropriate scaling of numerators S_A, S_T, S_C, and S_G), each of these four hyperbolas $H_{A,1}=S_A/n$, $H_{T,1}=S_T/n$, $H_{C,1}=S_C/n$, and $H_{G,1}=S_G/n$ reduces to the hyperbola (17.3):

$$Y = 1/x, \quad (17.3)$$

which we call the canonical (or reference) hyperbola of OS-representations (or OS-portraits) of nucleotide sequences. This canonical hyperbola (17.3) has already met above as the basis of the hyperbolic model of the main psychophysical Weber-Fechner law in Section 5 (Fig. 5.1). The author thinks that the principles of organizing sensory informatics according to Weber-Fechner law are structurally coordinated with the principles of informatics of DNA sequences. The transformation of one hyperbola point to another point is determined by the hyperbolic rotation, by which the hyperbole glides along itself.

The results presented indicate, at least for the human chromosome №1, that there exists a general hyperbolic rule on the total amounts of

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n-plets having a specific nucleotide in their first position (A, T, C, or G):

- for any of classes A_1-, T_1-, C_1-, or G_1-oligomers, the total quantities $\Sigma_{N,n,1}(n)$ of their *n*-plets, corresponding different *n*, are interrelated each other through the general expression $\Sigma_{N,n,1} \approx S_N/n$ with a high level of accuracy (here N means any of nucleotides A, T, C, or G). The phenomenological points with coordinates $[n, \Sigma_{N,n,1}]$ practically lie on the hyperbola $H_{N,1} = S_N/n$.

It should be noted that here not only each of the classes of A_1-, T_1-, C_1-, and G_1-oligomers shows separately the cooperative form of their organization associated with hyperbolas, but also all these four classes of N_1-oligomers are consistent with each other. This is confirmed by analyzing their summary deviations from the model magnitudes. As Fig. 17.4 shows, the sum of deviations $\Sigma\Delta\% = \Delta\%A + \Delta\%T + \Delta\%C + \Delta\%G$, each of which is taken from Fig. 17.3, is close to zero, that is, these deviations in the aggregate compensate each other to a noticeable extent.

N	2	3	4	5	6	7	8	9	10
Δ%A	-0.007	-0.016	-0.008	0.004	-0.008	-0.027	0.004	-0.017	0.005
Δ%T	0.005	0.008	0.013	0.026	0.001	-0.005	0.006	0.019	0.001
Δ%C	0.011	0.035	0.001	-0.013	0.043	-0.014	-0.022	0.046	0.033
Δ%G	-0.008	-0.023	-0.009	-0.029	-0.033	0.057	0.009	-0.049	-0.042
ΣΔ%	**0.001**	**0.003**	**-0.002**	**-0.012**	**0.003**	**0.012**	**-0.004**	**-0.001**	**0.001**

n	11	12	13	14	15	16	17	18	19	20
Δ%A	0.024	0.007	-0.017	-0.028	-0.020	-0.003	-0.028	-0.020	-0.030	-0.018
Δ%T	0.019	0.033	-0.025	0.037	0.077	0.000	0.038	0.012	0.110	0.052
Δ%C	-0.043	0.046	0.068	-0.033	0.026	-0.002	0.007	0.046	-0.088	0.024
Δ%G	-0.017	-0.102	-0.010	0.021	-0.106	0.007	-0.021	-0.036	-0.023	-0.072
ΣΔ%	**-0.017**	**-0.016**	**0.017**	**-0.004**	**-0.023**	**0.001**	**-0.004**	**0.003**	**-0.032**	**-0.014**

Fig. 17.4. In classes of A1-, T1-, C1-, and G1-oligomers, deviations Δ%A, Δ%T, Δ%C, and Δ%G (from Fig. 17.3) of real values from model ones are correlated with each other so that they significantly compensate each other: the sum $\Sigma\Delta\% = \Delta\%A + \Delta\%T + \Delta\%C + \Delta\%G$ of all four deviations for each kind of *n*-plets is significantly less than the maximum in them and is close to zero.

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But the human genome contains 22 autosomes and 2 sex chromosomes X and Y, which are very different from each other in length, molecular weight, gene content, etc. What can be said about the other 23 human chromosomes? Is there a similar rule for them? Yes, the author has got a positive answer to this question. For each of 24 human chromosomes, knowing its quantity S_N of the monomer N (that is A, T, C, or G) allows you to calculate the total amounts of *n*-plets, belonging to the class of N_1-oligomers, with a high level of accuracy by using the general expression (17.2). Fig. 17.5 shows confirmational results of studying all 24 human chromosomes. Appendix II contains more detailed data on parameters of the OS-representations of all human chromosomes with the indication of the GenBank sites, where initial data were taken from for analysis by the OS-method.

The author has obtained similar results for many other eukaryotic and prokaryotic genomes by the described OS-method. Their OS-representations (that is their OS-portraits) are also modeled with hyperbolas, which differ from the canonical hyperbola (17.3) only by their dilatations along the ordinate axis (that is only by numerators in their general expression (17.2)). The obtained results will be published soon in separate articles.

These results testify in favor of the existence of a general genomic rule, which at this stage of researches is a candidacy for the role of a universal genomic rule on the total amounts of *n*-plets having a specific nucleotide A, T, C, or G in their first position (much more genomes should be studied else for the confirmation of its universality):

- for any of classes A_1-, T_1-, C_1-, or G_1-oligomers in eukaryotic and prokaryotic genomes, the total quantities $\Sigma_{N,n,1}(n)$ of their *n*-plets, corresponding different *n*, are interrelated each other through the general expression $\Sigma_{N,n,1} \approx S_N/n$ with a high level of accuracy (here N means any of nucleotides A, T, C, or G). The phenomenological points with coordinates $[n, \Sigma_{N,n,1}]$ practically lie on the hyperbola $H_{N,1} = S_N/n$.

Let us call it the hyperbolic rule.

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№	S_A	Range %	S_T	Range %	S_C	Range %	S_G	Range %
1	67070277	-0.030 ÷0.024	67244164	-0.025 ÷0.110	48055043	-0.088 ÷0.068	48111528	-0.106 ÷0.057
2	71791213	-0.079 ÷0.087	71987932	-0.075 ÷0.095	48318180	-0.097 ÷0.072	48450903	-0.105 ÷0.141
3	59689091	-0.021 ÷0.045	59833302	-0.097 ÷0.098	39233483	-0.130 ÷0.081	39344259	-0.034 ÷0.088
4	58561236	-0.065 ÷0.044	58623430	-0.036 ÷0.128	36236976	-0.039 ÷0.127	36331025	-0.117 ÷0.075
5	54699094	-0.052 ÷0.040	54955010	-0.071 ÷0.078	35731600	-0.012 ÷0.132	35879674	-0.103 ÷0.085
6	51160489	-0.039 ÷0.057	51151754	-0.049 ÷0.022	33520786	-0.092 ÷0.061	33516767	-0.029 ÷0.069
7	47058248	-0.104 ÷0.040	47215040	-0.061 ÷0.030	32317984	-0.086 ÷0.091	32378859	-0.076 ÷0.069
8	42641072	-0.061 ÷0.068	42581941	-0.111 ÷0.071	28600559	-0.110 ÷0.069	28600963	-0.068 ÷0.050
9	31752642	-0.134 ÷0.090	31733822	-0.083 ÷0.065	22487631	-0.099 ÷0.141	22470915	-0.079 ÷0.143
10	38875926	-0.081 ÷0.052	39027555	-0.067 ÷0.099	27639505	-0.058 ÷0.085	27719976	-0.118 ÷0.085
11	39286730	-0.032 ÷0.084	39361954	-0.062 ÷0.042	27903257	-0.139 ÷0.056	27981801	-0.086 ÷0.112
12	39370109	-0.096 ÷0.056	39492225	-0.097 ÷0.094	27092804	-0.076 ÷0.078	27182678	-0.073 ÷0.105
13	29224840	-0.067 ÷0.077	29320872	-0.107 ÷0.069	18341128	-0.107 ÷0.141	18346620	-0.130 ÷0.065
14	25606393	-0.109 ÷0.100	25819249	-0.040 ÷0.086	17733667	-0.137 ÷0.077	17782016	-0.056 ÷0.142
15	24508669	-0.085 ÷0.179	24553812	-0.127 ÷0.088	17752941	-0.090 ÷0.162	17825903	-0.067 ÷0.113
16	22558319	-0.122 ÷0.080	22774906	-0.143 ÷0.104	18172742	-0.146 ÷0.074	18299976	-0.146 ÷0.173
17	22639499	-0.141 ÷0.105	22705261	-0.146 ÷0.070	18723944	-0.134 ÷0.072	18851500	-0.144 ÷0.105
18	22087028	-0.160 ÷0.071	22109347	-0.169 ÷0.121	14574701	-0.090 ÷0.134	14594335	-0.160 ÷0.210
19	15142293	-0.160 ÷0.024	15282753	-0.062 ÷0.062	13954580	-0.103 ÷0.097	14061132	-0.057 ÷0.226
20	16455618	-0.106 ÷0.129	16643030	-0.099 ÷0.089	13037092	-0.062 ÷0.116	13098788	-0.092 ÷0.155
21	9943435	-0.161 ÷0.083	9882679	-0.206 ÷0.173	6864570	-0.134 ÷0.277	6852178	-0.373 ÷0.219
22	10382214	-0.175 ÷0.084	10370725	-0.036 ÷0.209	9160652	-0.258 ÷0.155	9246186	-0.143 ÷0.235
X	46754807	-0.078 ÷0.084	46916701	-0.102 ÷0.055	30523780	-0.116 ÷0.179	30697741	-0.135 ÷0.067
Y	7886192	-0.244 ÷0.097	7956168	-0.063 ÷0.185	5285789	-0.181 ÷0.407	5286894	-0.247 ÷0.142

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Fig. 17.5. For each of all 24 human chromosomes, quantities S_A, S_T, S_C, and S_G of monomers A, T, C, and G are shown to define the modeling hyperbolas (17.2). The columns «Range %) show in percentages ranges of deviations of real total amounts of corresponding *n*-plets (*n* = 1, 2, …, 20) from their model values (in each case, an appropriate model value is taken as 100%).

In the frame of this hyperbolic rule, if you know for any analyzed eukaryotic or prokaryotic genome its total quantity S_N of the monomer N, you can predict – with a high level of accuracy – the total amounts of *n*-plets, belonging to the class of N_1-oligomers, by using the general expression (17.2). This rule indicates the existence of a genomic invariant of biological evolution. Preliminary author's results testify in favor that analogous rules are true in cases of classes of N_2-oligomers (and also of N_3-oligomers) that is for the total amounts of *n*-plets having the identical nucleotide N in their second position (and in their third position correspondingly).

The proposed OS-method gives interesting results in its application for analysis not only very long nucleotide sequences in genomes of different species but also relatively short sequences, for example, of viruses, bacteriophages, and separate genes. For instance, the application of the OS-method to some genes has discovered an unexpected phenomenon of regular rhythmic (wave-like) deviations of the real cooperative parameters of these genes from the corresponding values of reference hyperbolas (17.2) in their modeling OS-representations. Fig. 17.6 shows an example of such rhythmic deviations in the OS-representations of the TTN gene, whose DNA sequence contains 81940 nucleotides. The TTN gene provides instructions for making a very large protein called titin. This protein plays an important role in muscles the body uses for movement (skeletal muscles) and in heart (cardiac) muscle. Initial data on the TTN gene were accessed in the GenBank: https://www.ncbi.nlm.nih.gov/nuccore/X90568.1.

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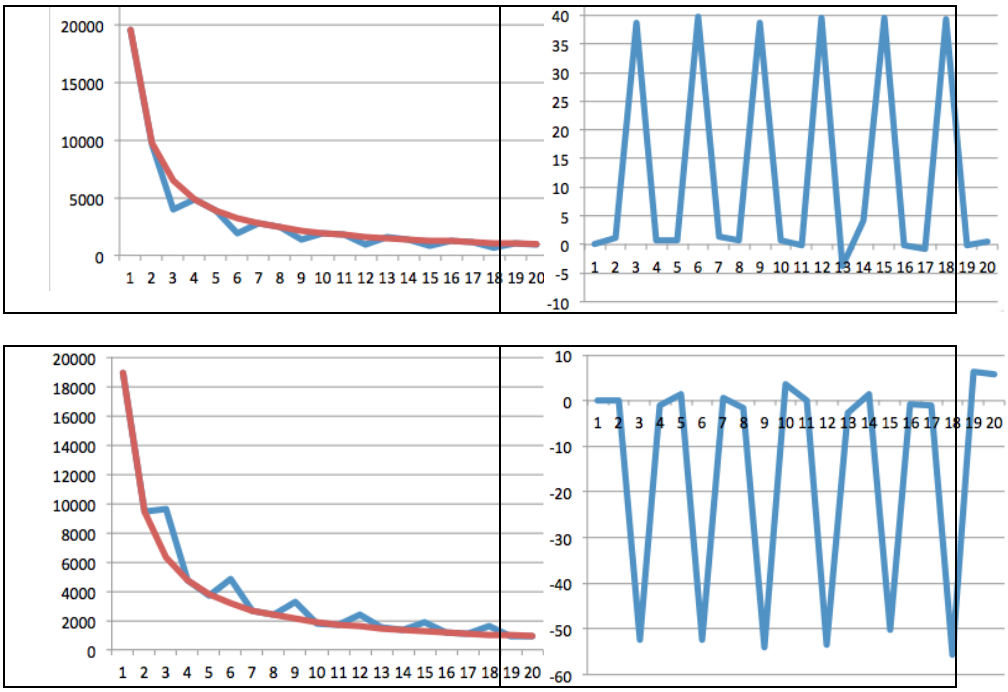

Fig. 17.6. Some results of the analysis of the TTN gene by the OS-method.

Left: blue curves represent the real total amounts of *n*-plets, having in their first

position the nucleotide T (up) and the nucleotide G (at bottom); red curves

represent the modeling hyperbolas $H_{T,1}(n) = 19569/n$ and $H_{G,1}(n) = 18901/n$,

corresponding the expression (17.2). On right: rhythmic deviations of the real

total amounts of such *n*-plets from the modeling values $19569/n$ and $18901/n$, in

percentages. Here $n = 1, 2, 3, \ldots, 20$.

Numeric features of such rhythmic deviations are related to triplets and bear important information about the genetic code system. The wide set of results, which are produced by the application of the OS-method to analyze DNA- and RNA-sequences, are systematically studied now by the author and his team. This new author's approach and its results are discussed at the International interdisciplinary semi-

nar "Algebraic Biology and System Theory" (Moscow, Russia, https://www.youtube.com/channel/UC8JLsuRzzPsRiHwrwEjMCtw).

The OS- allows you to see DNA sequences not as chaotic collections of individual types of oligomers, but as cooperative entities, built on the cooperative long-range coordination of many vast classes of oligomers. One can note that the considered above quantities $4^{(n-1)}$ of kinds of *n*-plets with the first nucleotide N (that is the nucleotide A, or T, or C, and or G) correspond not only to quantities of members of the quadrants of the (2^n*2^n)-matrices of the tensor family $[C, A; T, G]^{(n)}$ in Fig. 2.2 but also to quantities of such *n*-plets in the tensor families of vectors $[C, T, G, A]^{(n)}$.

Can any model be proposed for the formulated above hyperbolic rule of the eukaryotic and prokaryotic genomes? Using and developing his information-algorithmic model of probabilities of components in long DNA sequences, the author offers the following informational-algorithmic model of this hyperbolic rule. The previously published model introduced the notion “genetic qubits" formed based on different pairs of binary-oppositional indicators of adenine A, guanine G, cytosine C, and thymine T (see above Fig. 2.1). Appropriate 2*n*-qubit systems in so-called separable pure states were constructed, where nucleotides A, T, C, and G (and also DNA doublets and other *n*-plets) were represented by appropriate computational basis states [Petoukhov, 2018c; Petoukhov, Petukhova, Svirin, 2019]. For example, cytosine C was represented as the computational basis state |00> of the 2-qubit system, thymine T - as the computational basis state |01>, guanine G – as the computational basis state |10>, and adenine A - as the computational basis state |11> of the same 2-qubit system.

That model has shown that in such represented long DNA sequences, the individual probability (or percentage) P(A) of monomers A is equal to the following collective probabilities:

- The total probability $P_2(A_1)$ of all 4 doublets beginning with the nucleotide A;
- The total probability $P_3(A_1)$ of all 16 triplets beginning with A;
- … The total probability $P_n(A_1)$ of all 4^{n-1} n-plets also beginning with A.

The same is true for interrelations between individual probabilities of each nucleotide T, or C, or G and collective probabilities of *n*-plets beginning with such nucleotide. This is expressed by the following equations:

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$$P(A) = P_n(A_1), \quad P(T) = P_n(T_1), \quad P(T) = P_n(T_1), \quad P(G) = P_n(G_1) \qquad (17.4)$$

Knowing initially the quantities S_A, S_T, S_C, S_G of monomers A, T, C, G and also their sum $S=S_A+S_T+S_C+S_G$ in the analyzed DNA, one can calculate percentages of individual monomers $P(A)=S_A/S$, $P(T)=S_T/S$, $P(C)=S_C/S$, and $P(G)=S_G/S$, which are represented in equations (17.4) and whose sum is equal to 1 (percentages are calculated in fractions of the unit). The number of doublets in this DNA will be half that the number S of monomers, i.e., equal to S/2. Under different values *n*, the total number of *n*-plets will be equal to S/*n*. According to equalities (17.4), in this total number S/n of *n*-plets, the fractions of all *n*-plets with the first nucleotides A, T, C, and G are determined respectively by the quantities P(A)*S/*n*, P (T)*S/*n*, P(C)*S/*n*, and P(G)*S/*n*. These expressions determine those points of hyperbolas, which, as was shown above, model phenomenological data in OS-representations of genomes with high accuracy.

These calculations can be additionally explained by an example of the human chromosome №1, which was analyzed above (Figs. 17.2 and 17.3). It was determined that this chromosome contains the following quantities of monomers A, T, C, and G: S_A = 67070277, S_T = 67244164, S_C = 48055043/, and S_G = 48111528. Their sum S = 230481012. Correspondingly, percentage, for example, of nucleotide A in this chromosome is determined by the expression $P(A) = S_A/S$. In agreement with the equations (17.4), the total amount of all 4^{n-1} *n*-plets, which begin with the nucleotide A, is equal to $P_n(A_1)*S/n = P(A)*S/n = (S_A/S)*S/n = S_A/n$. But just this ratio determines the modeling points $H_{A,1} = S_A/n$ in Figs. 17.1 and 17.3. The similar considerations in cases of nucleotides T, C, and G lead to modeling expressions $H_{T,1}=S_T/n$, $H_{C,1}=S_C/n$, and $H_{G,1}=S_G/n$ used in Figs. 17.2-17.4.

From the proposed quantum-information model of the hyperbolic rule of genomes, the transition from the genome of one species of organisms to the genome of another species appears as a transition of the corresponding 2*n*-qubit system from one separable pure state to another separable pure state. At the same time, wave-like rhythmic deviations from the base hyperbola, which are found in relatively short sequences of the Titin gene type (Fig. 17.6), can also be considered in connection with separable pure states of DNA and their violations.

Returning to author's information-algorithmic model, which was published early [Petoukhov, 2018c; Petoukhov, Petukhova, Svirin, 2019], the author emphasizes that that model allows deducing or prognosis the existence of the phenomenological hyperbolic rule, whose discovery is repre-sented above. It can be considered as an example of usefulness of algebraic modeling in biology.

It should be noted that the genomic hyperbolic rule is fundamentally different from well-known hyperbolic Zipf's law. Zipf's law was originally formulated in terms of quantitative linguistics, stating that given some corpus of natural language utterances, the frequency of any word is inversely proportional to its rank in the frequency table (see, for example, [Fagan, Gençay, 2010]. In linguistics, Zipf's law speaks on the frequency of encounter of single words. In contrast, the genomic hyperbolic rule speaks on the total amounts of *n*-plets belonging to a numerous class of 4^{n-1} *n*-plets that are identical by their first position.

18. Regarding hyperbolic spectra for music timbres

There is a distant structural analogy between the described cooperative organization of genomes associated with the hyperbolic rule and the structure of vibrations of tensioned strings, having harmonic overtones. In a series of harmonic overtones, each of the overtone frequencies is n times less than the fundamental frequency. The timbre of a musical instrument is determined by which overtones it emphasizes.

Music can influence the state of the body and has different applications, including in music therapy [Shushardzhan, Petoukhov, 2020]. As known, living cells create sound. This discovery was made by J. Gimzewski in 2002 [Pelling, Sehati, Gralla, Valentine, Gimzewski, 2004]. Surprisingly, the sounds lie in the audible range. Gimzewski discovered that a yeast cell produced about 1,000 vibrations a second. «*When he amplified the signal, a musical hum filled the room. "It wasn't at all what I expected," he recalls. "It sounded beautiful"*» [Thompson, 2004].

Cell physiology is genetically inherited, and the fact that the sounds emitted by the cells are in the nature of a beautiful musical hum suggests that this genetically inherited hum is endowed with harmony. This harmony and its relationship with the concept of multi-resonance genetics [Petoukhov, 2016] should be studied in the future. The discov-

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ery of Gimzewski gave rise to a new scientific field called sonocytology. In particular, sonocytology is associated with the creation of new s for diagnosing cancer since harmony of cell sounds becomes cacophony when healthy cells become cancerous. A promising approach for such diagnostics on the basis of a CymaScope instrument is described in [Reid, Park, Ji, 2019].

In this regard, the question of the relative physiological activity of various types of timbres is interesting. Nowadays, computer technology allows you to synthesize a variety of timbres for each of the fundamental frequencies of musical notes. Considering the available data on the role of hyperbolic numbers, hyperbolic rotations and hyperbolic rules in different biological phenomena, the author puts forward the following hypothesis:

- Timbres having spectrum consisted of harmonic overtones, whose amplitudes decrease according to the hyperbolic rule $A_n = A_1/n$, have a special physiological activity.

One can think such “hyperbolic timbres” can be useful for enhancing the aesthetic perception of music and the effectiveness of music therapy. These timbres can be easily synthesized on a computer for each of the fundamental frequencies in any musical system (equal temperament, Pythagorean, Fibonacci-stages, etc.). Fig. 18.1 shows an example of such hyperbolic dependence of amplitudes of harmonic overtones from their serial number n for any possible fundamental frequency.

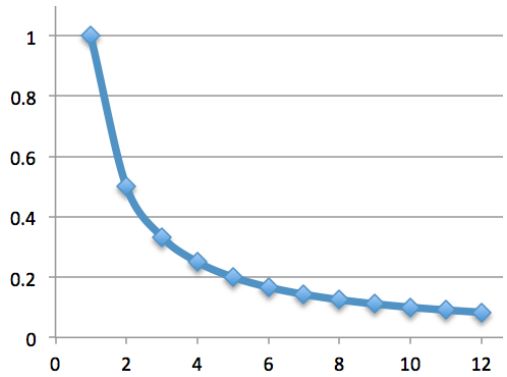

Fig. 18.1. For any fundamental frequency f_1, an example of hyperbolic spectra is shown. It represents the hyperbolic dependence $V_n=V_1/n$ of relative volumes V_n of their harmonic overtones from their

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serial numbers n = 1, 2, 3, ..., 12. The abscissa axis shows the serial numbers n of overtones, having frequencies nf_1. The ordinate axis shows the relative volumes V_n of these overtones. The relative volume V_1 of the fundamental frequency f_1 is taken as 1.

Oscillations with hyperbolic spectra can be useful not only in musical acoustics and its applications. It seems necessary to study the physiological effects of vibrational, electrical, magnetic, optical and other vibrations having a hyperbolic spectrum.

19 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]).

The presented article gives additional materials to the question about the dictatorial influence of genetic molecules DNA and RNA on the entire organism and about some algebraic rules of this influence. Here one can remind that else G.Mendel in his experiments on the crossing of organisms discovered that the inheritance of these characters occurs according to algebraic rules, despite the colossal heterogeneity of the molecular structure of bodies.

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

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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.

The described method of oligomeric sum, which allowed to discover the hyperbolic rule of the cooperative form of oligomeric organization of DNA sequences in genomes, gives new opportunities to study genetic systems and to discuss the problem of invariants in biological evolution.

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 matri-

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ces, 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 contain 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:

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

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 $110 \oplus 101 = 011$, which is equal to 3 in decimal notation ($\oplus$ is the symbol for modulo-2 addition). The set of binary numbers

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

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

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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 (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”).

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

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	0	1
0	0	1
1	1	0

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)

	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. The representations of human chromosomes by the oligomeric sum method

This Appendix shows more details from the author's results of the analysis of all 24 human chromosomes in addition to data shown above in Figs. 17.3-17.5. The results confirm the hyperbolic rule of the oligomer cooperative organization of genomes, formulated above in Section 17. By this rule, knowing the quantity S_N of the monomer N (that is A, T, C, or G) in any of human chromosomes allows you to calculate the total amounts of *n*-plets, belonging to the class of N_1-oligomers, with a high level of accuracy by using the general expression (17.2): $H_{N,1}(n) = S_N/n$. Initial data on all human chromosomes were taken in the GenBank:

№1 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000001.11;
№2- https://www.ncbi.nlm.nih.gov/nuccore/NC_000002.12;
№3- https://www.ncbi.nlm.nih.gov/nuccore/NC_000003.12;

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№4- https://www.ncbi.nlm.nih.gov/nuccore/NC_000004.12;
№5 – https://www.ncbi.nlm.nih.gov/nuccore/NC_000005.10;
№6 - https://www.ncbi.nlm.nih.gov/nuccore/CM000257.1;
№7 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000007.14;
№8 - https://www.ncbi.nlm.nih.gov/nuccore/NC_018919.2;
№9 - https://www.ncbi.nlm.nih.gov/nuccore/CM000260.1;
№10 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000010.11;
№11 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000011.10;
№12 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000012.12;
№13 - https://www.ncbi.nlm.nih.gov/nuccore/CM000264.1;
№14 - https://www.ncbi.nlm.nih.gov/nuccore/CM000265.1;
№15 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000015.10;
№16 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000016.10;
№17 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000017.11;
№18 - https://www.ncbi.nlm.nih.gov/nuccore/CM000269.1;
№19 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000019.10;
№20 - https://www.ncbi.nlm.nih.gov/nuccore/CM000271.1;
№21 - https://www.ncbi.nlm.nih.gov/nuccore/BA000005;
№22 - https://www.ncbi.nlm.nih.gov/nuccore/NC_000022.11;
X - https://www.ncbi.nlm.nih.gov/nuccore/NC_000023.11;
Y - https://www.ncbi.nlm.nih.gov/nuccore/NC_000024.10.

Below in all tables of this Appendix, the following data are shown:

- The real total amounts of n-plets (n = 1, 2, …, 20) having in their first position a certain nucleotide (A, T, C, or G) are shown (in blue) jointly with their model values (in red);
- Deviations Δ% of real quantities from model values in percent (model value is taken as 100%);
- n = 1, 2, 3, … , 20.

In the columns with n = 1, deviations Δ% is equal to zero for all chromosomes since the real quantity of any nucleotide is taken as the first value for the appropriate model hyperbola in the method of OS-representations.

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HUMAN CHROMOSOME № 1:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	67070277	33537501	22360413	16768845	13413532	11179286	9584038	8383461	7453552	6706672
Model	67070277	33535139	22356759	16767569	13414055	11178380	9581468	8383785	7452253	6707028
Δ%	0.000	-0.007	-0.016	-0.008	0.004	-0.008	-0.027	0.004	-0.017	0.005
T										
Real	67244164	33620498	22412993	16808862	13445360	11207274	9606748	8405040	7470145	6724359
Model	67244164	33622082	22414721	16811041	13448833	11207361	9606309	8405521	7471574	6724416
Δ%	0.000	0.005	0.008	0.013	0.026	0.001	-0.005	0.006	0.019	0.001
C										
Real	48055043	24024903	16012711	12013624	9612227	8005708	6865944	6008215	5336968	4803919
Model	48055043	24027522	16018348	12013761	9611009	8009174	6865006	6006880	5339449	4805504
Δ%	0.000	0.011	0.035	0.001	-0.013	0.043	-0.014	-0.022	0.046	0.033
G										
Real	48111528	24057606	16040889	12028924	9625086	8021235	6869132	6013412	5348337	4813156
Model	48111528	24055764	16037176	12027882	9622306	8018588	6873075	6013941	5345725	4811153
Δ%	0.000	-0.008	-0.023	-0.009	-0.029	-0.033	0.057	0.009	-0.049	-0.042

n	11	12	13	14	15	16	17	18	19	20
A										
Real	6095821	5588773	5160139	4792078	4472245	4192017	3946422	3726860	3531067	3354107
Model	6097298	5589190	5159252	4790734	4471352	4191892	3945310	3726127	3530015	3353514
Δ%	0.024	0.007	-0.017	-0.028	-0.020	-0.003	-0.028	-0.020	-0.030	-0.018
T										
Real	6111970	5601854	5173904	4801395	4479492	4202773	3954021	3735327	3535288	3360459
Model	6113106	5603680	5172628	4803155	4482944	4202760	3955539	3735787	3539167	3362208
Δ%	0.019	0.033	-0.025	0.037	0.077	0.000	0.038	0.012	0.110	0.052
C										
Real	4370502	4002753	3694018	3433636	3202830	3003511	2826568	2668499	2531448	2402186
Model	4368640	4004587	3696542	3432503	3203670	3003440	2826767	2669725	2529213	2402752
Δ%	-0.043	0.046	0.068	-0.033	0.026	-0.002	0.007	0.046	-0.088	0.024
G										
Real	4374518	4013372	3701250	3435824	3210839	3006763	2830698	2673815	2532772	2407301
Model	4373775	4009294	3700887	3436538	3207435	3006971	2830090	2672863	2532186	2405576
Δ%	-0.017	-0.102	-0.010	0.021	-0.106	0.007	-0.021	-0.036	-0.023	-0.072

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HUMAN CHROMOSOME № 2:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	71791213	35902934	23921769	17950960	14364606	11968957	10257354	8978505	7969867	7183064
Model	71791213	35895607	23930404	17947803	14358243	11965202	10255888	8973902	7976801	7179121
Δ%	0.000	-0.020	0.036	-0.018	-0.044	-0.031	-0.014	-0.051	0.087	-0.055
T										
Real	71987932	35986207	24000110	17989591	14395955	11995893	10279954	8993208	8003110	7194491
Model	71987932	35993966	23995977	17996983	14397586	11997989	10283990	8998492	7998659	7198793
Δ%	0.000	0.022	-0.017	0.041	0.011	0.017	0.039	0.059	-0.056	0.060
C										
Real	48318180	24157058	16108935	12077328	9660736	8052378	6905316	6037234	5368701	4831639
Model	48318180	24159090	16106060	12079545	9663636	8053030	6902597	6039773	5368687	4831818
Δ%	0.000	0.008	-0.018	0.018	0.030	0.008	-0.039	0.042	0.000	0.004
G										
Real	48450903	24227914	16151923	12119179	9688348	8074145	6921412	6059586	5385899	4845629
Model	48450903	24225452	16150301	12112726	9690181	8075151	6921558	6056363	5383434	4845090
Δ%	0	-0.010	-0.010	-0.053	0.019	0.012	0.002	-0.053	-0.046	-0.011

n	11	12	13	14	15	16	17	18	19	20
A										
Real	6529923	5983118	5522158	5129586	4787102	4489515	4221092	3987350	3777514	3592381
Model	6526474	5982601	5522401	5127944	4786081	4486951	4223013	3988401	3778485	3589561
Δ%	-0.053	-0.009	0.004	-0.032	-0.021	-0.057	0.045	0.026	0.026	-0.079
T										
Real	6543873	5995454	5537418	5138664	4798045	4497286	4237749	4002055	3789051	3595961
Model	6544357	5998994	5537533	5141995	4799195	4499246	4234584	3999330	3788839	3599397
Δ%	0.007	0.059	0.002	0.065	0.024	0.044	-0.075	-0.068	-0.006	0.095
C										
Real	4392191	4025318	3714356	3450916	3222061	3017709	2845008	2683355	2542985	2415881
Model	4392562	4026515	3716783	3451299	3221212	3019886	2842246	2684343	2543062	2415909
Δ%	0.008	0.030	0.065	0.011	-0.026	0.072	-0.097	0.037	0.003	0.001
G										
Real	4402032	4041798	3729777	3462852	3229338	3029757	2846046	2691030	2550885	2423189
Model	4404628	4037575	3726993	3460779	3230060	3028181	2850053	2691717	2550048	2422545
Δ%	0.059	-0.105	-0.075	-0.060	0.022	-0.052	0.141	0.026	-0.033	-0.027

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HUMAN CHROMOSOME № 3:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	59689091	29842467	19894622	14923443	11936984	9948767	8526840	7462677	6630316	5967608
Model	59689091	29844546	19896364	14922273	11937818	9948182	8527013	7461136	6632121	5968909
Δ%	0.000	0.007	0.009	-0.008	0.007	-0.006	0.002	-0.021	0.027	0.022
T										
Real	59833302	29916949	19953191	14957472	11967488	9976541	8545125	7476889	6653630	5982588
Model	59833302	29916651	19944434	14958326	11966660	9972217	8547615	7479163	6648145	5983330
Δ%	0.000	-0.001	-0.044	0.006	-0.007	-0.043	0.029	0.030	-0.083	0.012
C										
Real	39233483	19618919	13070698	9811281	7845439	6533612	5607340	4906443	4356506	3924168
Model	39233483	19616742	13077828	9808371	7846697	6538914	5604783	4904185	4359276	3923348
Δ%	0.000	-0.011	0.055	-0.030	0.016	0.081	-0.046	-0.046	0.064	-0.021
G										
Real	39344259	19671733	13114869	9832839	7870114	6557767	5620716	4916508	4370673	3935648
Model	39344259	19672130	13114753	9836065	7868852	6557377	5620608	4918032	4371584	3934426
Δ%	0.000	0.002	-0.001	0.033	-0.016	-0.006	-0.002	0.031	0.021	-0.031

n	11	12	13	14	15	16	17	18	19	20
A										
Real	5424387	4975057	4591954	4262899	3977476	3730186	3511401	3315812	3140856	2984905
Model	5426281	4974091	4591469	4263507	3979273	3730568	3511123	3316061	3141531	2984455
Δ%	0.035	-0.019	-0.011	0.014	0.045	0.010	-0.008	0.007	0.021	-0.015
T										
Real	5439947	4988894	4600200	4271861	3990969	3739900	3519732	3327281	3149388	2988724
Model	5439391	4986109	4602562	4273807	3988887	3739581	3519606	3324072	3149121	2991665
Δ%	-0.010	-0.056	0.051	0.046	-0.052	-0.009	-0.004	-0.097	-0.008	0.098
C										
Real	3566793	3266981	3019481	2804808	2614448	2454334	2308659	2178356	2066559	1964227
Model	3566680	3269457	3017960	2802392	2615566	2452093	2307852	2179638	2064920	1961674
Δ%	-0.003	0.076	-0.050	-0.086	0.043	-0.091	-0.035	0.059	-0.079	-0.130
G										
Real	3577977	3277411	3026837	2810441	2623780	2456840	2313158	2184113	2069520	1967151
Model	3576751	3278688	3026481	2810304	2622951	2459016	2314368	2185792	2070750	1967213
Δ%	-0.034	0.039	-0.012	-0.005	-0.032	0.088	0.052	0.077	0.059	0.003

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HUMAN CHROMOSOME № 4:

n	1	2	3	4	5	6	7	8	9	10
A	58561236	29281327	19524123	14640305	11717807	9761921	8368028	7321688	6508887	5859476
Real	58561236	29280618	19520412	14640309	11712247	9760206	8365891	7320155	6506804	5856124
Model	0	-0.002	-0.019	0.000	-0.047	-0.018	-0.026	-0.021	-0.032	-0.057
Δ%	58561236	29281327	19524123	14640305	11717807	9761921	8368028	7321688	6508887	5859476
T										
Real	58623430	29312376	19538396	14652392	11723156	9768719	8371542	7325734	6508115	5860902
Model	58623430	29311715	19541143	14655858	11724686	9770572	8374776	7327929	6513714	5862343
Δ%	0	-0.002	0.014	0.024	0.013	0.019	0.039	0.030	0.086	0.025
C										
Real	36236976	18113883	12075760	9058046	7248267	6037840	5175536	4528800	4025140	3624506
Model	36236976	18118488	12078992	9059244	7247395	6039496	5176711	4529622	4026331	3623698
Δ%	0	0.025	0.027	0.013	-0.012	0.027	0.023	0.018	0.030	-0.022
G										
Real	36331025	18168748	12112608	9087424	7261302	6056962	5192419	4542864	4041486	3630383
Model	36331025	18165513	12110342	9082756	7266205	6055171	5190146	4541378	4036781	3633103
Δ%	0	-0.018	-0.019	-0.051	0.067	-0.030	-0.044	-0.033	-0.117	0.075

n	11	12	13	14	15	16	17	18	19	20
A										
Real	5327218	4880301	4504431	4184775	3906567	3659836	3446321	3254739	3080802	2928682
Model	5323749	4880103	4504710	4182945	3904082	3660077	3444779	3253402	3082170	2928062
Δ%	-0.065	-0.004	0.006	-0.044	-0.064	0.007	-0.045	-0.041	0.044	-0.021
T										
Real	5328126	4881613	4510878	4185353	3909619	3662881	3449618	3252679	3085817	2928841
Model	5329403	4885286	4509495	4187388	3908229	3663964	3448437	3256857	3085444	2931172
Δ%	0.024	0.075	-0.031	0.049	-0.036	0.030	-0.034	0.128	-0.012	0.080
C										
Real	3294319	3020935	2787681	2586023	2412741	2265003	2129946	2013884	1907789	1812500
Model	3294271	3019748	2787459.692	2588355	2415798	2264811	2131587	2013165	1907209	1811849
Δ%	-0.001	-0.039	-0.008	0.090	0.127	-0.008	0.077	-0.036	-0.030	-0.036
G										
Real	3300579	3029871	2793368	2597611	2421247	2271823	2136034	2020510	1912574	1817609
Model	3302820	3027585	2794694	2595073	2422068	2270689	2137119	2018390	1912159	1816551
Δ%	0.068	-0.075	0.047	-0.098	0.034	-0.050	0.051	-0.105	-0.022	-0.058

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HUMAN CHROMOSOME № 5:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	54699094	27349201	18233370	13673573	10941267	9116388	7811014	6836959	6076042	5469235
Model	54699094	27349547	18233031	13674774	10939819	9116516	7814156	6837387	6077677	5469909
Δ%	0	0.001	-0.002	0.009	-0.013	0.001	0.040	0.006	0.027	0.012
T										
Real	54955010	27479169	18315808	13740635	10989091	9159314	7853719	6869850	6107501	5496647
Model	54955010	27477505	18318337	13738753	10991002	9159168	7850716	6869376	6106112	5495501
Δ%	0	-0.006	0.014	-0.014	0.017	-0.002	-0.038	-0.007	-0.023	-0.021
C										
Real	35731600	17867885	11909179	8935048	7143749	5954508	5103551	4467404	3971312	3571516
Model	35731600	17865800	11910533	8932900	7146320	5955267	5104514	4466450	3970178	3573160
Δ%	0	-0.012	0.011	-0.024	0.036	0.013	0.019	-0.021	-0.029	0.046
G										
Real	35879674	17936436	11963434	8967090	7178970	5980688	5126771	4483961	3985739	3589143
Model	35879674	17939837	11959891	8969919	7175935	5979946	5125668	4484959	3986630	3587967
Δ%	0	0.019	-0.030	0.032	-0.042	-0.012	-0.022	0.022	0.022	-0.033

n	11	12	13	14	15	16	17	18	19	20
A										
Real	4973852	4557691	4207081	3905897	3646914	3417315	3219256	3037636	2877734	2735393
Model	4972645	4558258	4207623	3907078	3646606	3418693	3217594	3038839	2878900	2734955
Δ%	-0.024	0.012	0.013	0.030	-0.008	0.040	-0.052	0.040	0.040	-0.016
T										
Real	4995666	4579475	4228635	3926752	3660823	3435258	3233874	3055229	2892482	2747595
Model	4995910	4579584	4227308	3925358	3663667	3434688	3232648	3053056	2892369	2747751
Δ%	0.005	0.002	-0.031	-0.036	0.078	-0.017	-0.038	-0.071	-0.004	0.006
C										
Real	3248776	2978774	2744952	2553097	2384078	2233507	2099761	1985819	1881323	1787061
Model	3248327	2977633	2748584.615	2552257	2382107	2233225	2101859	1985089	1880611	1786580
Δ%	-0.014	-0.038	0.132	-0.033	-0.083	-0.013	0.100	-0.037	-0.038	-0.027
G										
Real	3260377	2989513	2762824	2561783	2392545	2243011	2109780	1991615	1888742	1793221
Model	3261789	2989973	2759975	2562834	2391978	2242480	2110569	1993315	1888404	1793984
Δ%	0.043	0.015	-0.103	0.041	-0.024	-0.024	0.037	0.085	-0.018	0.043

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HUMAN CHROMOSOME № 6:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	51160489	25580315	17051523	12788672	10232910	8526747	7311290	6393180	5684167	5115376
Model	51160489	25580245	17053496	12790122	10232098	8526748	7308641	6395061	5684499	5116049
Δ%	0	0.000	0.012	0.011	-0.008	0.000	-0.036	0.029	0.006	0.013
T										
Real	51151754	25575618	17056499	12786603	10228151	8527823	7308684	6392743	5684184	5115669
Model	51151754	25575877	17050585	12787939	10230351	8525292	7307393	6393969	5683528	5115175
Δ%	0	0.001	-0.035	0.010	0.022	-0.030	-0.018	0.019	-0.012	-0.010
C										
Real	33520786	16759583	11170826	8383591	6707366	5583748	4785740	4192883	3723968	3353621
Model	33520786	16760393	11173595	8380197	6704157	5586798	4788684	4190098	3724532	3352079
Δ%	0	0.005	0.025	-0.041	-0.048	0.055	0.061	-0.066	0.015	-0.046
G										
Real	33516767	16759384	11171080	8378580	6701534	5586643	4787118	4189922	3724321	3350313
Model	33516767	16758384	11172256	8379192	6703353	5586128	4788110	4189596	3724085	3351677
Δ%	0	-0.006	0.011	0.007	0.027	-0.009	0.021	-0.008	-0.006	0.041

n	11	12	13	14	15	16	17	18	19	20
A										
Real	4649707	4263573	3936945	3655426	3411647	3196348	3007732	2841340	2693710	2557561
Model	4650954	4263374	3935422	3654321	3410699	3197531	3009441	2842249	2692657	2558024
Δ%	0.027	-0.005	-0.039	-0.030	-0.028	0.037	0.057	0.032	-0.039	0.018
T										
Real	4650508	4262761	3935263	3654213	3409923	3196365	3010400	2841860	2692655	2557660
Model	4650159	4262646	3934750	3653697	3410117	3196985	3008927	2841764	2692198	2557588
Δ%	-0.007	-0.003	-0.013	-0.014	0.006	0.019	-0.049	-0.003	-0.017	-0.003
C										
Real	3048543	2793128	2577889	2393822	2234568	2096327	1972066	1862539	1763557	1677584
Model	3047344	2793399	2578522	2394342	2234719	2095049	1971811	1862266	1764252	1676039
Δ%	-0.039	0.010	0.025	0.022	0.007	-0.061	-0.013	-0.015	0.039	-0.092
G										
Real	3046680	2793026	2576800	2392968	2233838	2095317	1971565	1862588	1763216	1674689
Model	3046979	2793064	2578213	2394055	2234451	2094798	1971575	1862043	1764040	1675838
Δ%	0.010	0.001	0.055	0.045	0.027	-0.025	0.000	-0.029	0.047	0.069

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HUMAN CHROMOSOME № 7:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	47058248	23530299	15686166	11764553	9411623	7840658	6723534	5880008	5229645	4707564
Model	47058248	23529124	15686083	11764562	9411650	7843041	6722607	5882281	5228694	4705825
Δ%	0	-0.005	-0.001	0.000	0.000	0.030	-0.014	0.039	-0.018	-0.037
T										
Real	47215040	23607686	15742888	11804663	9443865	7872181	6743183	5901787	5248651	4721265
Model	47215040	23607520	15738347	11803760	9443008	7869173	6745006	5901880	5246116	4721504
Δ%	0	-0.001	-0.029	-0.008	-0.009	-0.038	0.027	0.002	-0.048	0.005
C										
Real	32317984	16158125	10768945	8076952	6460853	5384305	4617629	4040019	3589340	3230819
Model	32317984	16158992	10772661	8079496	6463597	5386331	4616855	4039748	3590887	3231798
Δ%	0	0.005	0.034	0.031	0.042	0.038	-0.017	-0.007	0.043	0.030
G										
Real	32378859	16188955	10792044	8096367	6477686	5397876	4625671	4049454	3595711	3237365
Model	32378859	16189430	10792953	8094715	6475772	5396477	4625551	4047357	3597651	3237886
Δ%	0	0.003	0.008	-0.020	-0.030	-0.026	-0.003	-0.052	0.054	0.016

n	11	12	13	14	15	16	17	18	19	20
A										
Real	4278987	3920143	3618547	3363226	3136458	2939963	2768113	2614626	2479321	2354361
Model	4278023	3921521	3619865	3361303	3137217	2941141	2768132	2614347	2476750	2352912
Δ%	-0.023	0.035	0.036	-0.057	0.024	0.040	0.001	-0.011	-0.104	-0.062
T										
Real	4294332	3936000	3634128	3371872	3149286	2950864	2776699	2624006	2484604	2360053
Model	4292276	3934587	3631926	3372503	3147669	2950940	2777355	2623058	2485002	2360752
Δ%	-0.048	-0.036	-0.061	0.019	-0.051	0.003	0.024	-0.036	0.016	0.030
C										
Real	2935320	2691176	2485229	2308497	2154034	2019585	1902699	1794213	1699947	1615019
Model	2937999	2693165	2485998.769	2308427	2154532	2019874	1901058	1795444	1700947	1615899
Δ%	0.091	0.074	0.031	-0.003	0.023	0.014	-0.086	0.069	0.059	0.054
G										
Real	2943192	2700193	2490567	2311412	2158232	2025222	1903672	1798830	1702977	1619073
Model	2943533	2698238	2490681	2312776	2158591	2023679	1904639	1798826	1704150	1618943
Δ%	0.012	-0.072	0.005	0.059	0.017	-0.076	0.051	0.000	0.069	-0.008

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HUMAN CHROMOSOME № 8:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	42641072	21319741	14212284	10657826	8526586	7106173	6092948	5327368	4736841	4261328
Model	42641072	21320536	14213691	10660268	8528214	7106845	6091582	5330134	4737897	4264107
Δ%	0	0.004	0.010	0.023	0.019	0.009	-0.022	0.052	0.022	0.065
T										
Real	42581941	21295170	14193901	10648381	8518451	7101184	6079846	5327494	4730041	4261733
Model	42581941	21290970.5	14193980	10645485	8516388	7096990	6083134	5322743	4731327	4258194
Δ%	0	-0.020	0.001	-0.027	-0.024	-0.059	0.054	-0.089	0.027	-0.083
C										
Real	28600559	14300156	9534608	7150571	5719811	4765622	4086694	3574378	3179023	2860558
Model	28600559	14300279.5	9533520	7150140	5720112	4766760	4085794	3575070	3177840	2860056
Δ%	0	0.001	-0.011	-0.006	0.005	0.024	-0.022	0.019	-0.037	-0.018
G										
Real	28600963	14297203	9534022	7149344	5720049	4764450	4086867	3573810	3179020	2858824
Model	28600963	14300482	9533654	7150241	5720193	4766827	4085852	3575120	3177885	2860096
Δ%	0	0.023	-0.004	0.013	0.003	0.050	-0.025	0.037	-0.036	0.044

n	11	12	13	14	15	16	17	18	19	20
A										
Real	3874608	3551008	3282088	3045732	2842817	2664222	2508130	2369063	2243965	2130755
Model	3876461	3553423	3280082	3045791	2842738	2665067	2508298	2368948	2244267	2132054
Δ%	0.048	0.068	-0.061	0.002	-0.003	0.032	0.007	-0.005	0.013	0.061
T										
Real	3868322	3552444	3275805	3040563	2840277	2663163	2504274	2365051	2241113	2130802
Model	3871086	3548495	3275534	3041567	2838796	2661371	2504820	2365663	2241155	2129097
Δ%	0.071	-0.111	-0.008	0.033	-0.052	-0.067	0.022	0.026	0.002	-0.080
C										
Real	2602901	2381738	2198560	2043118	1905875	1786709	1682504	1589011	1504848	1430302
Model	2600051	2383380	2200043	2042897	1906704	1787535	1682386	1588920	1505293	1430028
Δ%	-0.110	0.069	0.067	-0.011	0.043	0.046	-0.007	-0.006	0.030	-0.019
G										
Real	2601862	2383526	2199268	2043781	1905993	1787439	1683031	1589352	1506126	1429348
Model	2600088	2383414	2200074	2042926	1906731	1787560	1682410	1588942	1505314	1430048
Δ%	-0.068	-0.005	0.037	-0.042	0.039	0.007	-0.037	-0.026	-0.054	0.049

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HUMAN CHROMOSOME № 9:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	31752642	15878637	10582404	7939808	6349428	5290553	4536832	3971949	3526209	3175997
Model	31752642	15876321	10584214	7938161	6350528	5292107	4536092	3969080	3528071	3175264
Δ%	0	-0.015	0.017	-0.021	0.017	0.029	-0.016	-0.072	0.053	-0.023
T										
Real	31733822	15871181	10578031	7938407	6346757	5292185	4534911	3967788	3524690	3173731
Model	31733822	15866911	10577941	7933456	6346764	5288970	4533403	3966728	3525980	3173382
Δ%	0	-0.027	-0.001	-0.062	0.000	-0.061	-0.033	-0.027	0.037	-0.011
C										
Real	22487631	11240118	7496094	5616960	4497621	3746338	3212089	2806998	2499785	2248072
Model	22487631	11243815.5	7495877	5621908	4497526	3747939	3212519	2810954	2498626	2248763
Δ%	0	0.033	-0.003	0.088	-0.002	0.043	0.013	0.141	-0.046	0.031
G										
Real	22470915	11232566	7491799	5616080	4495198	3745091	3208309	2808887	2498749	2246694
Model	22470915	11235458	7490305	5617729	4494183	3745153	3210131	2808864	2496768	2247092
Δ%	0	0.026	-0.020	0.029	-0.023	0.002	0.057	-0.001	-0.079	0.018

n	11	12	13	14	15	16	17	18	19	20
A										
Real	2886319	2644910	2441694	2269316	2114934	1985704	1868177	1763367	1670765	1589756
Model	2886604	2646054	2442511	2268046	2116843	1984540	1867802	1764036	1671192	1587632
Δ%	0.010	0.043	0.033	-0.056	0.090	-0.059	-0.020	0.038	0.026	-0.134
T										
Real	2884170	2646683	2441367	2268214	2117302	1982745	1866438	1763367	1669118	1586913
Model	2884893	2644485	2441063	2266702	2115588	1983364	1866695	1762990	1670201	1586691
Δ%	0.025	-0.083	-0.012	-0.067	-0.081	0.031	0.014	-0.021	0.065	-0.014
C										
Real	2045193	1871955	1729423	1605263	1499667	1405314	1321799	1249138	1184728	1123642
Model	2044330	1873969	1729817.769	1606259	1499175	1405477	1322802	1249313	1183560	1124382
Δ%	-0.042	0.107	0.023	0.062	-0.033	0.012	0.076	0.014	-0.099	0.066
G										
Real	2042951	1873526	1729437	1603276	1497763	1404053	1322702	1248847	1183021	1121937
Model	2042810	1872576	1728532	1605065	1498061	1404432	1321819	1248384	1182680	1123546
Δ%	-0.007	-0.051	-0.052	0.111	0.020	0.027	-0.067	-0.037	-0.029	0.143

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HUMAN CHROMOSOME № 10:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	38875926	19443685	12956218	9721728	7775819	6480654	5553092	4861979	4318362	3889657
Model	38875926	19437963	12958642	9718982	7775185	6479321	5553704	4859491	4319547	3887593
Δ%	0	-0.029	0.019	-0.028	-0.008	-0.021	0.011	-0.051	0.027	-0.053
T										
Real	39027555	19512977	13010825	9755195	7802617	6503211	5571860	4877988	4339289	3899745
Model	39027555	19513777.5	13009185	9756889	7805511	6504593	5575365	4878444	4336395	3902756
Δ%	0	0.004	-0.013	0.017	0.037	0.021	0.063	0.009	-0.067	0.077
C										
Real	27639505	13815852	9214019	6910447	5528002	4606316	3949304	3454683	3070056	2763201
Model	27639505	13819752.5	9213168	6909876	5527901	4606584	3948501	3454938	3071056	2763951
Δ%	0	0.028	-0.009	-0.008	-0.002	0.006	-0.020	0.007	0.033	0.027
G										
Real	27719976	13858969	9239926	6928371	5546156	4620314	3963311	3463219	3079286	2773695
Model	27719976	13859988	9239992	6929994	5543995	4619996	3959997	3464997	3079997	2771998
Δ%	0	0.007	0.001	0.023	-0.039	-0.007	-0.084	0.051	0.023	-0.061

n	11	12	13	14	15	16	17	18	19	20
A										
Real	3532326	3241515	2990990	2777145	2593835	2429763	2287328	2160483	2046461	1944638
Model	3534175	3239661	2990456	2776852	2591728	2429745	2286819	2159774	2046101	1943796
Δ%	0.052	-0.057	-0.018	-0.011	-0.081	-0.001	-0.022	-0.033	-0.018	-0.043
T										
Real	3548039	3251197	3002242	2786346	2599362	2439264	2294993	2169313	2054532	1949446
Model	3547960	3252296	3002120	2787683	2601837	2439222	2295739	2168198	2054082	1951378
Δ%	-0.002	0.034	-0.004	0.048	0.095	-0.002	0.032	-0.051	-0.022	0.099
C										
Real	11	12	13	14	15	16	17	18	19	20
Model	2513904	2304198	2124300	1972970	1843443	1728465	1626424	1534509	1455140	1382146
Δ%	2512682	2303292	2126115.769	1974250	1842634	1727469	1625853	1535528	1454711	1381975
G										
Real	2520545	2308333	2133465	1982325	1847559	1731446	1630247	1539193	1457707	1386920
Model	2519998	2309998	2132306	1979998	1847998	1732499	1630587	1539999	1458946	1385999
Δ%	-0.022	0.072	-0.054	-0.118	0.024	0.061	0.021	0.052	0.085	-0.066

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HUMAN CHROMOSOME № 11:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	39286730	19639369	13095063	9817484	7856874	6545830	5614211	4907052	4363348	3927062
Model	39286730	19643365	13095577	9821683	7857346	6547788	5612390	4910841	4365192	3928673
Δ%	0	0.020	0.004	0.043	0.006	0.030	-0.032	0.077	0.042	0.041
T										
Real	39361954	19682193	13116231	9842156	7873104	6558220	5622154	4921159	4372287	3937213
Model	39361954	19680977	13120651	9840489	7872391	6560326	5623136	4920244	4373550	3936195
Δ%	0	-0.006	0.034	-0.017	-0.009	0.032	0.017	-0.019	0.029	-0.026
C										
Real	27903257	13954370	9302239	6978435	5578255	4650740	3984719	3489875	3102280	2789601
Model	27903257	13951628.5	9301086	6975814	5580651	4650543	3986180	3487907	3100362	2790326
Δ%	0	-0.020	-0.012	-0.038	0.043	-0.004	0.037	-0.056	-0.062	0.026
G										
Real	27981801	13990939	9331049	6995362	5598516	4667502	3998020	3498631	3110281	2799499
Model	27981801	13990901	9327267	6995450	5596360	4663634	3997400	3497725	3109089	2798180
Δ%	0	0.000	-0.041	0.001	-0.039	-0.083	-0.016	-0.026	-0.038	-0.047

n	11	12	13	14	15	16	17	18	19	20
A										
Real	3570154	3271475	3022297	2805914	2617723	2453975	2309047	2180924	2067228	1963354
Model	3571521	3273894	3022056	2806195	2619115	2455421	2310984	2182596	2067723	1964337
Δ%	0.038	0.074	-0.008	0.010	0.053	0.059	0.084	0.077	0.024	0.050
T										
Real	3577554	3280509	3028297	2812286	2623952	2461014	2316844	2186486	2070821	1968921
Model	3578359	3280163	3027843	2811568	2624130	2460122	2315409	2186775	2071682	1968098
Δ%	0.023	-0.011	-0.015	-0.026	0.007	-0.036	-0.062	0.013	0.042	-0.042
C										
Real	2537260	2325531	2148116	1991978	1860497	1744088	1643017	1550809	1470634	1395653
Model	2536660	2325271	2146404.385	1993090	1860217	1743954	1641368	1550181	1468592	1395163
Δ%	-0.024	-0.011	-0.080	0.056	-0.015	-0.008	-0.100	-0.041	-0.139	-0.035
G										
Real	2545372	2333633	2150039	1999373	1866746	1749283	1644843	1555881	1472041	1398760
Model	2543800	2331817	2152446	1998700	1865453	1748863	1645988	1554545	1472726	1399090
Δ%	-0.062	-0.078	0.112	-0.034	-0.069	-0.024	0.070	-0.086	0.047	0.024

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HUMAN CHROMOSOME № 12:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	39370109	19681670	13127127	9844635	7874716	6561545	5623971	4921422	4375081	3936072
Model	39370109	19685055	13123370	9842527	7874022	6561685	5624301	4921264	4374457	3937011
Δ%	0	0.017	-0.029	-0.021	-0.009	0.002	0.006	-0.003	-0.014	0.024
T										
Real	39492225	19746627	13164611	9871129	7899772	6583644	5641418	4937178	4391619	3950054
Model	39492225	19746112.5	13164075	9873056	7898445	6582038	5641746	4936528	4388025	3949223
Δ%	0	-0.003	-0.004	0.020	-0.017	-0.024	0.006	-0.013	-0.082	-0.021
C										
Real	27092804	13547188	9029476	6773021	5418240	4514513	3870916	3386388	3009188	2708923
Model	27092804	13546402	9030935	6773201	5418561	4515467	3870401	3386601	3010312	2709280
Δ%	0	-0.006	0.016	0.003	0.006	0.021	-0.013	0.006	0.037	0.013
G										
Real	27182678	13593425	9058057	6795670	5434837	4529932	3883386	3397240	3017203	2718735
Model	27182678	13591339	9060893	6795670	5436536	4530446	3883240	3397835	3020298	2718268
Δ%	0	-0.015	0.031	0.000	0.031	0.011	-0.004	0.018	0.102	-0.017

n	11	12	13	14	15	16	17	18	19	20
A										
Real	3579052	3281962	3030056	2811233	2626741	2460584	2318120	2185997	2071129	1968383
Model	3579101	3280842	3028470	2812151	2624674	2460632	2315889	2187228	2072111	1968505
Δ%	0.001	-0.034	-0.052	0.033	-0.079	0.002	-0.096	0.056	0.047	0.006
T										
Real	3589516	3290323	3038934	2820732	2633641	2468091	2320877	2196134	2079937	1974181
Model	3590202	3291019	3037863	2820873	2632815	2468264	2323072	2194013	2078538	1974611
Δ%	0.019	0.021	-0.035	0.005	-0.031	0.007	0.094	-0.097	-0.067	0.022
C										
Real	2708923	2463763	2256749	2082722	1936038	1804770	1692941	1593730	1505326	1427017
Model	2709280	2462982	2257734	2084061.846	1935200	1806187	1693300	1593694	1505156	1425937
Δ%	0.013	-0.032	0.044	0.064	-0.043	0.078	0.021	-0.002	-0.011	-0.076
G										
Real	2471107	2265783	2089656	1941841	1810705	1699498	1598908	1509087	1429171	1360125
Model	2471153	2265223	2090975	1941620	1812179	1698917	1598981	1510149	1430667	1359134
Δ%	0.002	-0.025	0.063	-0.011	0.081	-0.034	0.005	0.070	0.105	-0.073

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HUMAN CHROMOSOME № 13:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	29224840	14609701	9740813	7305359	5848600	4869437	4176765	3653520	3246021	2923336
Model	29224840	14612420	9741613	7306210	5844968	4870807	4174977	3653105	3247204	2922484
Δ%	0	0.019	0.008	0.012	-0.062	0.028	-0.043	-0.011	0.036	-0.029
T										
Real	29320872	14658068	9775410	7328793	5860372	4887057	4187059	3665263	3261374	2930648
Model	29320872	14660436	9773624	7330218	5864174	4886812	4188696	3665109	3257875	2932087
Δ%	0	0.016	-0.018	0.019	0.065	-0.005	0.039	-0.004	-0.107	0.049
C										
Real	18341128	9174248	6113318	4586059	3666775	3058126	2619260	2292140	2036479	1833225
Model	18341128	9170564	6113709	4585282	3668226	3056855	2620161	2292641	2037903	1834113
Δ%	0	-0.040	0.006	-0.017	0.040	-0.042	0.034	0.022	0.070	0.048
G										
Real	18346620	9174712	6114944	4588159	3670945	3057621	2621694	2293259	2037612	1836135
Model	18346620	9173310	6115540	4586655	3669324	3057770	2620946	2293328	2038513	1834662
Δ%	0	-0.015	0.010	-0.033	-0.044	0.005	-0.029	0.003	0.044	-0.080

n	11	12	13	14	15	16	17	18	19	20
A										
Real	2656650	2433527	2247628	2087855	1948879	1826491	1717987	1622898	1539154	1462224
Model	2656804	2435403	2248065	2087489	1948323	1826553	1719108	1623602	1538149	1461242
Δ%	0.006	0.077	0.019	-0.018	-0.029	0.003	0.065	0.043	-0.065	-0.067
T										
Real	2664773	2443866	2254356	2092899	1954262	1833345	1724723	1629904	1542565	1465169
Model	2665534	2443406	2255452	2094348	1954725	1832555	1724757	1628937	1543204	1466044
Δ%	0.029	-0.019	0.049	0.069	0.024	-0.043	0.002	-0.059	0.041	0.060
C										
Real	1667135	1528575	1413297	1309588	1221832	1145462	1079773	1018561	964064	915763
Model	1667375	1528427	1410856	1310081	1222742	1146321	1078890	1018952	965323	917056
Δ%	0.014	-0.010	-0.173	0.038	0.074	0.075	-0.082	0.038	0.130	0.141
G										
Real	1669031	1530151	1410365	1312044	1223930	1146799	1079495	1019381	966507	918519
Model	1667875	1528885	1411278	1310473	1223108	1146664	1079213	1019257	965612	917331
Δ%	-0.069	-0.083	0.065	-0.120	-0.067	-0.012	-0.026	-0.012	-0.093	-0.130

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HUMAN CHROMOSOME № 14:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	25606393	12799463	8536879	6398418	5121176	4268077	3659882	3198871	2844433	2561480
Model	25606393	12803197	8535464	6401598	5121279	4267732	3658056	3200799	2845155	2560639
Δ%	0	0.029	-0.017	0.050	0.002	-0.008	-0.050	0.060	0.025	-0.033
T										
Real	25819249	12909111	8605806	6455564	5164155	4300865	3686847	3227393	2868634	2582715
Model	25819249	12909624.5	8606416	6454812	5163850	4303208	3688464	3227406	2868805	2581925
Δ%	0	0.004	0.007	-0.012	-0.006	0.054	0.044	0.000	0.006	-0.031
C										
Real	17733667	8871974	5912056	4435723	3546079	2958415	2534244	2217687	1971632	1772674
Model	17733667	8866833.5	5911222	4433417	3546733	2955611	2533381	2216708	1970407	1773367
Δ%	0	-0.058	-0.014	-0.052	0.018	-0.095	-0.034	-0.044	-0.062	0.039
G										
Real	17782016	8890114	5925692	4445622	3556858	2962863	2539216	2223714	1975450	1777268
Model	17782016	8891008	5927339	4445504	3556403	2963669	2540288	2222752	1975780	1778202
Δ%	0	0.010	0.028	-0.003	-0.013	0.027	0.042	-0.043	0.017	0.053

n	11	12	13	14	15	16	17	18	19	20
A										
Real	2328958	2134374	1969599	1828781	1706342	1599657	1507905	1421156	1348571	1281424
Model	2327854	2133866	1969723	1829028	1707093	1600400	1506258	1422577	1347705	1280320
Δ%	-0.047	-0.024	0.006	0.014	0.044	0.046	-0.109	0.100	-0.064	-0.086
T										
Real	2346873	2150075	1986319	1843352	1720883	1612313	1518316	1434358	1358380	1291484
Model	2347204	2151604	1986096	1844232	1721283	1613703	1518779	1434403	1358908	1290962
Δ%	0.014	0.071	-0.011	0.048	0.023	0.086	0.031	0.003	0.039	-0.040
C										
Real	1613681	1479759	1363482	1268063	1183151	1109870	1042857	986293	932633	886064
Model	1612152	1477806	1364128.231	1266691	1182244	1108354	1043157	985204	933351	886683
Δ%	-0.095	-0.132	0.047	-0.108	-0.077	-0.137	0.029	-0.111	0.077	0.070
G										
Real	1614245	1480907	1368389	1269895	1185716	1111994	1045118	988265	936274	888098
Model	1616547	1481835	1367847	1270144	1185468	1111376	1046001	987890	935896	889101
Δ%	0.142	0.063	-0.040	0.020	-0.021	-0.056	0.084	-0.038	-0.040	0.113

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HUMAN CHROMOSOME № 15:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	24508669	12257215	8173351	6127496	4901186	4086075	3500690	3063805	2725130	2449776
Model	24508669	12254335	8169556	6127167	4901734	4084778	3501238	3063584	2723185	2450867
Δ%	0	-0.024	-0.046	-0.005	0.011	-0.032	0.016	-0.007	-0.071	0.045
T										
Real	24553812	12277116	8182954	6139451	4911929	4093347	3510119	3069731	2725799	2458502
Model	24553812	12276906	8184604	6138453	4910762	4092302	3507687	3069227	2728201	2455381
Δ%	0	-0.002	0.020	-0.016	-0.024	-0.026	-0.069	-0.016	0.088	-0.127
C										
Real	17752941	8875159	5918553	4439589	3550957	2957640	2535156	2219552	1972944	1775282
Model	17752941	8876470.5	5917647	4438235	3550588	2958824	2536134	2219118	1972549	1775294
Δ%	0	0.015	-0.015	-0.031	-0.010	0.040	0.039	-0.020	-0.020	0.001
G										
Real	17825903	8911174	5938915	4453796	3564193	2969826	2545651	2227076	1980717	1780573
Model	17825903	8912952	5941968	4456476	3565181	2970984	2546558	2228238	1980656	1782590
Δ%	0	0.020	0.051	0.060	0.028	0.039	0.036	0.052	-0.003	0.113

n	11	12	13	14	15	16	17	18	19	20
A										
Real	2224072	2043423	1885563	1750172	1635302	1531950	1441010	1361323	1288636	1224799
Model	2228061	2042389	1885282	1750619	1633911	1531792	1441686	1361593	1289930	1225433
Δ%	0.179	-0.051	-0.015	0.026	-0.085	-0.010	0.047	0.020	0.100	0.052
T										
Real	2234532	2046465	1890145	1755772	1637110	1534779	1444412	1364249	1292898	1229106
Model	2232165	2046151	1888755	1753844	1636921	1534613	1444342	1364101	1292306	1227691
Δ%	-0.106	-0.015	-0.074	-0.110	-0.012	-0.011	-0.005	-0.011	-0.046	-0.115
C										
Real	1614439	1479412	1363399	1267510	1183122	1110374	1044478	986123	935203	887647
Model	1613904	1479412	1365610.846	1268067	1183529	1109559	1044291	986275	934365	887647
Δ%	-0.033	0.000	0.162	0.044	0.034	-0.073	-0.018	0.015	-0.090	0.000
G										
Real	1621622	1484144	1371763	1272355	1187220	1112980	1049005	990598	938070	890515
Model	1620537	1485492	1371223	1273279	1188394	1114119	1048583	990328	938205	891295
Δ%	-0.067	0.091	-0.039	0.073	0.099	0.102	-0.040	-0.027	0.014	0.088

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HUMAN CHROMOSOME № 16:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	22558319	11276313	7520193	5639012	4511596	3759105	3223921	2821345	2508088	2254369
Model	22558319	11279160	7519440	5639580	4511664	3759720	3222617	2819790	2506480	2255832
Δ%	0	0.025	-0.010	0.010	0.002	0.016	-0.040	-0.055	-0.064	0.065
T										
Real	22774906	11392435	7591638	5696104	4555284	3797040	3252955	2846589	2529069	2278531
Model	22774906	11387453	7591635	5693727	4554981	3795818	3253558	2846863	2530545	2277491
Δ%	0	-0.044	0.000	-0.042	-0.007	-0.032	0.019	0.010	0.058	-0.046
C										
Real	18172742	9087743	6056202	4544425	3634337	3028789	2597284	2272410	2018809	1818837
Model	18172742	9086371	6057581	4543186	3634548	3028790	2596106	2271593	2019194	1817274
Δ%	0	-0.015	0.023	-0.027	0.006	0.000	-0.045	-0.036	0.019	-0.086
G										
Real	18299976	9146481	6100612	4571945	3659972	3049387	2612402	2285400	2033583	1828858
Model	18299976	9149988	6099992	4574994	3659995	3049996	2614282	2287497	2033331	1829998
Δ%	0	0.038	-0.010	0.067	0.001	0.020	0.072	0.092	-0.012	0.062

n	11	12	13	14	15	16	17	18	19	20
A										
Real	2050851	1880478	1733865	1611591	1503601	1411360	1326703	1254763	1187413	1127605
Model	2050756	1879860	1735255	1611309	1503888	1409895	1326960	1253240	1187280	1127916
Δ%	-0.005	-0.033	0.080	-0.018	0.019	-0.104	0.019	-0.122	-0.011	0.028
T										
Real	2069922	1897886	1754413	1627184	1518712	1422617	1338652	1265541	1197438	1139313
Model	2070446	1897909	1751916	1626779	1518327	1423432	1339700	1265273	1198679	1138745
Δ%	0.025	0.001	-0.143	-0.025	-0.025	0.057	0.078	-0.021	0.104	-0.050
C										
Real	1650838	1515238	1397538	1298309	1211787	1135601	1070110	1009041	956160	909967
Model	1652067	1514395	1397903.231	1298053	1211516	1135796	1068985	1009597	956460	908637
Δ%	0.074	-0.056	0.026	-0.020	-0.022	0.017	-0.105	0.055	0.031	-0.146
G										
Real	1665290	1523558	1406945	1306196	1219631	1143296	1076647	1015430	964562	913413
Model	1663634	1524998	1407690	1307141	1219998	1143749	1076469	1016665	963157	914999
Δ%	-0.100	0.094	0.053	0.072	0.030	0.040	-0.017	0.122	-0.146	0.173

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HUMAN CHROMOSOME № 17:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	22639499	11319059	7546872	5656791	4530288	3774212	3233070	2827679	2515252	2264946
Model	22639499	11319750	7546500	5659875	4527900	3773250	3234214	2829937	2515500	2263950
Δ%	0	0.006	-0.005	0.054	-0.053	-0.025	0.035	0.080	0.010	-0.044
T										
Real	22705261	11355846	7571879	5676660	4539969	3786215	3244213	2839343	2523060	2270552
Model	22705261	11352630.5	7568420	5676315	4541052	3784210	3243609	2838158	2522807	2270526
Δ%	0	-0.028	-0.046	-0.006	0.024	-0.053	-0.019	-0.042	-0.010	-0.001
C										
Real	18723944	9358265	6241205	4680627	3743834	3118529	2674871	2339739	2080736	1871247
Model	18723944	9361972	6241315	4680986	3744789	3120657	2674849	2340493	2080438	1872394
Δ%	0	0.040	0.002	0.008	0.025	0.068	-0.001	0.032	-0.014	0.061
G										
Real	18851500	9426933	6280113	4715974	3769947	3141080	2693587	2358271	2094311	1885275
Model	18851500	9425750	6283833	4712875	3770300	3141917	2693071	2356438	2094611	1885150
Δ%	0	-0.013	0.059	-0.066	0.009	0.027	-0.019	-0.078	0.014	-0.007

n	11	12	13	14	15	16	17	18	19	20
A										
Real	2061045	1885696	1741112	1616907	1508271	1413484	1330996	1257604	1191079	1131835
Model	2058136	1886625	1741500	1617107	1509300	1414969	1331735	1257750	1191553	1131975
Δ%	-0.141	0.049	0.022	0.012	0.068	0.105	0.056	0.012	0.040	0.012
T										
Real	2062947	1892699	1745337	1623386	1515901	1419780	1334857	1261999	1195292	1134722
Model	2064115	1892105	1746559	1621804	1513684	1419079	1335604	1261403	1195014	1135263
Δ%	0.057	-0.031	0.070	-0.098	-0.146	-0.049	0.056	-0.047	-0.023	0.048
C										
Real	1702241	1560061	1442233	1336746	1247637	1170134	1101482	1039495	985747	935527
Model	1702177	1560329	1440303.385	1337425	1248263	1170247	1101408	1040219	985471	936197
Δ%	-0.004	0.017	-0.134	0.051	0.050	0.010	-0.007	0.070	-0.028	0.072
G										
Real	1711969	1571560	1449795	1345831	1256203	1179116	1110323	1047582	992104	943928
Model	1713773	1570958	1450115	1346536	1256767	1178219	1108912	1047306	992184	942575
Δ%	0.105	-0.038	0.022	0.052	0.045	-0.076	-0.127	-0.026	0.008	-0.144

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HUMAN CHROMOSOME № 18:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	22087028	11049099	7363151	5524275	4415580	3685073	3156485	2761565	2455849	2209991
Model	22087028	11043514	7362343	5521757	4417406	3681171	3155290	2760879	2454114	2208703
Δ%	0	-0.051	-0.011	-0.046	0.041	-0.106	-0.038	-0.025	-0.071	-0.058
T										
Real	22109347	11053769	7369923	5528493	4426314	3684363	3156935	2765073	2455495	2211975
Model	22109347	11054673.5	7369782	5527337	4421869	3684891	3158478	2763668	2456594	2210935
Δ%	0	0.008	-0.002	-0.021	-0.101	0.014	0.049	-0.051	0.045	-0.047
C										
Real	14574701	7283090	4859734	3641818	2914111	2427781	2081248	1820311	1620861	1456680
Model	14574701	7287350.5	4858234	3643675	2914940	2429117	2082100	1821838	1619411	1457470
Δ%	0	0.058	-0.031	0.051	0.028	0.055	0.041	0.084	-0.090	0.054
G										
Real	14594335	7296744	4862343	3646792	2917064	2430361	2086099	1823746	1619525	1457882
Model	14594335	7297168	4864778	3648584	2918867	2432389	2084905	1824292	1621593	1459434
Δ%	0	0.006	0.050	0.049	0.062	0.083	-0.057	0.030	0.128	0.106

n	11	12	13	14	15	16	17	18	19	20
A										
Real	2009122	1843374	1697799	1578470	1471651	1380514	1299476	1229025	1163180	1104916
Model	2007912	1840586	1699002	1577645	1472469	1380439	1299237	1227057	1162475	1104351
Δ%	-0.060	-0.151	0.071	-0.052	0.056	-0.005	-0.018	-0.160	-0.061	-0.051
T										
Real	2009333	1841971	1702311	1578552	1476451	1381727	1300674	1227935	1162244	1105916
Model	2009941	1842446	1700719	1579239	1473956	1381834	1300550	1228297	1163650	1105467
Δ%	0.030	0.026	-0.094	0.044	-0.169	0.008	-0.010	0.029	0.121	-0.041
C										
Real	1324115	1214443	1120714	1039657	970778	910034	857501	809817	766563	728705
Model	1324973	1214558	1121130.846	1041050	971647	910919	857335	809706	767090	728735
Δ%	0.065	0.010	0.037	0.134	0.089	0.097	-0.019	-0.014	0.069	0.004
G										
Real	1327030	1214002	1122685	1043713	972153	913074	857965	809097	769352	728731
Model	1326758	1216195	1122641	1042453	972956	912146	858490	810796	768123	729717
Δ%	-0.021	0.180	-0.004	-0.121	0.082	-0.102	0.061	0.210	-0.160	0.135

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HUMAN CHROMOSOME № 19:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	15142293	7574216	5049052	3785784	3029069	2526143	2162672	1893041	1683010	1515756
Model	15142293	7571147	5047431	3785573	3028459	2523716	2163185	1892787	1682477	1514229
Δ%	0	-0.041	-0.032	-0.006	-0.020	-0.096	0.024	-0.013	-0.032	-0.101
T										
Real	15282753	7642102	5095598	3821187	3056901	2548586	2183929	1910559	1698282	1528245
Model	15282753	7641376.5	5094251	3820688	3056551	2547126	2183250	1910344	1698084	1528275
Δ%	0	-0.009	-0.026	-0.013	-0.011	-0.057	-0.031	-0.011	-0.012	0.002
C										
Real	13954580	6976934	4650271	3489519	2789221	2324833	1993407	1744902	1551581	1394570
Model	13954580	6977290	4651527	3488645	2790916	2325763	1993511	1744323	1550509	1395458
Δ%	0	0.005	0.027	-0.025	0.061	0.040	0.005	-0.033	-0.069	0.064
G										
Real	14061132	7027127	4685331	3513700	2812961	2340563	2008671	1756592	1560546	1405505
Model	14061132	7030566	4687044	3515283	2812226	2343522	2008733	1757642	1562348	1406113
Δ%	0	0.049	0.037	0.045	-0.026	0.126	0.003	0.060	0.115	0.043

n	11	12	13	14	15	16	17	18	19	20
A										
Real	1377415	1262596	1166660	1082823	1009795	946200	891264	842158	797482	758078
Model	1376572	1261858	1164792	1081592	1009486	946393	890723	841239	796963	757115
Δ%	-0.061	-0.059	-0.160	-0.114	-0.031	0.020	-0.061	-0.109	-0.065	-0.127
T										
Real	1388879	1274240	1175902	1091889	1018553	955193	898425	849567	804361	764251
Model	1389341	1273563	1175596	1091625	1018850	955172	898985	849042	804355	764138
Δ%	0.033	-0.053	-0.026	-0.024	0.029	-0.002	0.062	-0.062	-0.001	-0.015
C										
Real	1269321	1163395	1072616	995786	929903	873060	820402	775579	735008	697821
Model	1268598	1162882	1073429.231	996756	930305	872161	820858	775254	734452	697729
Δ%	-0.057	-0.044	0.076	0.097	0.043	-0.103	0.056	-0.042	-0.076	-0.013
G										
Real	1277181	1169833	1080265	1003841	937799	878093	827601	779405	738979	701888
Model	1278285	1171761	1081626	1004367	937409	878821	827125	781174	740060	703057
Δ%	0.086	0.165	0.126	0.052	-0.042	0.083	-0.057	0.226	0.146	0.166

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HUMAN CHROMOSOME № 20:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	16455618	8229975	5484278	4115241	3289454	2742600	2350654	2057494	1828885	1645507
Model	16455618	8227809	5485206	4113905	3291124	2742603	2350803	2056952	1828402	1645562
Δ%	0	-0.026	0.017	-0.032	0.051	0.000	0.006	-0.026	-0.026	0.003
T										
Real	16643030	8316491	5548589	4159012	3330684	2772383	2379936	2079142	1850401	1664869
Model	16643030	8321515	5547677	4160758	3328606	2773838	2377576	2080379	1849226	1664303
Δ%	0	0.060	-0.016	0.042	-0.062	0.052	-0.099	0.059	-0.064	-0.034
C										
Real	13037092	6520503	4345713	3260325	2606410	2173376	1861524	1629800	1448575	1303152
Model	13037092	6518546	4345697	3259273	2607418	2172849	1862442	1629637	1448566	1303709
Δ%	0	-0.030	0.000	-0.032	0.039	-0.024	0.049	-0.010	-0.001	0.043
G										
Real	13098788	6550295	4366257	3274054	2620355	2184056	1869956	1637885	1453749	1309922
Model	13098788	6549394	4366263	3274697	2619758	2183131	1871255	1637349	1455421	1309879
Δ%	0	-0.014	0.000	0.020	-0.023	-0.042	0.069	-0.033	0.115	-0.003

n	11	12	13	14	15	16	17	18	19	20
A										
Real	1496007	1371789	1265386	1175105	1095622	1029567	968278	914478	866222	823656
Model	1495965	1371302	1265817	1175401	1097041	1028476	967978	914201	866085	822781
Δ%	-0.003	-0.036	0.034	0.025	0.129	-0.106	-0.031	-0.030	-0.016	-0.106
T										
Real	1512478	1385879	1279293	1188990	1110146	1039270	978127	925428	875327	832115
Model	1513003	1386919	1280233	1188788	1109535	1040189	979002	924613	875949	832152
Δ%	0.035	0.075	0.073	-0.017	-0.055	0.088	0.089	-0.088	0.071	0.004
C										
Real	1185877	1086994	1003471	931671	869195	814890	766756	724319	686373	651100
Model	1185190	1086424	1002853.231	931221	869139	814818	766888	724283	686163	651855
Δ%	-0.058	-0.052	-0.062	-0.048	-0.006	-0.009	0.017	-0.005	-0.031	0.116
G										
Real	1190595	1091548	1008352	935267	874004	818432	771222	726582	689678	654856
Model	1190799	1091566	1007599	935628	873253	818674	770517	727710	689410	654939
Δ%	0.017	0.002	-0.075	0.039	-0.086	0.030	-0.092	0.155	-0.039	0.013

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HUMAN CHROMOSOME № 21:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	9943435	4970936	3313355	2487369	1989007	1656802	1421123	1244934	1104807	994803
Model	9943435	4971718	3314478	2485859	1988687	1657239	1420491	1242929	1104826	994344
Δ%	0	0.016	0.034	-0.061	-0.016	0.026	-0.045	-0.161	0.002	-0.046
T										
Real	9882679	4943311	3294026	2470227	1974626	1646396	1410786	1234295	1097760	988154
Model	9882679	4941339.5	3294226	2470670	1976536	1647113	1411811	1235335	1098075	988268
Δ%	0	-0.040	0.006	0.018	0.097	0.044	0.073	0.084	0.029	0.012
C										
Real	6864570	3430992	2287342	1715863	1372069	1144468	980695	857828	762589	684712
Model	6864570	3432285	2288190	1716143	1372914	1144095	980653	858071	762730	686457
Δ%	0	0.038	0.037	0.016	0.062	-0.033	-0.004	0.028	0.018	0.254
G										
Real	6852178	3426192	2286230	1712258	1372870	1142809	979231	855800	761826	686617
Model	6852178	3426089	2284059	1713045	1370436	1142030	978883	856522	761353	685218
Δ%	0	-0.003	-0.095	0.046	-0.178	-0.068	-0.036	0.084	-0.062	-0.204

n	11	12	13	14	15	16	17	18	19	20
A										
Real	903739	829760	764723	710220	662894	621827	584895	552523	522905	497692
Model	903949	828620	764880	710245	662896	621465	584908	552413	523339	497172
Δ%	0.023	-0.138	0.020	0.004	0.000	-0.058	0.002	-0.020	0.083	-0.105
T										
Real	898955	822131	760965	705748	657856	617208	581111	549253	521214	493623
Model	898425	823557	760206	705906	658845	617667	581334	549038	520141	494134
Δ%	-0.059	0.173	-0.100	0.022	0.150	0.074	0.038	-0.039	-0.206	0.103
C										
Real	623023	572393	527261	490069	456929	428977	404134	381875	360969	342279
Model	624052	572048	528043.8462	490326	457638	429036	403798	381365	361293	343229
Δ%	0.165	-0.060	0.148	0.053	0.155	0.014	-0.083	-0.134	0.090	0.277
G										
Real	623635	570953	527272	489883	458515	428418	402966	379841	360327	343548
Model	622925	571015	527091	489441	456812	428261	403069	380677	360641	342609
Δ%	-0.114	0.011	-0.034	-0.090	-0.373	-0.037	0.026	0.219	0.087	-0.274

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HUMAN CHROMOSOME № 22:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	10382214	5190842	3459864	2595694	2077171	1731161	1483055	1299585	1153447	1038681
Model	10382214	5191107	3460738	2595554	2076443	1730369	1483173	1297777	1153579	1038221
Δ%	0	0.005	0.025	-0.005	-0.035	-0.046	0.008	-0.139	0.011	-0.044
T										
Real	10370725	5185385	3456366	2593027	2072914	1727140	1481917	1296304	1152409	1035658
Model	10370725	5185362.5	3456908	2592681	2074145	1728454	1481532	1296341	1152303	1037073
Δ%	0	0.000	0.016	-0.013	0.059	0.076	-0.026	0.003	-0.009	0.136
C										
Real	9160652	4579249	3054480	2290057	1832851	1526026	1308193	1144240	1018445	916325
Model	9160652	4580326	3053551	2290163	1832130	1526775	1308665	1145082	1017850	916065
Δ%	0	0.024	-0.030	0.005	-0.039	0.049	0.036	0.073	-0.058	-0.028
G										
Real	9246186	4624413	3082546	2311165	1849021	1542299	1321091	1154840	1026784	925316
Model	9246186	4623093	3082062	2311547	1849237	1541031	1320884	1155773	1027354	924619
Δ%	0	-0.029	-0.016	0.017	0.012	-0.082	-0.016	0.081	0.055	-0.075

n	11	12	13	14	15	16	17	18	19	20
A										
Real	943041	865385	799039	741397	692782	650027	611022	577311	547254	519683
Model	943838	865185	798632	741587	692148	648888	610718	576790	546432	519111
Δ%	0.084	-0.023	-0.051	0.026	-0.092	-0.175	-0.050	-0.090	-0.150	-0.110
T										
Real	942204	864308	797990	741032	690936	647455	608940	575783	544903	517451
Model	942793	864227	797748	740766	691382	648170	610043	576151	545828	518536
Δ%	0.062	-0.009	-0.030	-0.036	0.064	0.110	0.181	0.064	0.169	0.209
C										
Real	832972	763117	704336	653318	610194	572505	539776	508635	483384	458159
Model	832787	763388	704665.5385	654332	610710	572541	538862	508925	482140	458033
Δ%	-0.022	0.035	0.047	0.155	0.085	0.006	-0.170	0.057	-0.258	-0.028
G										
Real	841763	770501	710928	661382	616739	577496	543782	513809	485496	462695
Model	840562	770516	711245	660442	616412	577887	543893	513677	486641	462309
Δ%	-0.143	0.002	0.045	-0.142	-0.053	0.068	0.020	-0.026	0.235	-0.083

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HUMAN CHROMOSOME X:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	46754807	23379570	15586222	11691762	9347711	7796517	6678814	5842454	5195039	4676912
Model	46754807	23377404	15584936	11688702	9350961	7792468	6679258	5844351	5194979	4675481
Δ%	0	-0.009	-0.008	-0.026	0.035	-0.052	0.007	0.032	-0.001	-0.031
T										
Real	46916701	23458854	15637186	11727912	9386193	7817480	6701049	5864619	5211521	4692629
Model	46916701	23458350.5	15638900	11729175	9383340	7819450	6702386	5864588	5212967	4691670
Δ%	0	-0.002	0.011	0.011	-0.030	0.025	0.020	-0.001	0.028	-0.020
C										
Real	30523780	15259528	10174897	7628008	6104748	5085872	4359615	3815823	3392971	3050051
Model	30523780	15261890	10174593	7630945	6104756	5087297	4360540	3815473	3391531	3052378
Δ%	0	0.015	-0.003	0.038	0.000	0.028	0.021	-0.009	-0.042	0.076
G										
Real	30697741	15348565	10232706	7675576	6139953	5115637	4388099	3838736	3410804	3069712
Model	30697741	15348871	10232580	7674435	6139548	5116290	4385392	3837218	3410860	3069774
Δ%	0	0.002	-0.001	-0.015	-0.007	0.013	-0.062	-0.040	0.002	0.002

n	11	12	13	14	15	16	17	18	19	20
A										
Real	4250061	3897979	3594446	3340416	3114934	2921407	2749805	2597296	2458714	2339575
Model	4250437	3896234	3596524	3339629	3116987	2922175	2750283	2597489	2460779	2337740
Δ%	0.009	-0.045	0.058	-0.024	0.066	0.026	0.017	0.007	0.084	-0.078
T										
Real	4269518	3908087	3609269	3349357	3128846	2931491	2759688	2606740	2470003	2346786
Model	4265155	3909725	3608977	3351193	3127780	2932294	2759806	2606483	2469300	2345835
Δ%	-0.102	0.042	-0.008	0.055	-0.034	0.027	0.004	-0.010	-0.028	-0.041
C										
Real	2771659	2543281	2346589	2180109	2037286	1907746	1795586	1695309	1607013	1523460
Model	2774889	2543648	2347983.077	2180270	2034919	1907736	1795516	1695766	1606515	1526189
Δ%	0.116	0.014	0.059	0.007	-0.116	-0.001	-0.004	0.027	-0.031	0.179
G										
Real	2789946	2558411	2364541	2193908	2045136	1920171	1806271	1705825	1616529	1534831
Model	2790704	2558145	2361365	2192696	2046516	1918609	1805749	1705430	1615671	1534887
Δ%	0.027	-0.010	-0.135	-0.055	0.067	-0.081	-0.029	-0.023	-0.053	0.004

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HUMAN CHROMOSOME Y:

n	1	2	3	4	5	6	7	8	9	10
A										
Real	7886192	3943767	2628327	1972285	1575702	1315547	1127472	986328	877065	788691
Model	7886192	3943096	2628731	1971548	1577238	1314365	1126599	985774	876244	788619
Δ%	0	-0.017	0.015	-0.037	0.097	-0.090	-0.078	-0.056	-0.094	-0.009
T										
Real	7956168	3979257	2653031	1990291	1589884	1326685	1136107	994568	883575	794453
Model	7956168	3978084	2652056	1989042	1591234	1326028	1136595	994521	884019	795617
Δ%	0	-0.029	-0.037	-0.063	0.085	-0.050	0.043	-0.005	0.050	0.146
C										
Real	5285789	2643050	1761782	1320660	1058536	880195	755403	660391	586535	529537
Model	5285789	2642894.5	1761930	1321447	1057158	880965	755113	660724	587310	528579
Δ%	0	-0.006	0.008	0.060	-0.130	0.087	-0.038	0.050	0.132	-0.181
G										
Real	5286894	2641447	1761874	1320524	1058883	880083	754592	660593	587831	528820
Model	5286894	2643447	1762298	1321724	1057379	881149	755271	660862	587433	528689
Δ%	0	0.076	0.024	0.091	-0.142	0.121	0.090	0.041	-0.068	-0.025

n	11	12	13	14	15	16	17	18	19	20
A										
Real	716673	658783	607174	563899	525387	493101	464190	439070	414918	394355
Model	716927	657183	606630	563299	525746	492887	463894	438122	415063	394310
Δ%	0.035	-0.244	-0.090	-0.106	0.068	-0.043	-0.064	-0.216	0.035	-0.012
T										
Real	723083	663210	611104	567935	529710	496740	467855	441926	417973	397615
Model	723288	663014	612013	568298	530411	497261	468010	442009	418746	397808
Δ%	0.028	-0.030	0.149	0.064	0.132	0.105	0.033	0.019	0.185	0.049
C										
Real	480691	439316	407258	377448	352984	330530	310832	292459	278430	264369
Model	480526	440482	406599.1538	377556	352386	330362	310929	293655	278199	264289
Δ%	-0.034	0.265	-0.162	0.029	-0.170	-0.051	0.031	0.407	-0.083	-0.030
G										
Real	480922	439947	406383	377501	352916	330573	310943	294052	278944	264408
Model	480627	440575	406684	377635	352460	330431	310994	293716	278258	264345
Δ%	-0.061	0.142	0.074	0.036	-0.129	-0.043	0.016	-0.114	-0.247	-0.024

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Appendix III. 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	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	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	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	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	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	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_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	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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

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

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	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	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_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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	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
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**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	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	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: 13 April 2020 doi:10.20944/preprints201908.0284.v4

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

e_{11} :

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

e_{12} :

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

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	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_{14} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	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_{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	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	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_{16} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	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	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	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	0	0	0	0	0	0	1	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	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	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	0	1	0	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	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	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: 13 April 2020 doi:10.20944/preprints201908.0284.v4

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

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

0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	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_{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	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	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_{22} :

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

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

e_{24} :

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 13 April 2020 doi:10.20944/preprints201908.0284.v4

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	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	1
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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	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	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	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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
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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
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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	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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
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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	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	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} :

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

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

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 13 April 2020 doi:10.20944/preprints201908.0284.v4

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	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	1	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	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	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} :

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

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	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_{28} :

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	**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	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	**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
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	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	0	**1**	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	**1**	0	0	0	0	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	0	**1**	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	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	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	**1**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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e_{31} :

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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	0	0
1	0	0	0	0	0	0	0	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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