The genetic system and algebras of projection operators *Sergey Petoukhov* Head of Lab of Biomechanical systems, Russian Academy of Sciences, Moscow





Science has led to a new understanding of life itself: **«Life is a partnership between genes and mathematics»** (Stewart I. Life's other secret: The new mathematics of the living world. 1999, New-York: Penguin).

But what kind of mathematics is a partner with the genetic code and defines the structure of living matter? This lecture shows that phenomenology of ensembles of molecular-genetic elements is connected with ensembles of **projection operators**, which are well-known in physics, informatics, chemistry, etc.

Information from the micro-world of genetic molecules dictates constructions in the macro-world of living organisms under strong noise and interference. This dictation is realized by means of unknown algorithms of multi-channel noise-immunity coding. For example, in accordance with Mendel's laws of independent inheritance of traits, colors of human skin, eye and hairs are genetically defined independently. So, each living organism is an algorithmic machine of multi-channel noise-**<u>immunity</u>** coding. To understand this machine we should use the theory of noise-immunity coding, which is based on **matrix representations** of digital information. Correspondingly we search mathematics of genetic systems in matrix representations of ensembles of genetic elements.



Our visual perception and a "projection method" in the drawing are based on projections of external objects on retina and a drawing plane. In mathematics, such operations of projections are expressed by means of **square matrices**, which are called "projection operators" (or "projectors"). The following matrix P is an example of a projector, which makes a projection of vector [x, y, z] on the plane [x, y, 0]:



A necessary and sufficient condition that a matrix P is a projection operator is given by the criterion: $P^2 = P$. Many matrices in this lecture will satisfy this criterion.

Projection operators are used widely in math, physics (including quantum mechanics), chemistry, informatics, logics, etc. Two kinds of projectors exist: orthogonal

projectors are expressed by symmetric matrices; **oblique projectors** – by asymmetric matrices (they are less studied).



This lecture shows that **projectors can be also used in studying and modeling properties of the genetic code system and many inherited biological ensembles** including ensembles of cyclic processes, phyllotaxis patterns, etc. **EXPLANATION ABOUT GENETIC MATRICES R₈ AND H₈** Theory of noise-immunity coding is based on matrix methods. For example, matrix methods allow transferring high-quality photos of Mar's surface via millions of kilometers of strong interference. In particularly, Kronecker families of Hadamard matrices are used for this aim.



Here (n) means a Kronecker power.

By analogy with theory of noise-immunity coding, the 4-letter alphabet of RNA (adenine A, cytosine C, guanine G and uracil U) can be represented in a form of a (2*2)-matrix [C U; A G] as a kernel of a Kronecker family of matrices [C U; A G]^(N), where (N) means a Kronecker power. The third Kronecker power of this alphabetic $(2\bar{*}2)$ -matrix gives the (8*8)-matrix of 64 triplets disposed in a strong order. These 64 triplets encode amino acids of proteins.

	CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
	CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
	CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
=	CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
	ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
	ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
	AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
	AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG

C U (3)

Two first positions of each triplet is termed as a "root" of the triplet. The phenomenological fact is that the set of 64 triplets is divided by the nature into two equal subsets with 32 triplets in each. The first subset contains 32 triplets with "strong roots" CC, CU, CG, AC, UC, GC, GU, GG (it means that all triplets, which have one of these roots, encode the same amino acid). The second subset contains 32 triplets with "weak roots" CA, AA, AU, AG, UA, UU, UG, GA (it means that all triplets, which have one of these roots, encode not the same amino acid).

Whether any symmetry exists in a disposition of triplets with strong and weak roots in the matrix of triplets [C U; A G]⁽³⁾ constructed formally ?

THE STA	NDARD CODE					
8 subfamilies of triplets with strong	8 subfamilies of triplets with weak roots					
roots («black triplets») and amino	(«white triplets») and amino acids, which					
acids, which are encoded by them	are encoded by them					
CCC, CCT, CCA, CCG \rightarrow Pro	CAC, CAT, CAA, CAG → His, His, Gln, Gln					
CTC, CTT, CTA, CTG → Leu	AAC, AAT, AAA, AAG 🗲 Asn, Asn, Lys, Lys					
CGC, CGT, CGA, CGG → Arg	ATC, ATT, ATA, ATG → Ile, Ile, Ile, Met					
ACC, ACT, ACA, ACG 🏼 → Thr	AGC, AGT, AGA, AGG 🗲 Ser, Ser, Arg, Arg					
TCC, TCT, TCA, TCG 🔶 Ser	TAC, TAT, TAA, TAG 🗲 Tyr, Tyr, Stop, Stop					
GCC, GCT, GCA, GCG → Ala	TTC, TTT, TTA, TTG 🗲 Phe, Phe, Leu, Leu					
GTC, GTT, GTA, GTG → Val	TGC, TGT, TGA, TGG → Cys, Cys, Stop, Trp					
GGC, GGT, GGA, GGG → Gly	GAC, GAT, GAA, GAG → Asp, Asp, Glu, Glu					
THE VERTEBRATE	MITOCHONDRIAL CODE					
CCC, CCT, CCA, CCG 🔶 Pro	CAC, CAT, CAA, CAG 🗲 His, His, Gln, Gln					
CTC, CTT, CTA, CTG 🗦 Leu	AAC, AAT, AAA, AAG 🗲 Asn, Asn, Lys, Lys					
CGC, CGT, CGA, CGG 🗲 Arg	ATC, ATT, ATA, ATG 🗦 lle, lle, Met, Met					
ACC, ACT, ACA, ACG \rightarrow Thr	AGC, AGT, AGA, AGG→ Ser, Ser, Stop, Stop					
TCC, TCT, TCA, TCG 🗲 Ser	TAC, TAT, TAA, TAG → Tyr, Tyr, Stop, Stop					
GCC, GCT, GCA, GCG → Ala	<u>TTC, TTT, TTA, TTG</u> \rightarrow Phe, Phe, Leu, Leu					
GTC, GTT, GTA, GTG → Val	<u>TG</u> C, <u>TG</u> T, <u>TG</u> A, <u>TG</u> G → Cys, Cys, Trp, Trp					
GGC, GGT, GGA, GGG 🗲 Gly	GAC, GAT, GAA, GAG 🗲 Asp, Asp, Glu, Glu					

Figure shows triplets with strong roots (black color) and weak roots (white color) in the Standard Genetic Code and the Vertebrate Mitochondrial Genetic Code It should be noted that a huge quantity $64! \approx 10^{89}$ of variants exists for dispositions of 64 triplets in the (8*8)-matrix. For comparison, the modern physics estimates time of existence of the Universe in 10^{17} seconds. It is obvious that an accidental disposition of the 20 amino acids and the corresponding triplets in a (8*8)-matrix will give almost never any symmetry.

But unexpectedly the phenomenological disposition of the 32 triplets with strong roots (black color) and the 32 triplets with weak roots (white color) has a symmetric character: 1) both quadrants along each of diagonals are identical by their mosaic; 2) the upper half and the lower half of the matrix are mirror-antisymmetric to each other in its colors: any pair of cells, disposed by mirror-symmetrical manner in these halves, possesses the opposite colors.

					CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
					CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
ſ	5	U	(3)		CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
1	1	G		=	CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
					ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
					ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
					AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
					AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG

	CCC	CCU	CUC	cw	VCC	UCU	WC	W
	CCA	CCG	C UA	CUG	UCA	UCG	UUA	WG
$\mathbf{T} \mathbf{A} \mathbf{C} \mathbf{I}(2)$	CAC	CAU	CCC	C GU	VAC	UAU	UGC	UGU
$U; AG^{(5)} =$	CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
	ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
	ACA	ACG	A UA	AUG	GCA	GC C	GUA	GUG
	AA C	AAU	AGC	A GU	GAC	GAU	GGC	GGU
	AAA	AAG	AGA	AGG	GAA	GA G	GGA	GGG
	<u> </u>	1	1			1	1	Ι
		Г				Г		

The most important fact || || || || || || is that a mosaic character of each of columns corresponds to an <u>odd meander-like function</u>. But such odd meander-like functions are well-known in theory of signal processing under the name "<u>Rademacher</u> functions".

[C]





Examples of Rademacher functions:

 $r_n(t) = sign(sin2^n \pi t)$

Rademacher functions contain only rad(1, t)elements "+1" and "-1". Each of the matrix columns presents one of the rad(2, t)Rademacher functions if each black (white) cell is interpreted such rad(3, t)that it contains the number +1 (-1).



				CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU		1	1	1	1	1	1	-1	-1
				CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG		1	1	1	1	1	1	-1	-1
С	U	(3)		CAC	CAU	CCC	CGU	UAC	UAU	UGC	UGU		-1	-1	1	1	-1	-1	-1	-1
A	G		=	CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG		-1	-1	1	1	-1	-1	-1	-1
	-		-	4.00	L CITT	110		0.00	0.011	0110	0.000	$\mathbf{R}_{\mathbf{a}} =$	1	1	-1	-1	1	1	1	1
				ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU	108 -	-	_			_	_	_	_
				ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG		1	1	-1	-1	1	1	1	1
				AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU		-1	-1	-1	-1	-1	-1	1	1
				AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG		-1	-1	-1	-1	-1	-1	1	1

Here we show a transformation of the mosaic genomatrix [C U; A G]⁽³⁾ into the numeric matrix R_8 in the result of such replacements of triplets with strong and weak roots by means of numbers "+1" and "-1" correspondingly. This numeric matrix R_8 is called the "Rademacher form" of the genetic matrix of triplets [C U; A G]⁽³⁾ or briefly the "**Rademacher matrix**" R_8 .

Taking into account another phenomenological fact about a unique status of uracil U (which is replaced by thymine T in DNA), a simple U-algorithm exists, which transforms the matrix [C U; A G]⁽³⁾ into the matrix [C T; A G⁽³⁾ with a new black-and-white mosaic (a triplet changes its color, if it has U in its odd position; this algorithm can be described below [Petoukhov, 2008]). This new mosaic corresponds to mosaic of one of Hadamard matrices H₈.

								_								
CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU		CCC	CCT	CTC	CTT	TCC	TCT	TTC	TTT
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG		CCA	CCG	CTA	CTG	TCA	TCG	TTA	TTG
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU		CAC	CAT	CGC	CGT	TAC	TAT	TGC	TGT
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG		CAA	CAG	CGA	CGG	TAA	TAG	TGA	TGG
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU		ACC	ACT	ATC	ATT	GCC	GCT	GTC	GTT
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG		ACA	ACG	ATA	ATG	GCA	GCG	GTA	GTG
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU		AAC	AAT	AGC	AGT	GAC	GAT	GGC	GGT
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG		AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG

Hadamard matrices also contain only entries "+1" and "-1". Columns of a Hadamard matrix form a complete orthogonal set of Walsh functions. If each black (white) cell of this symbolic matrix is interpreted as a container of number +1 (-1), then the **Hadamard matrix H₈** arises. Each of columns of the numeric matrix H₈ presents one of the Walsh functions.

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

H ₈	=

1	-1	1	-1	-1	1	1	-1
1	1	1	1	-1	-1	1	1
-1	1	1	-1	1	-1	1	-1
-1	-1	1	1	1	1	1	1
1	-1	-1	1	1	-1	1	-1
1 1	-1 1	-1 -1	1 -1	1	-1 1	1 1	-1 1
1 1 -1	-1 1 1	-1 -1 -1	1 -1 1	1 1 -1	-1 1 1	1 1 1	-1 1 -1

Hadamard matrices are intensively explored in digital signal processing including noise-immunity coding. For example, codes based on Hadamard matrices have been used on spacecrafts «Mariner» and «Voyadger», which allowed obtaining high-quality photos of Mars, Jupiter, Saturn, Uranus and Neptune in spite of the distortion and

weakening of the incoming signals.

Hadamard matrices are used to create quantum computers, which are based on Hadamard gates. They are used in quantum mechanics in the form of unitary operators.

Now we reveal and study the connection of the genetic code with a special kind of Hadamard matrices.

The main mathematical objects of the lecture will be these two (8*8)-matrices, which reflect phenomenological properties of the moleculargenetic ensembles: the Rademacher matrix R₈ and the Hadamard matrix H₈.



What secrets of the genetic code and living matter are hidden in these mosaic matrices? Let's study these matrices using their "Rademacher decomposition" and "Walsh decomposition" correspondingly.

	_							
	1	1	1	1	1	1	-1	-1
	1	1	1	1	1	1	-1	-1
	-1	-1	1	1	-1	-1	-1	-1
R8 =	-1	-1	1	1	-1	-1	-1	-1
	1	1	-1	-1	1	1	1	1
	1 1	1 1	-1 -1	-1 -1	1 1	1 1	1 1	1 1
	1 1 -1	1 1 -1	-1 -1 -1	-1 -1 -1	1 1 -1	1 1 -1	1 1 1	1 1 1
	1 1 -1	1 1 -1	-1 -1 -1	-1 -1 -1	1 1 -1	1 1 -1	1 1 1	1 1 1

	1	-1	1	-1	-1	1	1	-1
	1	1	1	1	-1	-1	1	1
	-1	1	1	-1	1	-1	1	-1
	-1	-1	1	1	1	1	1	1
H8 =	1	-1	-1	1	1	-1	1	-1
	1	1	-1	-1	1	1	1	1
	-1	1	-1	1	-1	1	1	-1
	-1	-1	-1	-1	-1	-1	1	1

Each of matrices R_8 and H_8 is a sum of 8 sparse matrices, in which only one of columns is non-zero (all these columns coincide with Rademacher or Walsh functions):

 $R_8 = s_0 + s_1 + s_2 + s_3 + s_4 + s_5 + s_6 + s_7;$ $H_8 = u_0 + u_1 + u_2 + u_3 + u_4 + u_5 + u_6 + u_7$

$R_8 = \begin{smallmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 & 0 \\$	$H_8 =$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$
$ \begin{vmatrix} 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 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$	L 0 0 1 00000 00000 L 0 0 1 00000 00000 00000 1 0 0 0 1 00000 00000 00000 1 0 0 0 1 000000 + 000000 + L 0 0 0 1 000000 + 000000 + L 0 0 0 -1 000000 + 000000 - L 0 0 0 -1 000000 - + 000000 - L 0 0 0 -1 000000 -	$\begin{array}{c c c c c c c c c c c c c c c c c c c $
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R ₈ =	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
$\left \begin{array}{cccccc} 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ \end{array} \right +$	$ \begin{smallmatrix} 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ \end{smallmatrix} $	$\left \begin{array}{cccccccccccc} 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \end{array}\right +$
$\left \begin{array}{cccccccccc} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \end{array}\right $	$\left(\begin{array}{ccccccccccc} 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{array}\right)$	$ \begin{smallmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 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 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 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 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 &$

	1 0000000	0 -1 000000
	1 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0
	-1 0000000	0 1 0 0 0 0 0 0
	-1 0000000	0 -1 0 0 0 0 0 0
Ш —	10000000 +	- 0 -1 0 0 0 0 0 -
Пд —	10000000	0 1 0 0 0 0 0 0
0	-1 0000000	0 1 0 0 0 0 0 0
	-1 0000000	0 -1 000000
	-1 0000000	0 -1 000000
00 1 00000 1		
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00 1 00000		0000 -1 000
00 1 00000	000-10000	0000 1 000
00 1 00000	000 10000	0000 1 000
00 -1 00000 +	000 1 0000 +	0000 1 000
00 -1 00000	000 -10000	0000 1 000
00 -1 00000	000 10000	0000 -1 000
00 -1 00000	000 -10000	0000 -1 000
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00000100	000000 10	0000000-1
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00000-100	000000 10	0000000-1
00000 10 0	000000 10	0000000 1
00000-100 +	000000 10 +	- 0000000 -1
00000 10 0	000000 10	0000000 1
00000 10 0	000000 10	0000000 -1
00000-10 0	000000 10	0000000 1

In these decompositions of $R_8 = s_0 + s_1 + s_2 + s_3 + s_4 + s_5 + s_6 + s_7$ and $H_8 = u_0 + u_1 + u_2 + u_3 + u_4 + u_5 + u_6 + u_7$, every of 16 sparse matrices s_0 , ..., s_7 , u_0 , ..., u_7 is <u>a projection operator</u> because it satisfies the criterion $P^2 = P$. It means that genetic matrices R_8 and H_8 are sums of oblique projectors; the genetic system is connected with projectors.

Now let us show how these "genetic" projectors allow modeling genetically inherited bio-ensembles.

INHERITED ENSEMBLES OF BIOLOGICAL CYCLES Any living organism is a huge ensemble of inherited cyclic processes, which form a hierarchy at different levels. Even every protein is involved in a cycle of its "birth-death," because after a certain time it breaks down into its constituent amino acids and they are then collected into a new protein. According to chrono-medicine and bio-rhythmology, various diseases of living bodies are associated with disturbances (dys-synchronization) in these cooperative ensembles of biocycles.

It is known that mathematical cyclic groups are useful to model natural cyclic processes. But combinations of the considered genetic projectors lead to a great number of cyclic groups. For example, take sum of two projectors s_0 and s_2 :

$$\mathbf{s}_0 + \mathbf{s}_2 = \begin{bmatrix} 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Exponentiation $(2^{-0.5*}(s_0+s_2))^N$ gives a **cyclic group** with its period 8: $(2^{-0.5*}(s_0+s_2))^N = (2^{-0.5*}(s_0+s_2))^{N+8}$ (here N=1, 2, 3, ...).

Iterative actions of this operator $Y = (2^{-0.5}*(s_0+s_2))$ on an arbitrary 8-dimensional vector $X = [x_0, x_1, x_2, x_3, x_4, x_5]$ x_5 , x_6 , x_7] give a cyclic set of vectors, in which only two coordinates with appropriate indexes 0 and 2 are cyclic changed, all other coordinates are equal to 0:

$$X^{*}Y^{1} = 2^{-0.5} * [(x_{0} + x_{1} - x_{2} - x_{3} + x_{4} + x_{5} - x_{6} - x_{7}), 0, (x_{0} + x_{1} + x_{2} + x_{3} - x_{4} - x_{5} - x_{6} - x_{7}), 0, 0, 0, 0, 0, 0]$$

$$X^*Y^2 = [(x_4-x_3-x_2+x_5), 0, (x_0+x_1-x_6-x_7), 0, 0, 0, 0, 0]$$

$$X^{*}Y^{*} = [(x_{4}-x_{3}-x_{2}+x_{5}), 0, (x_{0}+x_{1}-x_{6}-x_{7}), 0, 0, 0, 0, 0]$$

$$X^{*}Y^{3} = 2^{-0.5}*[(x_{4}-x_{1}-x_{2}-x_{3}-x_{0}+x_{5}+x_{6}+x_{7}), 0, (x_{0}+x_{1}-x_{2}-x_{3}+x_{4}+x_{5}-x_{6}-x_{7}), 0, 0, 0, 0]$$

$$X^{*}Y^{4} = [(x_{6}-x_{1}-x_{0}+x_{7}), 0, (x_{4}-x_{3}-x_{2}+x_{5}), 0, 0, 0, 0, 0]$$

$$X^{*}Y^{5} = 2^{-0.5}*[(x_{2}-x_{1}-x_{0}+x_{3}-x_{4}-x_{5}+x_{6}+x_{7}), 0, (x_{4}-x_{1}-x_{2}-x_{3}-x_{0}+x_{5}+x_{6}+x_{7}), 0, 0, 0, 0, 0]$$

$$X^{*}Y^{6} = [(x_{2}+x_{3}-x_{4}-x_{5}), 0, (x_{6}-x_{1}-x_{0}+x_{7}), 0, 0, 0, 0, 0]$$

$$X^*Y^4 = [(x_6-x_1-x_0+x_7), 0, (x_4-x_3-x_2+x_5), 0, 0, 0, 0, 0]$$

$$X^{*}Y^{5} = 2^{-0.5} \times [(x_{2}-x_{1}-x_{0}+x_{3}-x_{4}-x_{5}+x_{6}+x_{7}), 0, (x_{4}-x_{1}-x_{2}-x_{3}-x_{0}+x_{5}+x_{6}+x_{7}), 0, 0, 0, 0, 0]$$

$$X^*Y^0 = [(x_2+x_3-x_4-x_5), 0, (x_6-x_1-x_0+x_7), 0, 0, 0, 0, 0]$$

$$X * Y' = 2^{-0.5} * [(x_0 + x_1 + x_2 + x_3 - x_4 - x_5), 0, (x_0 - x_1 - x_0 + x_7), 0, (x_2 - x_1 - x_0 + x_3 - x_4 - x_5 + x_6 + x_7), 0, 0, 0, 0, 0, 0]$$

$$X*Y^8 = [(x_0+x_1-x_6-x_7), 0, (x_2+x_3-x_4-x_5), 0, 0, 0, 0, 0]$$

$$X^{*}Y^{9} = 2^{-0.5} * [(x_{0} + x_{1} - x_{2} - x_{3} + x_{4} + x_{5} - x_{6} - x_{7}), 0, (x_{0} + x_{1} + x_{2} + x_{3} - x_{4} - x_{5} - x_{6} - x_{7}), 0, 0, 0, 0, 0, 0]$$

It means that this cyclic group of operators allows a selective control (or a selective coding) of cyclic changes of vectors in 2-dimensional plane (x_0, x_2) of a 8-dimensional vector space. Other cyclic groups, which are based on exponentiation of pairs of the genetic projectors, possess the same property of a selective control of cyclic changes in corresponding 2-dimensional planes.

Exponentiation of sums of different pairs of these genetic projectors give three kinds of results, represented in the following symmetric tables by three colors.



Green cells contain pairs of projectors, exponentiation of which give similar cyclic groups with the period 8. All these cyclic groups possess the property of a **selective control of cyclic changes in corresponding 2-dimensional planes** inside an 8-dimensional vector space.





Let's return to sets of cyclic groups in green cells. The property of a simultaneously selective control of different subspaces of a multidimensional space by means of many cyclic groups is useful for modeling ensembles of cyclic processes in organisms including different animal gaits, etc. The simplest example is our model of human gaits, where cyclic movements of separate hands and foots can be defined independently. Fractional exponents for cyclic groups, for example $(2^{-0.5*}(s_0 + s_2))^{N/K}$, allow getting any approximation to smooth (uninterrupted) movements.











But what one can do if big ensembles with thousands and more cyclic processes should be simulated?

A proposed decision is based on extensions of the Rademacher's and Hadamard's (8*8)-matrices R₈ and H_8 into $(2^{N*}2^{N})$ -matrices by the following expressions: $R_8 \otimes [1 \ 1; 1 \ 1]^{(N)}$, $H_8 \otimes [1 \ -1; 1 \ 1]^{(N)}$, where \otimes means Kronecker multiplication; (N) – Kronecker power, N = 1, 2, 3, ...; [1 1; 1 1] and [1 -1; 1 1] matrix representations of complex number and double number with unit coordinates. Each of these $(2^{N*}2^{N})$ -matrices are sums of 2^{N} -projectors of the same "column type". Exponentiation of sums of different pairs of these new projectors gives as much cyclic groups as you want. These cyclic groups possess the same property of a selective control of 2-dimensional subspaces inside 2^{N} -dimensional space.

The revealed matrix approach gives new opportunities not only for studying inherited biological phenomena but also for biotechnical applications including systems of artificial intellect and robotics.



The problem of inherited ensembles of biological cycles is closely connected with a fundamental problem of biological time and biological watch.

The author puts forward a "projectors conception", which interprets living bodies as colonies of projection operators and multidimensional constructions on a basis of direct sums of vector sub-spaces. Any organism is a whole entity, and it is naturally to think that not only visual perception is based on projectors but that all bioinformatics is connected with them.

The evolution of living organisms is connected with their absorption of solar energy that is projected on surfaces of biological bodies by means of solar rays. Perhaps this fact can be considered as one of reasons of importance of projection operators in living bodies.



ABOUT DIRECTION OF ROTATIONS

In configurations and functions of biological objects frequently one direction of rotation is preferable (it concerns the famous problem of biological dissymmetry). Taking this into account, it is interesting what one can say about a direction of rotation of vectors under influence of the cyclic groups of the considered operators? The following tables give the answer.





Here green cells correspond to cyclic groups on a basis of sums of pairs of projectors. The symbol \bigcirc means counterclockwise rotation, the symbol \bigcirc means clockwise rotation. For example, the action $[x_0, x_1, x_2, x_3, x_4, x_5, x_6, x_7]^*(2^{-0.5*}(s_0+s_2))^N$ gives counter-clockwise rotations of vectors in (x_0, x_2) -plane. Tables show **dis-symetric** sets of cases of both directions of rotation: 1) the left table contains only counter-clockwise rotation; 2) the right table contains the ratio of cases $\bigcirc: \bigcirc = 5:3$. It generates some associations with a general problem of biological dis-symmetry.

ABOUT HAMILTON QUATERNIONS

Till now we considered sums of pairs of the genetic projectors. Now let us consider sums of 4 projectors. Hadamard matrix H_8 is sum of two sparse (8*8)matrices $H_8 = HL_8 + HR_8$, each of which is sum of 4

projectors:



1	0	1	0	-1	0	1	0	
1	0	1	0	-1	0	1	0	
-1	0	1	0	1	0	1	0	
-1	0	1	0	1	0	1	0	+
1	0	-1	0	1	0	1	0	
1	0	-1	0	1	0	1	0	
-1	0	-1	0	-1	0	1	0	
-1	0	-1	0	-1	0	1	0	

0	-1	0	-1	0	1	0	-1
0	1	0	1	0	-1	0	1
0	1	0	-1	0	-1	0	-1
0	-1	0	1	0	1	0	1
0	-1	0	1	0	-1	0	-1
0	1	0	-1	0	1	0	1
0	1	0	1	0	1	0	-1
0	-1	0	-1	0	-1	0	1

Each of the matrices HL₈ and HR₈ can be decomposed into 4 sparse matrices, set of which is closed in relation to multiplication and defines a known table of multiplication of Hamilton quaternions:
$HL_8 = HL_{80} + HL_{81}$	+ HL	₈₂ + HL ₈₃ =	$HR_{g} = HR_{g0} + HR_{g1} + HR_{g2}$	$+ HR_{0}$	в =
10000000		00100000	0-10 00 0 0 0		0 0 0 - 1 0 0 0 0
10000000		00100000	01000000		0 0 0 1 0 0 0 0
00100000		-10000000	000-10000		0 1 0 0 0 0 0 0
00100000	+	-100000000	0 0 0 1 0 0 0 0		0-1000000
00001000		00000010	0 0 0 0 0 - 1 0 0	+	0 0 0 0 0 0 0 -1
00001000		00000010	0 0 0 0 0 1 0 0		0 0 0 0 0 0 0 1
00000010		0000-1000	0 0 0 0 0 0 0 -1		0 0 0 0 0 1 0 0
00000010		0000-1000	0 0 0 0 0 0 0 1		0 0 0 0 0 -1 0 0
00 00 - 10 00		00 00 0010	00000100		0 0 0 0 0 0 0 -1
00 00 - 10 00		00 00 0010	00000-100		0 0 0 0 0 0 0 1
00 00 00 10		00 00 10 00	000000-1	+	0 0 0 0 0 - 1 0 0
00 00 00 10	+	00 00 10 00	00000001		0 0 0 0 0 1 0 0
10 00 00 00		00-100000	0-10 00 0 0 0		0 0 0 1 0 0 0 0
10 00 00 00		00-100000	01000000		0 0 0 - 1 0 0 0 0
00-100000		-10 00 00 00	00010000		01000000
00-100000		-10 00 00 00	000-10000		0-1000000

	HL ₈₀	HL ₈₁	HL ₈₂	HL ₈₃
HL ₈₀	HL ₈₀	HL ₈₁	HL ₈₂	HL ₈₃
HL ₈₁	HL ₈₁	- HL ₈₀	HL ₈₃	- HL ₈₂
HL ₈₂	HL ₈₂	- HL ₈₃	- HL ₈₀	HL ₈₁
HL83	HL83	HL ₈₂	- HL ₈₁	- HL ₈₀

+

	HR ₈₀	HR ₈₁	HR ₈₂	HR83
HR ₈₀	HR ₈₀	HR ₈₁	HR ₈₂	HR ₈₃
HR ₈₁	HR ₈₁	- HR ₈₀	HR ₈₃	- HR ₈₂
HR ₈₂	HR ₈₂	- HR ₈₃	- HR ₈₀	HR ₈₁
HR83	HR83	HR ₈₂	- HR ₈₁	- HR ₈₀

The multiplication table of Hamilton quaternions.

It means that the (8*8)-matrix H₈ is sum of two Hamilton quaternions with unit coordinates or, figuratively speaking, a "double quaternion". This fact generates an association with a double helix of DNA.



Hamilton quaternions are closely related to Pauli matrices, the theory of the electromagnetic field (Maxwell wrote his equation on the language of these quaternions),



the special theory of relativity, the theory of spins, quantum theory of chemical valences, etc. In the twentieth century thousands of works were devoted to quaternions in physics [http://arxiv.org/abs/mathph/0511092]. Now Hamilton quaternions are manifested in the genetic code system. Our scientific direction - "matrix genetics" - has led to the discovery of an important bridge among physics, biology and informatics for their mutual enrichment.

The connections of the genetic code with hypercomplex numbers seem to be interesting since classical theory of noise-immunity communication is based on multi-dimensional geometry: information sequences are represented as sequences of multidimensional vectors



THE 8 PROJECTORS AND HAMILTON BIQUATERNION

The genetic (8*8)-matrix H₈, which is sum of the 8 projectors, can be decomposed also in another way into a set of new 8 sparse matrices:

1	-1	1	-1	-1	1	1	-1
1	1	1	1	-1	-1	1	1
-1	1	1	-1	1	-1	1	-1
-1	-1	1	1	1	1	1	1
1	-1	-1	1	1	-1	1	-1
1	1	-1	-1	1	1	1	1
-1	1	-1	1	-1	1	1	-1
-1	-1	-1	-1	-1	-1	1	1

 $H_8 = H_{80} + H_{81} + H_{82} + H_{83} + H_{84} + H_{85} + H_{86} + H_{87} =$

1	0	0	0	0	0	0	0		Γ	(0.1	. 0	0	0	0 (0 0			0	0	1	0	0	0	0	0			0	0	0	-1	. 0	0	0	0		
0	1	0	0	0	0	0	0			-1	. 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	1	0	0	0	0	0			1	0.0	0	-1	0.1	0.0	0 0			_1	0	0	0	0	0	0	0			0	1	0	0	0	- a	0	0		
Lā	Ē.	ā	ĩ.	ñ.	ñ.	ñ.	ñ.		+	Ĩ	n n	n.	ñ.	ñ i	n n	i n		+	n.	ñ	ā	ñ.	n.	ā.	'n.	ā.		+	1	ិ	ា	- ñ	n a	ιā	n o	n.		
		SP.	÷.,	w.	ъ.	122	92 1			- 3	8 W	ан. С	ъ.	97 S	9 B	a w			200		, a	. W.	- 12	200		. W.				. w		1.5	8 N		8 U	. w		
0	0.	0	0.	1	0	0	0			- 0	0 0	0	0	0 - ,	1 (00			0	0	0	0	- 0	-0	1	0			0	-0	0	- 0) () (0 0) _1		÷.
0	0	0	0	0	1	0	0			- (0 0	0	0	1 (0 0	0 (0	0	0	0	0	0	0	1			0	0	0	- 0) () (01	. 0		
0	0	0	0	0	0	1	0			(0 0	0	0	0 (0 0	1-1			0	0	0	0	-1	.0	0	0			0	0	0	- () ()]	10	0		
0	0	0.1	0	0	0	0	1			- (0.0	0	0	0.0	0 1	0			0	0	0	0	0	.1	0	0			0	0	0	0	L LI	1.0	n o	0		
		20.		ω.		192					ar rea	- 1	Sec.						100		- W.	1995	196	- - - -	100	1996			100	100					. w			
																																					_	
ĺ	0	0	0	0	-1	0	0	0	- ר	Γ	0	0	0	0	0	1	0	0	7	Г	Q	0	0	0	0	0	1	0		Г	0	0	0 1	0	0 (0 0	-1	٦
	0	0	0 0	0	-1 0	0 -1	0 0	0		ſ	0	0	0	0	0 -1	1 0	0	0	1	Γ	0	0	0 0	0 0	0 0	0 0	1	0		Γ	0	0	0 (0	0 (00	-1 0	7
	0 0 0	0 0 0	0 0 0	0 0 0	-1 0 0	0 -1 0	0 0 1	0 0 0		ſ	0000	0000	0000	0000	0 -1 0	1 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	1 0 0	0 1 0			0 0 0	0	0 (0 (0 (0	0 (0 0 0 1 1 0	-1]
	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 1 0	0 0 0 1].	-	000000	00000	000000	000000	0 -1 0 0	1 0 0 0	0 0 0 1	0 0 -1 0	+		0 0 0 0	0 0 0 0	0 0 0 0	0 0 0 0	0 0 1 0	0 0 0 1	1 0 0 0	0 1 0 0	+		0 0 0 0	0		0	0 (0 (0 -		-1	
	0 0 0 0 1	0 0 0 0	0000000	000000	-1 0 0 0 0	0 -1 0 0 0	0 0 1 0 0	0 0 0 1 0].	-	000000		0000000	0000000	0.1000	1 0 0 0 0	00010	0 -1 0 0	+		000000	0000000	0 0 0 0 -1	000000	00100	0 0 0 1 0	1 0 0 0 0	0 1 0 0	+		000000	0 0 0 0		0 0 0 1	0 (0 - 1 (0 (-1 0 0 0	
	0 0 0 1 0	0 0 0 0 0	0000000	000000000	-100000000000	0-1-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0	001000	0 0 0 1 0].	-	00000	000010	000000000	000000000	0-10000	10000000	000100	0 -1 0 0	+		000000000000000000000000000000000000000	000000000000000000000000000000000000000	0 0 0 0 -1 0	000000	0 0 1 0 0	0 0 0 1 0 0	1 0 0 0 0 0 0	0 1 0 0 0	+		00000000	000000000000000000000000000000000000000		0 0 0 1	0 (0 - 1 (0 (
	0 0 0 1 0	0 0 0 0 1	000000	0000000	-1000000	0-10000	001000	0001000].	-	0000010	0000100	000000000	000000	0.100000	1 0 0 0 0 0	0001000	0 0 -1 0 0 0 0	+		000000	000000	0000-100	00000.10	001000	0001000	1 0 0 0 0 0	010000	+		000000000000000000000000000000000000000	000000000000000000000000000000000000000		0	0 (
	0 0 0 1 0	0 0 0 0 1	000000	00000000	-10000000000000000000000000000000000000	0 1 0 0 0 0 0	001000	0001000	-	-	0000010	00000-100	000000000000000000000000000000000000000	000000000000000000000000000000000000000	0100000	10000000	0001000	0 -1 0 0 0	+		0 0 0 0 0 0 0	0000000	0000100	00000-10	0010000	0001000		0 1 0 0 0 0	+		000000000000000000000000000000000000000	0 0 0 0 0 1	0 (0 (0 (0 (1 (0 0 0 1 0 0	0 0 0 1 0 0			

This set of 8 matrices is also closed in relation to multiplication and defines a known multiplication table of Hamilton biquaternions :

	0 0 1 0 0 0
	00000100
	00000-10
	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 1 0 0
	0000-1000
	0 0 0 0 0 0 0 -1
	0 (0 (0 (0 (0 (0 (
	0 0 1 0 0 0 0
	0 -1 0 0 0 0
	+
	0 0 0 0 0 -1 0
	0 0 0 0 0 0
	0 0 0 1 0 0 0
	0 0 0 0 -1 0 0
	0 0 0 0 1 0 0 1 0 0 0 0
	0 1 0 0 0 0 0
	+
-	000000000000000000000000000000000000000
	0 0 0 0 -1 0
	000000000000000000000000000000000000000
	0 0 1 0 0 0
	0 -1 0 0 0 0
	0 - 1 0 0 0 0 0 0 0
	.1 0 0 0 0 0 0 0

	1	H_{s_1}	H_{s_2}	H _{so}	H_{s_4}	H _{s5}	H_{sc}	H_{s7}
1	1	H_{s_1}	H_{52}	H _{s3}	H.,	H _{s5}	H _{se}	H_{s7}
H _m	H_{s_1}	-1	H _{sp}	$-H_{82}$	H _{s5}	$-H_{84}$	H_{s7}	$-H_{sc}$
H_{s_2}	H_{s_2}	H _{so}	-1	$-H_{81}$	$-\mathbf{H}_{ss}$	$-H_{87}$	H_{s_4}	H _{ss}
H _{so}	H_{s_3}	$-H_{82}$	$-H_{81}$	1	$-H_{87}$	H_{se}	H_{ss}	$-H_{84}$
H_{g_4}	H_{g_4}	H _{s5}	H_{se}	H_{s7}	-1	$-H_{81}$	$-\mathbf{H}_{82}$	$-H_{83}$
H ₈₅	H_{gs}	$-H_{84}$	H_{s7}	$-H_{86}$	$-H_{81}$	1	- H ₈₃	H_{s_2}
H_{ss}	H_{gs}	H_{s7}	- H ₈₄	$-H_{85}$	H_{s_2}	H _{so}	-1	$-H_{81}$
H_{87}	H_{87}	$-H_{ss}$	- H ₈₅	H_{54}	H _{s3}	$-H_{82}$	$-H_{s1}$	1

The multiplication table of Hamilton biquaternions (or Hamilton quaternions over field of complex numbers)

ABOUT SPLIT-QUATERNIONS BY J.COCKLE

The Rademacher matrix R_8 is also sum of 2 sparse (8*8)-matrices $R_8 = RL_8 + RR_8$, each of which is sum of 4 projectors:

K		<u>аг"+</u>	KK _s	=										
1	0	1	0	1	0	-1	0		0	1	0	1	0	
1	0	1	0	1	0	-1	0		0	1	0	1	0	
-1	0	1	0	7	0	-1	0		0	7	0	1	0	
-1	0	1	0	7	0	-1	0	+	0	7	0	1	0	
1	0	-1	0	1	0	1	0		0	1	0	-1	0	
1	0	-1	0	1	0	1	0		0	1	0	-1	0	
-1	0	-1	0	-1	0	1	0		0	-1	0	-1	0	
-1	0	-1	0	7	0	1	0		0	-1	0	-1	0	



Each of the matrices RL₈ and RR₈ can be decomposed into 4 sparse matrices, set of which is closed in relation to multiplication and defines a known table of multiplication of split-quaternions by J.Cockle (1849 year, <u>HTTP://EN.WIKIPEDIA.ORG/WIKI/SPLIT-QUATERNION</u>).

RL8 =RL80+RL81+RL82+RL83=

10000000 10000000 00100000 00100000 00001000 00001000 000001000 000000	+	00100000 00100000 -10000000 -100000000 00000010 0000010 0000-1000 0000-1000
00001000 00001000 000000-10 000000-10 10000000 10000000 00-100000 00-100000	+	00 00 00-10 00 00 00-10 00 00-10 00 00 00-10 00 00-10 00 00 00-10 00 00 -10 00 00 00

RR8 = RR80 + RR81 + RR82 + RR83 =

01000000		0 0 0 1 0 0 0 0
01000000		0 0 0 1 0 0 0 0
00010000		0-1000000
00010000		0-1000000
00000100	+	0 0 0 0 0 0 0 0 1
00000100		0 0 0 0 0 0 0 1
00000001		0 0 0 0 0 -1 0 0
00000001		0 0 0 0 0 -1 0 0
0000001		0 0 0 0 0 -1 0 0
	-	
00000100		0000000-1
00000100		0000000-1 0000000-1
000 0010 0 000 0010 0 000 0000-1		0000000-1 0000000-1 00000-100
$\begin{array}{c} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & -1 \end{array}$		0000000-1 0000000-1 00000-100 00000-100
$\begin{array}{c} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{array}$	+	0000000-1 000000-1 00000-100 00000-100 0000-10000
$\begin{array}{c} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \end{array}$	+	0000000-1 000000-1 00000-100 00000-100 000-10000 000-10000
$\begin{array}{c} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \end{array}$	+	$\begin{array}{c} 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 \end{array}$
$\begin{array}{c} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \end{array}$	÷	$\begin{array}{c} 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ -1 \\ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ -1 \\ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ -1 \ 0 \ 0 \\ 0 \ 0 \ 0 \ 0 \ -1 \ 0 \ 0 \ 0 \\ 0 \ 0 \ 0 \ -1 \ 0 \ 0 \ 0 \ 0 \\ 0 \ 0 \ 0 \ 0 \ 0 \ 0$

	RL _{to}	RL _m	RL ₁₀	RL ₁₀		RR ₈₀	RR ₈₁	RR _{itt}	RR _{K3}
RL ₁₀	RL ₁₀	RL _m	RL ₁₀	RL ₈₃	RR ₈₀	RR ₈₀	RR ₈₁	RR ₈₂	RR ₆₃
RL _m	RL _m	- RL ₈₀	RL ₁₀	-RL ₈₂	RR ₈₁	RR ₈₁	- RR _{go}	RR ₁₀	- RR ₈₂
RL ₈₂	RL ₈₂	- RL ₈₃	RL ₁₀	-RL _M	RR _{st}	RR ₈₂	- RR ₆₃	RR ₈₀	- RR ₈₁
RL ₁₀	RL ₁₀	RL ₈₂	RL _m	RL ₁₀	RR ₈₃	RR ₆₃	RR _{st}	RR ₅₁	RR ₈₀

THE MULTIPLICATION TABLE OF SPLIT-QUATERNIONS BY J.COCKLE. Split-quaternions by Cockle are also used in mathematics and physics, for example, in A.Poincare's model of Lobachevskiy's geometry (http://en.wikipedia.org/wiki/Split-quaternion).





The 8 projectors and Cockle's bi-split-quaternions

The genetic (8*8)-matrix R_8 , which is sum of the 8 projectors, can be decomposed also in another way into a set of new 8 sparse matrices: $R_8 = R_{80} + R_{81} + R_{82} + R_{83} + R_{84} + R_{85} + R_{86} + R_{87} =$

1	1	1	1	1	1	-1	-1
1	1	1	1	1	1	-1	-1
-1	-1	1	1	-1	-1	-1	-1
-1	-1	1	1	-1	-1	-1	-1
1	1	-1	-1	1	1	1	1
1 1	1	-1 -1	-1 -1	1 1	1	1 1	1
1 1 -1	1 1 -1	-1 -1 -1	-1 -1 -1	1 1 -1	1 1 -1	1 1 1	1 1 1



This set of 8 matrices are also closed in relation to multiplication and defines a known multiplication table of Cockle's biquaternions :

$\begin{array}{c} 1 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \$	+	0100000000000000000000000000000000000	+	0 0 -1 0 0 0 0 0	$\begin{array}{c} 0 \ 1 \ 0 \ 0 \ 0 \\ 0 \ 0 \ 1 \ 0 \ 0 \\ 0 \ 0 \ 0 \ 0 \ 0 \\ 0 \ 0 \ 0$	0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0	0 0 + -1 0 0 0	00 01 -10 00 00 00 00	1000 0000 0000 0000 0001 00-10 0-100	0 0 0 1 0 0 0 0 0 0 0
$\begin{array}{c} 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 \end{array}$	+	$\begin{array}{c} 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 &$	0 -1 10 0 0	+	$\begin{array}{c} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 &$) 0 -1 () 0 0 - 1 0 0 () -1 0 (0 0 0 (0 0 0 () 0 0 0 (0 1) +)	0 0 0 0 0 -1	00000 0000- 000-1 00-10 0-100 1000 00-00	0 0 -1 0 -1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	The late	D1 D3		TD-2	D .4	THE:	D.4		TO F	1

	R0 _s	Rls	R2 ₈	R3 ₈	R4 _s	$R5_8$	R6 ₈	R7 _s
R0 _s	R0 _s	R1 _s	R2 ₈	R3 ₈	R4 _s	$R5_8$	R6 _s	R7 _s
Rls	R1 _s	R0 _s	R3 ₈	R2 ₈	$R5_8$	R4 _s	R7 ₈	Rő _s
R2 _s	R2 _s	R3 _s	- R0 _s	- R1,	Rős	R7 _s	- R4 _s	- R5 ₈
R3 _s	R3 _s	R2 _s	- R1,	- R0 _s	R7 _s	R6 _s	- R5 ₈	- R4 ₈
R4 _s	R4 _s	$R5_8$	- R6 _s	- R7 _s	R0 _s	R1 _s	- R2 _s	- R3 ₈
$R5_{g}$	$R5_8$	R4 _s	- R7 _s	- R6 _s	Rls	R0 _s	- R3 _s	- R2 ₈
Rős	Rős	R7 _s	R4 _s	$R5_8$	R2 ₈	R3 ₈	R0 ₈	Rls
R7 _s	R7 ₈	Rős	R5 _s	R4 _s	R3 _s	R2 _s	Rls	R0 _s

The multiplication table of bisplit-quaternion by J.Cockle (or split-quaternions over field of complex numbers)

Here we have received new examples of the effectiveness of mathematics: abstract mathematical structures, which have been derived by mathematicians at the tip of the pen 160 years ago, are embodied long ago in the information basis of living matter - the system of genetic coding. The mathematical structures, which are discovered by mathematicians in a result of painful reflections (like Hamilton, who has wasted 10 years of continuous thought to reveal his quaternions), are already represented in the genetic coding system.

Let's return to (8*8)-matrix representations **HL₈** and **HR₈** of Hamilton quaternions with unit coordinates.



Exponentiation of each of these matrices (with a coefficient 0.5) leads to a cyclic group with its period 6 (n = 1, 2, 3, ...): (0.5*HL₈)ⁿ⁺⁶ =(0.5*HL₈)ⁿ; $(0.5^*HR_8)^{n+6} = (0.5^*HR_8)^{n}$ A similar expression is true for a classical (4*4)-matrix $O = 0.5^{*}$ representation of Hamilton quaternion **Q** with unit coordinates: (0.5*Q)ⁿ⁺⁶ =(0.5*Q)ⁿ

One can dispose all 6 members of any of these cyclic groups (for example, members of the group of (4*4)-matrices $(0.5*Q)^{n+6} = (0.5*Q)^n$) on a circle to show a complete analogy of their set to famous Newton's color circle of inborn properties of human color perception.





The Newton's color circle shows the following: 1) each of 6 colors on the circle is the sum of two adjacent colors (the same is true for these 6 quaternions on the circle);

2) the three colors in vertices



3) complementary colors, which are opposite each other on this circle, neutralize each other in their summation (sum of any two diagonal quaternions on the circle is also equal to 0).



Briefly speaking, the red, magenta, blue, cyan, green and yellow colors are formally expressed by means of the Hamilton quaternions Q¹, Q², Q³, Q⁴, Q⁵, Q⁶ correspondingly. The problem of mixing of colors can now be solved in terms of the cyclic group of Hamilton quaternions Qⁿ.

Using the mentioned $(2^{n*}2^{n})$ -matrix representations of Hamilton quaternions allows encoding (or controlling) different colors in different sub-spaces of an internal space of a living body.

Algebraic invariances and positional permutations in triplets

The theory of signal processing pays a special attention to permutations of information elements. Six variants of permutations of positions inside a triplet exist: 1-2-3, 2-3-1, 3-1-2, 3-2-1, 2-1-3, 1-3-2, 3-2-1. Let us study transformations of the Rademacher and Hadamard representations of the genomatrix [C T; A G]⁽³⁾ in all these cases of positional permutations in all triplets. A simultaneous permutation of positions in triplets transforms the most of the triplets in its matrix cells. For example, in the case of the transformation of the order of positions 1-2-3 into the order 2-3-1, the "white" triplet <u>CAG</u> with the weak root CA is transformed into the "black" triplet AGC with the strong root AG. In the result, the quite new mosaic genomatrices arises.

In the result of these positional permutations in triplets, five additional Rademachér matrices arise from the initial Rademacher genomatrix R_8 ; each of them is a new matrix representation of the same bi-spit-quaternion by Cockle with unit coordinates. Also in the result of these permutations, five new Hadamard matrices come from the initial Hadamard genomatrix H_8 ; each of them is a new representation of the same Hamilton's **biquaternion** with unit coordinates



Each of these 5 new Rademacher matrices can be also decomposed into 8 projectors with Rademacher functions in their non-zero columns

Each of these 5 new Hadamard matrices can be also decomposed into 8 projectors with Walsh functions in their non-zero columns **All ideology of projectors and their combinations is conserved for these new matrices, which arise due to positional permutations in triplets.**



The invariance of matrix algebras with different permutations of elements in genomatrices is interesting, in particular, due to the metamorphosis of the organisms. For example, in the metamorphosis of a butterfly, chrysalis does not eat at all and has a fixed atomic composition, but - by means of genetically determined permutations of elements – chrysalis turns into a butterfly, which is a quite different organism with the same DNA.

It seems that the nature likes projectors. For example, electromagnetic vectors are represented as sums of their projections in a form of electric and magnetic vectors.

CYCLIC CHANGES AND THE "I-CHING"

In the field of molecular genetics, Nobel prize winner F.Jacob, a famous Prof. G.Stent (1965) and some other authors already noted some parallelisms between the molecular genetic system and a symbolic system of the Ancient Chinese book "I-Ching" ("The Book of Changes"), which was written a few thousand years ago.

This book had a great influences on different aspects of life of people not only in China but also in many other countries.

The state flag of South Korea with symbols of triplets from "I-Ching"





Cyclic and other patterns, which arise in "matrix genetics", have many new analogies with the system of "I-Ching", Chinese circular calendars, the Zodiac system and patterns of Ancient Oriental medicine. In other words, here we get new materials for a problem of "a connection of times".



"I-Ching" deals with Yin-Yang symbols including the four basic digrams: Old Yang (), Old Yin ()), Young Yang () and Young Yin ()). The famous table of 64 hexagrams in Fu-Xi's order exists in this symbolic system:

	111	110	101	100	011	010	001	000
	CHYAN	TUI	LI	CHEN	HSUN	KAN	KEN	KUN
	<u>1111</u> 111	<u>111</u> 110	<u>111</u> 101	<u>111</u> 100	<u>111</u> 011	<u>111</u> 010	<u>111</u> 001	<u>111</u> 000
<u>110</u> TUI	<u>110</u> 111	<u>110</u> 110	<u>110</u> 101	<u>110</u> 100	<u>110</u> 011	<u>110</u> 010	<u>110</u> 001	<u>110</u> 000
<u>101</u> LI	<u>101</u> 111	<u>101</u> 110	<u>101</u> 101	<u>101</u> 100	<u>101</u> 011	<u>101</u> 010	<u>101</u> 001	<u>101</u> 000
<u>100</u> CHEN	<u>100</u> 111	<u>100</u> 110	<u>100</u> 101	<u>100</u> 100	<u>100</u> 011	<u>100</u> 010	<u>100</u> 001	<u>100</u> 000
011 HSUN	<u>011</u> 111	<u>011</u> 110	<u>011</u> 101	<u>011</u> 100	<u>011</u> 011	<u>011</u> 010	011 001	<u>011</u> 000
010 KAN	<u>010</u> 111	010110	<u>010</u> 101	<u>010</u> 100	<u>010</u> 011	010010	010 001	010000
<u>001</u> KEN	<u>001</u> 111	<u>001</u> 110	<u>001</u> 101	001100	<u>001</u> 011	001010	001 001	001000
<u>000</u> KUN			<u>000</u> 101					

The ancient Chinese claimed that the system of "I-Ching" is a universal archetype of nature, a universal classification system. They knew nothing about the genetic code, but the genetic code is constructed in accordance with the "I-Ching". Briefly about ensembles of phyllotaxis patterns Let us briefly note that a study of sums of genetic projectors has given new possibilities of modeling some other inherited biological phenomena including a phenomenon of ensembles of phyllotaxis patterns inside one organism.



It is known that an organism can have many phyllotaxis patterns in its parts. Figure shows an example of a spruce with many phyllotaxis cones. Each of



these cones can be interpreted as a sub-space of a multi-dimensional internal space of this tree. The proposed approach of genetic projectors and their sums allows modeling such ensemble of phyllotaxis patterns, each of which is realized in its own subspace with an individual velocity and a phase shift of development (see some details in the article [Petoukhov, 2013, <u>http://arxiv.org/abs/1307.7882</u>]).



An example of modeling three phyllotaxis patterns, each of which belongs to its own 2-dimensional sub-space of a general multi-dimensional internal space.

PROJECTORS AND THE EXCLUSION PRINCILE OF EVOLUTION OF DIALECTS OF THE GENETIC CODE Science knows 19 dialects of the genetic code http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprint

gc.cgi . Some of them have another black-and-white mosaic in their matrix presentation [C U; A G]⁽³⁾ (another system of triplets with strong and weak roots).

The Standard Code The Vertebrate Mitochondrial Code The Yeast Mitochondrial Code The Mold. Protozoan. and Coelenterate Mitochondrial Code and Mycoplasma/Spiroplasma Code The Invertebrate Mitochondrial Code The Ciliate, Dasycladacean and Hexamita Nuclear Code The Echinoderm and Flatworm Mitochondrial Code The Euplotid Nuclear Code The Bacterial, Archaeal and Plant Plastid Code The Alternative Yeast Nuclear Code The Ascidian Mitochondrial Code The Alternative Flatworm Mitochondrial Code Blepharisma Nuclear Code Chlorophycean Mitochondrial Code Trematode Mitochondrial Code Scenedesmus Obliquus Mitochondrial Code Thraustochytrium Mitochondrial Code Pterobranchia Mitochondrial Code Candidate Division SR1 and Gracilibacteria Code

Some of the dialects have another black-and-white mosaic in their matrix presentation [C U; A G]⁽³⁾ (another system of triplets with strong and weak

The Vertebrate Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Тут	Тут	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Met	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lys	Lys	Stop	Stop	Glu	Ghu	Gly	Gly

The Standard Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lys	Lys	Arg	Arg	Glu	Glu	Gly	Gly

The Invertebrate Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
ACC Thr	ACU Thr	AUC Ile	AUU Ile	GCC Ala	GCU Ala	GUC Val	GUU Val
ACC Thr ACA	ACU Thr ACG	AUC Ile AUA	AUU Ile AUG	GCC Ala GCA	GCU Ala GCG	GUC Val GUA	GUU Val GUG
ACC Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Met	AUU Ile AUG Met	GCC Ala GCA Ala	GCU Ala GCG Ala	GUC Val GUA Val	GUU Val GUG Val
ACC Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Met AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	GCU Ala GCG Ala GAU	GUC Val GUA Val GGC	GUU Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Met AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU Gly
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Met AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	GCU Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Тут	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
ACC Thr	ACU Thr	AUC Ile	AUU Ile	GCC Ala	GCU Ala	GUC Val	GUU Val
ACC Thr ACA	ACU Thr ACG	AUC Ile AUA	AUU Ile AUG	GCC Ala GCA	GCU Ala GCG	GUC Val GUA	GUU Val GUG
ACC Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Ile	AUU Ile AUG Met	GCC Ala GCA Ala	GCU Ala GCG Ala	GUC Val GUA Val	GUU Val GUG Val
ACC Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Ile AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	GCU Ala GCG Ala GAU	GUC Val GUA Val GGC	GUU Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Ile AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU GIy
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Ile AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	GCU Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

The Yeast Mitochondrial Code:

The Euplotid Nuclear Code:

CCC	CCU	CUC	CUA	UCC	UCU	UUC	UUU
Pro	Pro	Thr	Thr	Ser	Ser	Phe	Phe
CCA	CCG	CUU	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Thr	Thr	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Met	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
	т	A	A	C1	Clu	C1	Class

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Cys	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
ACC Thr	ACU Thr	AUC Ile	AUU Ile	GCC Ala	GCU Ala	GUC Val	GUU Val
ACC Thr ACA	ACU Thr ACG	AUC Ile AUA	AUU Ile AUG	GCC Ala GCA	GCU Ala GCG	GUC Val GUA	GUU Val GUG
ACC Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Ile	AUU Ile AUG Met	GCC Ala GCA Ala	GCU Ala GCG Ala	GUC Val GUA Val	GUU Val GUG Val
ACC Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Ile AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	GCU Ala GCG Ala GAU	GUC Val GUA Val GGC	GUU Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Ile AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU Gly
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Ile AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	GCU Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

The Bacterial, Archaeal and Plant Plastid Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lvs	Lvs	Arg	Arg	Glu	Glu	Gly	Gly

The Alternative Yeast Nuclear Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Ser	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Stop	trp
100				000	~ ~ ~ ~	~~~~~	
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	ACU Thr	AUC Ile	AUU Ile	GCC Ala	GCU Ala	GUC Val	GUU Val
Thr ACA	ACU Thr ACG	AUC Ile AUA	AUU Ile AUG	GCC Ala GCA	GCU Ala GCG	GUC Val GUA	GUU Val GUG
ACC Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Ile	AUU Ile AUG Met	GCC Ala GCA Ala	GCU Ala GCG Ala	GUC Val GUA Val	GUU Val GUG Val
ACC Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Ile AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	GCU Ala GCG Ala GAU	GUC Val GUA Val GGC	GUU Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Ile AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU Gly
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Ile AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	GCU Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

The Ascidian Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	ALIC	ATTT	000	COLL	OLIC	CIUI
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
Thr ACA	Thr ACG	Ile AUA	Ile AUG	Ala GCA	Ala GCG	Val GUA	Val GUG
Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Met	AUU Ile AUG Met	Ala GCA Ala	Ala GCG Ala	GUC Val GUA Val	Val GUG Val
Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Met AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	Ala GCG Ala GAU	GUC Val GUA Val GGC	Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Met AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU Gly
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Met AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

Blepharisma Nuclear Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Gln	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lys	Lys	Arg	Arg	Glu	Glu	Gly	Gly

The Alternative Flatworm Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
71511	71511						
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG

Chlorophycean Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Leu	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
ACC Thr	ACU Thr	AUC Ile	AUU Ile	GCC Ala	GCU Ala	GUC Val	GUU Val
ACC Thr ACA	ACU Thr ACG	AUC Ile AUA	AUU Ile AUG	GCC Ala GCA	GCU Ala GCG	GUC Val GUA	GUU Val GUG
ACC Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Ile	AUU Ile AUG Met	GCC Ala GCA Ala	GCU Ala GCG Ala	GUC Val GUA Val	GUU Val GUG Val
ACC Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Ile AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	GCU Ala GCG Ala GAU	GUC Val GUA Val GGC	GUU Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Ile AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU Gly
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Ile AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	GCU Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
ACC Thr	ACU Thr	AUC Ile	AUU Ile	GCC Ala	GCU Ala	GUC Val	GUU Val
ACC Thr ACA	ACU Thr ACG	AUC Ile AUA	AUU Ile AUG	GCC Ala GCA	GCU Ala GCG	GUC Val GUA	GUU Val GUG
ACC Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Met	AUU Ile AUG Met	GCC Ala GCA Ala	GCU Ala GCG Ala	GUC Val GUA Val	GUU Val GUG Val
ACC Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Met AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	GCU Ala GCG Ala GAU	GUC Val GUA Val GGC	GUU Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Met AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU Gly
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Met AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	GCU Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

Trematode Mitochondrial Code:

Thraustochytrium Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Stop	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lys	Lys	Arg	Arg	Glu	Glu	Gly	Gly

Scenedesmus Obliquus Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Stop	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Leu	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
Thr ACA	Thr ACG	Ile AUA	Ile AUG	Ala GCA	Ala GCG	Val GUA	Val GUG
Thr ACA Thr	Thr ACG Thr	Ile AUA Ile	Ile AUG Met	Ala GCA Ala	Ala GCG Ala	Val GUA Val	Val GUG Val
Thr ACA Thr AAC	Thr ACG Thr AAU	Ile AUA Ile AGC	Ile AUG Met AGU	Ala GCA Ala GAC	Ala GCG Ala GAU	Val GUA Val GGC	Val GUG Val GGU
Thr ACA Thr AAC Asn	Thr ACG Thr AAU Asn	Ile AUA Ile AGC Ser	Ile AUG Met AGU Ser	Ala GCA Ala GAC Asp	Ala GCG Ala GAU Asp	Val GUA Val GGC Gly	Val GUG Val GGU Gly
Thr ACA Thr AAC Asn AAA	Thr ACG Thr AAU Asn AAG	Ile AUA Ile AGC Ser AGA	Ile AUG Met AGU Ser AGG	Ala GCA Ala GAC Asp GAA	Ala GCG Ala GAU Asp GAG	Val GUA Val GGC Gly GGA	Val GUG Val GGU Gly GGG

Pterobranchia Mitochondrial Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
ACC Thr	ACU Thr	AUC Ile	AUU Ile	GCC Ala	GCU Ala	GUC Val	GUU Val
ACC Thr ACA	ACU Thr ACG	AUC Ile AUA	AUU Ile AUG	GCC Ala GCA	GCU Ala GCG	GUC Val GUA	GUU Val GUG
ACC Thr ACA Thr	ACU Thr ACG Thr	AUC Ile AUA Ile	AUU Ile AUG Met	GCC Ala GCA Ala	GCU Ala GCG Ala	GUC Val GUA Val	GUU Val GUG Val
ACC Thr ACA Thr AAC	ACU Thr ACG Thr AAU	AUC Ile AUA Ile AGC	AUU Ile AUG Met AGU	GCC Ala GCA Ala GAC	GCU Ala GCG Ala GAU	GUC Val GUA Val GGC	GUU Val GUG Val GGU
ACC Thr ACA Thr AAC Asn	ACU Thr ACG Thr AAU Asn	AUC Ile AUA Ile AGC Ser	AUU Ile AUG Met AGU Ser	GCC Ala GCA Ala GAC Asp	GCU Ala GCG Ala GAU Asp	GUC Val GUA Val GGC Gly	GUU Val GUG Val GGU Gly
ACC Thr ACA Thr AAC Asn AAA	ACU Thr ACG Thr AAU Asn AAG	AUC Ile AUA Ile AGC Ser AGA	AUU Ile AUG Met AGU Ser AGG	GCC Ala GCA Ala GAC Asp GAA	GCU Ala GCG Ala GAU Asp GAG	GUC Val GUA Val GGC Gly GGA	GUU Val GUG Val GGU Gly GGG

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Gly	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	ΔΙΙΔ	ALIC	CCA	000	CILLA	OIIG
	1100	лол	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	GUA Val	GUG Val
Thr AAC	Thr AAU	Ile AGC	Met AGU	Ala GAC	Ala GAU	Val GGC	GUG Val GGU
Thr AAC Asn	Thr AAU Asn	Ile AGC Ser	Met AGU Ser	GCA Ala GAC Asp	GCG Ala GAU Asp	GUA Val GGC Gly	GUG Val GGU Gly
Thr AAC Asn AAA	Thr AAU Asn AAG	Ile AGC Ser AGA	Met AGU Ser AGG	GCA Ala GAC Asp GAA	Ala GAU Asp GAG	GUA Val GGC Gly GGA	GUG Val GGU Gly GGG

Candidate Division SR1 and Gracilibacteria Code:

The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code:

		-	-	-	-		
CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr		Met	Ala	Ala	Val	Val
		Ile					
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lys	Lys			Glu	Glu	Gly	Gly
		Arg	Arg				

The Ciliate, Dasycladacean and Hexamita Nuclear Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Gln	Gln	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lys	Lys	Arg	Arg	Glu	Glu	Gly	Gly

The set of 19 dialects of the genetic code contains 13 dialects with a "typical mosaic" of their matrix representations and 6 dialects with non-typical mosai
CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Gly	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
		San	Ser	Asp	Asn	Glv	Glv
Asn	Asn	Ser	501	110p	110p	01)	01
Asn AAA	Asn AAG	AGA	AGG	GAA	GAG	GGA	GGG

Candidate Division SR1 and Gracilibacteria Code:

The Mold, Protozoan, and Coelenterate Mitochondrial

Code and the Mycoplasma/Spiroplasma Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Stop	Stop	Trp	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	Ile	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr		Met	Ala	Ala	Val	Val
		Ile					
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Lys	Lys			Glu	Glu	Gly	Gly
		Arg	Arg				

The Ciliate, Dasycladacean and Hexamita Nuclear Code:

CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU
Pro	Pro	Leu	Leu	Ser	Ser	Phe	Phe
CCA	CCG	CUA	CUG	UCA	UCG	UUA	UUG
Pro	Pro	Leu	Leu	Ser	Ser	Leu	Leu
CAC	CAU	CGC	CGU	UAC	UAU	UGC	UGU
His	His	Arg	Arg	Tyr	Tyr	Cys	Cys
CAA	CAG	CGA	CGG	UAA	UAG	UGA	UGG
Gln	Gln	Arg	Arg	Gln	Gln	Stop	trp
ACC	ACU	AUC	AUU	GCC	GCU	GUC	GUU
Thr	Thr	Ile	lle	Ala	Ala	Val	Val
ACA	ACG	AUA	AUG	GCA	GCG	GUA	GUG
Thr	Thr	Ile	Met	Ala	Ala	Val	Val
AAC	AAU	AGC	AGU	GAC	GAU	GGC	GGU
Asn	Asn	Ser	Ser	Asp	Asp	Gly	Gly
AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG
Taux	I and	Arca	Arca	Ghu	Chu	Chu	Chu

The set of 19 dialects of the genetic code contains 13 dialects with a "typical mosaic" of their matrix representations and 6 dialects with non-typical mosaics. The author notes the following non-trivial phenomenological fact: If each of black (white) triplets is replaced by +1(-1) in the matrices, every of these numeric matrices of the genetic dialects is sum of projector operators. One can name this fact as the "projection rule" of dialects of the genetic code. So the following exclusion principle is proposed:

 nature forbids such dialects of the genetic code, in which the division of the set of 64 triplets into two subsets of triplets with strong and weak roots leads to a violation of "the projection rule".

Discovering exclusive principles of nature is an important task of mathematical natural science (the exclusive principle by Pauli in quantum mechanics is one of examples). About the main role of informatics in living matter:

"Notions of "information" or "valuable information" are not utilized in physics of non-biological nature because they are not needed there. On the contrary, in biology notions "information" and especially "valuable information" are main ones; understanding and description of phenomena in biological nature are impossible without these notions. A specificity of "living substance" lies in these notions" (Chernavskiy, 2000, "The problem of origin of life and thought from the viewpoint of the modern physics",- "Progress of Physical Sciences", 170(2), p.157-183 ("Uspehi Physicheskih Nauk", in Russian)). Prof. Chernavskiy is a head of Department of theoretical biophysics in Physical Institute of the Russian Academy of Sciences.

The author has published four books about matrix genetics in Russia (2001, 2008) and in the USA (2010 and 2011 years) and many thematic articles (see his personal web site <u>http://petoukhov.com/</u>).

PREMIER REFERENCE SOURCE

Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics

Advanced Patterns and Applications



Sergey Petoukhov & Matthew He

Wiley Series on Bioinformatics . Yi Pan, Albert Y. Zomaya Series Editors

Mathematics of Bioinformatics

THEORY, PRACTICE, AND APPLICATIONS



MATTHEW HE Sergey Petoukhov

WILEY

РОССИЙСКАЯ АКАДЕМИЯ НАУК

С.В. Петухов

МАТРИЧНАЯ ГЕНЕТИКА, АЛГЕБРЫ ГЕНЕТИЧЕСКОГО КОДА, ПОМЕХОУСТОЙЧИВОСТЬ



Москва 2008

But materials of this lecture are presented mainly in the article:

S.Petoukhov "The genetic code, algebra of projection operators and problems of inherited biological ensembles " http://arxiv.org/abs/1307.7882

CONCLUSIONS

Projection operators are one of the most useful notions and mathematical instruments to study the genetic coding system and genetically inherited biological phenomena including ensembles of cyclic processes. Living matter is an algebraic essence in its informational fundamentals. A development of algebraic biology is possible with using approaches of matrix genetics.

THANK YOU FOR YOUR ATTENTION!

S.Petoukhov: <u>http://petoukhov.com/</u>, <u>http://symmetry.hu/isabm/petoukhov.html</u> Acknowledgments. Described researches were made by the author in a frame of a long-term cooperation between Russian and Hungarian Academies of Sciences. The author is grateful to Darvas G., Stepanyan I.V., Svirin V.I. for their collaboration. Fractal genetic networks and rules of long nucleotide sequences are presented in the article:

"Fractal genetic nets and symmetry principles in long nucleotide sequences" - "Symmetries in genetic information and algebraic biology", специальный выпуск журнала "Symmetry: Culture and Science", Guest editor: S. Petoukhov, 2012, vol. 23, № 3-4, p. 303-322. <u>http://symmetry.hu/scs_online/SCS_23_3-</u> <u>4.pdf</u>

Genetic Hadamard matrices

Now we will show that properties of genetic alphabets bind the genetic system with a special sub-family of Hadamard matrices which are one of the most famous tools in technology of signal processing.

Two of essential properties of the 4-letter alphabet of nitrogenous bases A, C, G, T are connected with <u>unique</u> status of thymine T:

- 1) each of three bases A, C, G has the important amino-group NH₂, but the fourth base T has not it;
- 2) the letter T is a single base in DNA, which is replaced in RNA by another base U (uracil).



- Taking into account this unique status of the letter T, we have revealed the following "<u>T-algorithm</u>" (or "U-algorithm"), which can be used in computer of organisms and which transforms the Rademacher matrix R_8 into a Hadamard matrix H_8 :



By definition the T-algorithm contains two steps:

1) each of triplets in the black-and-white (8*8)genomatrix (for example, in the matrix [C T; A G]⁽³⁾) changes its color into the opposite color each time when the letter T stands in an odd position of the triplet (in the first or in the third position);
2) then black triplets and white triples are interpreted as entries "+1" and "-1" correspondingly.

CCC	ССТ	СТС	CTT	TCC	ТСТ	TTC	TTT
CCA	CCG	СТА	CTG	TCA	TCG	TTA	TTG
CAC	CAT	CGC	CGT	TAC	TAT	TGC	TGT
CAA	CAG	CGA	CGG	TAA	TAG	TGA	TGG
ACC	ACT	ATC	ATT	GCC	GCT	GTC	GTT
ACA	ACC	ATA	ATC	CCA	CCC	CTLA	CTTC
110/1	ACG	AIA	AIG	GCA	ենե	GTA	GIG
AAC	AAT	AGC	AGT	GAC	GAT	GTA GGC	GGT

CCC	ССТ	CTC	CTT	TCC	TCT	TTC	TTT
CCA	CCG	СТА	CTG	TCA	TCG	TTA	TTG
CAC	CAT	CGC	CGT	TAC	TAT	TGC	TGT
CAA	CAG	CGA	CGG	TAA	TAG	TGA	TGG
ACC	ACT	ATC	ATT	GCC	GCT	GTC	GTT
ACA	ACG	ATA	ATG	GCA	GCG	GTA	GTG
ACA AAC	ACG AAT	ATA AGC	ATG AGT	GCA GAC	GCG GAT	GTA GGC	GTG GGT

By definition a Hadamard matrix of dimension "n" is the (n*n)-matrix H(n) with elements "+1" and "-1". It satisfies the condition $H(n)*H(n)^T = n*I_n$, where $H(n)^T$ is the transposed matrix and I_n is the identity (n*n)-matrix.

Rows of Hadamard matrices form a complete orthogonal system of Walsh functions. Tens of thousands of publications are devoted to applications of Hadamard matrices in signal processing techniques: noise-immunity coding, data compression, etc.