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### **The Atomic Genetic Code**

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#### **Abstract**

The modern science mainly treats the biochemical basis of sequencing in bio-macromolecules and processes in biochemistry. One can ask weather the language of biochemistry is the adequate scientific language to explain the phenomenon in that science. Is there maybe some other language, out of biochemistry, that determines how the biochemical processes will function and what the structure and organization of life systems will be? The research results provide some answers to these questions. They reveal to us that the process of sequencing in bio-macromolecules is conditioned and determined not only through biochemical, but also through cybernetic and information principles.

**Keywords:** Digital genetics; Genetics code; RNA code; Amino acids code; Evolution

### **Methods**

The genetic code tables used by the modern science are characterized and determined by principles of biochemistry. However, if in those tables, instead of the UCAG nucleotides we put the number of atoms of those nucleotides, we will get the new tables of the genetic code characterized and determined by programmatic and information principles. Therefore, biochemistry can be explained through a phenomenon out of biochemistry. Particularly interesting results we will get when determining numeric values for the information content of atoms and molecules. We will then find out that those values express physical and chemical characteristics of molecules. For example: in a DNA molecule, the polynucleotide chains are connected through an exact cyber-information connections. In those molecules there are also mathematical matrixes of DNA, represented by the number of atoms of four ATCG bases. These matrixes determine the positioning of nucleotides in that molecule. With this, the biological particularities of DNA are determined. Similar mathematical matrixes determine the positioning of nucleotides in the RNA molecule. In the amino acid proteins, they are interconnected into the respective mathematical chains. In those chains are also matrixes where particular mathematical principles apply, the principles that determine the positioning of each amino acid in the chain.

#### Results

The herewith discussed research results show that the process of sequencing in bio-macromolecules is conditioned and determined not only through biochemical, but also through cybernetic information principles.

We would particularly like to stress here that the genetic, as well as biochemical information in a broader sense of the word, is determined and characterized by very complex cybernetic and information principles. The constantans in those principles are: the number of atoms and molecules, atomic numbers, atomic weight, physical and chemical parameters, even and odd values, codes and analogue codes, standard deviations, frequencies, primary and secondary values, and many other things. How functioning of biochemistry is determined through cybernetic information principles, will be discussed further in this text.

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The Atomic Genetic Code (RNA)

A = 15 atoms; U = 12 atoms; C = 13 atoms; G = 16 atoms; Number of atoms

UUU= <mark>36</mark>	UUC=37	CUC=38	UUA= <mark>39</mark>	UUG=40	CUG=41	CGC=42	GAU=43	GAC=44	CGG=45	AGA=46	AGG=47	GGG=48
Phe=23	Phe=23	Leu=22	Leu=22	Leu=22	Leu=22	Arg=26	Asp=16	Asp=16	Arg=26	Arg=26	Arg=26	Gly= <mark>10</mark>
	UCU=37	UCC=38	AUU=39	AUC=40	UGC=41	AUA=42	AUG=43	UGG=44	AAA=45	AAG=46	GGA=47	
	Ser= <mark>14</mark>	Ser=14	lle= <mark>22</mark>	lle= <mark>22</mark>	Cys=14	lle= <mark>22</mark>	Met=20	Trp=27	Lys= <mark>24</mark>	Lys= <mark>24</mark>	Gly=10	
	CUU=37	CCU=38	CCC=39	CUA=40	CCA=41	CCG=42	AAC=43	ACG=44	GGC=45	GAA=46	GAG=47	
	Leu= <mark>22</mark>	Pro=17	Pro=17	Leu=22	Pro=17	Pro=17	Asn= <mark>17</mark>	Thr= <mark>17</mark>	Gly= <mark>10</mark>	Glu=19	Glu=19	
			UAU= <mark>39</mark>	GUU= <mark>40</mark>	GUC=41	GCC=42	GUA=43	GUG=44	GCG=45			
			Tyr= <mark>24</mark>	Val= <mark>19</mark>	Val= <mark>19</mark>	Ala= <mark>13</mark>	Val= <mark>19</mark>	Val= <mark>19</mark>	Ala= <mark>13</mark>			
				UCA=40	UCG=41	UAA=42	AGU=43	AGC=44				
				Ser= <mark>14</mark>	Ser= <mark>14</mark>	STOP	Ser=14	Ser= <mark>14</mark>				
				ACU=40	ACC=41	AAU=42	ACA=43	GGU=44				
				Thr=17	Thr=17	Asn= <mark>17</mark>	Thr=17	Gly=10				
				UAC=40	GCU=41		UAG=43	GCA=44				
				Tyr= <mark>24</mark>	Ala= <mark>13</mark>		STOP	Ala= <mark>13</mark>				
				CAU=40	CAC=41		CAA=43	CAG=44				
				His= <mark>20</mark>	His= <mark>20</mark>		Gln= <mark>20</mark>	GIn= <mark>20</mark>				
				UGU= <mark>40</mark>	CGU=41		UGA=43	CGA=44				
				Cys= <mark>14</mark>	Arg= <mark>26</mark>		STOP	Arg= <mark>26</mark>				

Number of atoms in triplets UCAG

UUU	UUC	CUC	UUA	UUG	CUG	CGC	GAU	GAC	CGG	AGA	AGG	GGG
36	37	38	39	40	41	42	43	44	45	46	47	48
	UCU	UCC	AUU	AUC	UGC	AUA	AUG	UGG	AAA	AAG	GGA	
	37	38	39	40	41	42	43	44	45	46	47	
	CUU	CCU	CCC	CUA	CCA	CCG	AAC	ACG	GGC	GAA	GAG	
	37	38	39	40	41	42	43	44	45	46	47	
			UAU	GUU	GUC	GCC	GUA	GUG	GCG			
			39	40	41	42	43	44	45			
				UCA	UCG	UAA	AGU	AGC				
				40	41	42	43	44				
				ACU	ACC	AAU	ACA	GGU				
				40	41	42	43	44				
				UAC	GCU		UAG	GCA				
				40	41		43	44				
				CAU	CAC		CAA	CAG				
				40	41		43	44				
				UGU	CGU		UGA	CGA				
				40	41		43	44				

$$.(36+48) = (37+47) = (38+46) = (39+45) = (40+44) = (41+43)$$
 etc.

In fact, we discovered that the *mathematical balance* in the distribution of codons and amino acids in the genetic code is achieved.

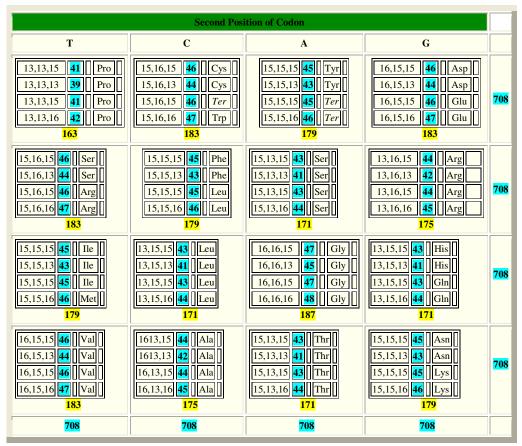
### Mathematical Position of the Nucleotides in Codon

The development of prediction methods based on digital theory is focused on the exploration of new digital formulas and algorithms. The genetic code is stored in DNA molecules as sequences of bases: adenine (A) which pairs with thymine (T), and cytosine (C) which pairs with guanine (G), The analog of DNA in a digital genetic algorithm is a number of atoms, atomic numbers, analog codes, etc.

At mathematical evolution of genetic processes, nucleotides TCAG are being transformed to codons UCAG and later to amino acids and various organic composition.

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#### Number of atoms



Diagonal D1 = 708; Diagonal D2 = 708;

The digital genetic code describe a genotype, which is translated into an organism a phenotype by the processes of cell division.

Mathematical evolution of genetic processes is manifested in different ways. Evolution of groups of atoms is especially interesting. Here are some examples

#### **Digital Codon Square**

A digital codon square of order n is an arrangement of  $n^2$  numbers, usually distinct integers, in a square, such that the n numbers in all rows, all columns, and both diagonals sum to the same constant. A digital square contains the integers from 1 to  $n^2$ . The term "digital square" is also sometimes used to refer to any of various types of word square.

#### Number of atoms

163	183	179	183	708
183	179	171	175	708
179	171	187	171	708
183	175	171	179	708
708	708	708	708	

D1 = (163+179+187+179) = 708;

D2 = (183 + 171 + 171 + 183) = 708;

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The constant sum in every row, column and diagonal is called the magic analogue constant or magic sum, M.

163	183	179	183
183	179	171	175
179	171	187	171
183	175	171	179

(163+183+183+179)=708; (179+183+171+175)=708; (179+171+183+175)=708; 187+171+171+179)=708;

163	183	179	183
183	179	171	175
179	171	187	171
183	175	171	179



163	183	179	183
183	179	171	175
179	171	187	171
183	175	171	179



etc.

#### **Analogue Atomic Genetic Code**

How could we adapt the program, ciberfnetic, and informational system to convey more information? Here's one way. This is an analogue code.

"Theoretically the ancient book of DNA could have been analogue. But, for the same reason as for our analogue armada beacons, any ancient book copied and recopied in analogue language would degrade to meaninglessness in very few scribe generations. Fortunately, human writing is digital, at least in the sense we care about here. And the same is true of the DNA books of ancestral wisdom that we carry around inside us. Genes are digital, and in the full sense not shared by nerves" (20).

#### Correlation of the Code and Analogue Code

The atomic and analogue genetic code is the set of rules by which information encoded in genetic material (DNA or RNA sequences) is translated into proteins (amino acid sequences) by living cells. Specifically, those codes defines a mapping between tri-nucleotide sequences called codons and amino acids; every triplet of nucleotides in a nucleic acid sequence specifies a single amino acid. Because the vast majority of genes are encoded with exactly the same code.

Those codes are universal. The same codons are assigned to the same amino acids and to the same START and STOP signals in the vast majority of genes in animals, plants, and microorganisms.

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Analogue Code | | Code Code

#### **Example:**

Analogue Code of the number 12 is number 21:

21 | 12;

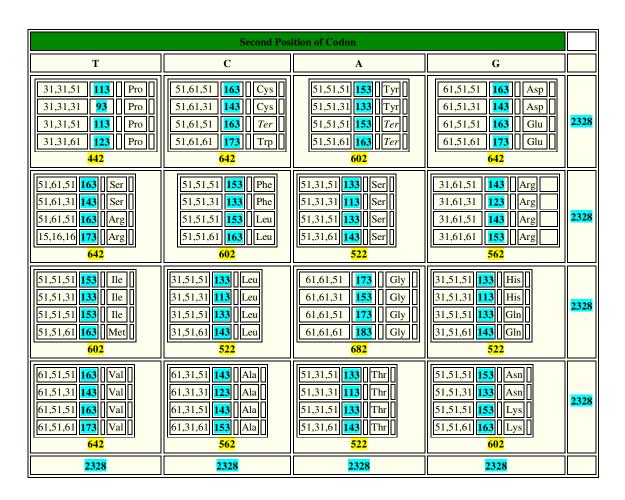
Analogue Code of the number 15 is number 51:

51 | | 15;

At this stage of our research we replaced nucleotides from the Amino Acid Code Matrix with analogue numbers of the atoms in those nucleotides.

#### **Analogue Codon Table**

#### Mathematical position of the nucleotides in codon



Diagonal D1 = 2328; Diagonal D2 = 2328;

Row 1 = Column 1; Row 2 = Column 2; Row 3 = Column 3; Row 4 = Column 4;

### **Analogue Codon Square**

A analogue codon square of order n is an arrangement of  $n^2$  numbers, usually distinct integers, in a square, such that the n numbers in all rows, all columns, and both diagonals sum to the same constant.

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442	642	602	642	2328
642	602	522	562	2328
602	522	682	522	2328
642	562	522	602	2328
2328	2328	2328	2328	

D1 = (442+602+682+602) = 2328;

D2 = (642+522+522+642) = 2328;

The constant sum in every row, column and diagonal is called the magic analogue constant or magic sum, M = 2328;

### **Correlation:**

442	642	602	642
642	602	522	562
602	522	682	522
642	562	522	602

(442+642+642+602) = 2328;

(602+642+522+562) = 2328;

etc.

442	642	602	642				
642	602	522	562				
602	522	682	522				
642	562	522	602				



442	642	602	642				
642	602	522	562				
602	522	682	522				
642	562	522	602				
<b>y</b>							
0000							

2328

#### Determinants in Digital analogue Genetic Code

DET (4 x 4)

442	642	602	642
642	602	522	562
602	522	682	522
642	562	522	602



2681856000 = (2328 + 2328 + 2328..., + 2328);

There is a mathematical balance within all of the phenomena in the analogue genetic code matrix.

Mathematical correlation of groups of nucleotides are a proof that genetic processes have evolved from one mathematical shape to another one. They are a proof that we can uncover some of hidden secrets in that science, with the help of mathematics.

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				Atomic numbers	
		U	C	A	G
	U	58,58,58 174 Phe 58,58,58 174 Phe 58,58,70 186 Leu 58,58,78 194 Leu 728	70,78,58     206     Ser       70,78,58     206     Ser       70,78,70     218     Arg       70,78,78     226     Arg	58,70,58     186     Tyr       58,70,58     186     Tyr       58,70,70     198     Ter       58,70,78     206     Ter	58,78,58       194       Cys         58,78,58       194       Cys         58,78,70       206       Ter       3168         58,78,78       214       Trp
F i r s t	С	78,70,58 206   Asp   78,70,58 206   Asp   78,70,70 218   Glu   78,70,78 226   Glu   856	58,58,58     174     Ser       58,58,58     174     Ser       58,58,58     174     Ser       58,58,70     186     Ser       58,58,78     194     Ser       728	58,70,58 <b>186</b> His 58,70,58 <b>186</b> His 58,70,70 <b>198</b> Gln 58,70,78 <b>206</b> Gln <b>776</b>	58,78,58     194     Arg       58,78,58     194     Arg       58,78,70     206     Arg     3168       58,78,78     214     Arg
o s i t i o n	A	70,58,58 186	70,58,58 186   Thr   70,58,58 186   Thr   70,58,70 198   Thr   70,58,78 206   Thr   70,58,78 206   Thr   776	78,78,58 214 Gly 78,78,58 214 Gly 78,78,70 226 Gly 78,78,78 234 Gly 888	58,58,58 174 Leu 58,58,58,70 186 Leu 58,58,78 194 Leu 728
	G	78,58,58 194   Val   78,58,58 194   Val   78,58,70 206   Val   78,58,78 214   Val   808	78,58,58   194	58,58,58 174   Pro     58,58,58 174   Pro     58,58,70 186   Pro     58,58,78 194   Pro     728	70,70,58 198 Asn 70,70,58 198 Asn 70,70,70 210 Lys 3168 70,70,78 218 Lys 824
		3168	3168	3168	3168

Diagonal D1 = **3168**; Diagonal D2 = **3168**;

The atomic genetic code describe a genotype, which is translated into an organism a phenotype by the processes of cell division.

Mathematical evolution of genetic processes is manifested in different ways. Evolution of groups of atoms is especially interesting. Here are some examples.

#### **Digital Codon Square**

A atomic codon square of order n is an arrangement of  $n^2$  numbers, usually distinct integers, in a square, such that the n numbers in all rows, all columns, and both diagonals sum to the same constant. A digital square contains the integers from 1 to  $n^2$ . The term "digital square" is also sometimes used to refer to any of various types of word square.

Number of atoms

728	856	776	808	3168
856	728	776	808	3168
776	776	888	728	3168
808	808	728	824	3168
3168	3168	3168	3168	

D1 = (728+856+776+808) = 3168; D2 = (808+776+776+808) = 3168;

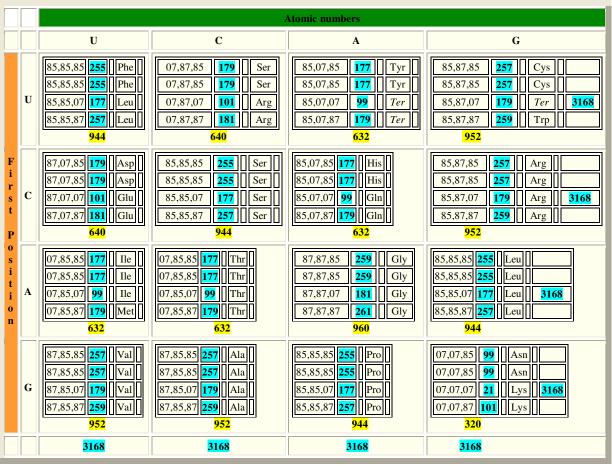
The constant sum in every row, column and diagonal is called the magic analogue constant or magic sum, M

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728	856	776	808		
856	728	776	808		
776	776	888	728		
808	808	728	824		
	7	/			
	31	<mark>68</mark>			
728	856	776	808		
856	728	776	808		
776	776	888	728		
808	808	728	824		
		Ψ			
	3	<b>168</b>			
728	856	776	808		
856	728	776	808		
776	776	888	728		
808	808	728	824		
Ψ					
3168					
	et	c.			

At this stage of our research we replaced nucleotides from the Amino Acid Code Matrix with analogue of the atomic numbers in those nucleotides.

### Analogue Codon Table



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Diagonal D1 = 3168; Diagonal D2 = 3168;

Row 1 = Column 1; Row 2 = Column 2; Row 3 = Column 3; Row 4 = Column 4;

#### **Analogue Codon Square**

A analogue codon square of order n is an arrangement of  $n^2$  numbers, usually distinct integers, in a square, such that the n numbers in all rows, all columns, and both diagonals sum to the same constant.

944	640	632	952	3168
640	944	632	952	3168
632	632	960	944	3168
952	952	944	320	3168
3168	3168	3168	3168	

D1 = (944+944+960+320) = 3168;

D2 = (952+632+632+952) = 3168;

The constant sum in every row, column and diagonal is called the magic analogue constant or magic sum, M = 3168;

#### **Correlation:**

944	640	632	952
640	944	632	952
632	632	960	944
952	952	944	320



944	640	632	952
640	944	632	952
632	632	960	944
952	952	944	320



944	640	632	952
640	944	632	952
632	632	960	944
952	952	944	320

**↓**3168

### Determinants in Digital analogue Genetic Code

DET (4 x 4)

	DEI (4 X 4)						
944	640	632	952				
640	944	632	952				
632	632	960	944				
952	952	944	320				

197237145600

197237145600 = (3168 + 3168 + 3168..., + 3168);

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There is a mathematical balance within all of the phenomena in the analogue genetic code matrix.

Mathematical correlation of groups of nucleotides are a proof that genetic processes have evolved from one mathematical shape to another one. They are a proof that we can uncover some of hidden secrets in that science, with the help of mathematics.

Atomic Weight						
С	Н	N	0	S		

	С	Η	Z	0	S	
Α	5	5	5	0	0	15
U	4	4	2	2	0	12
С	4	5	3	1	0	13
G	5	5	5	1	0	16

C = 12,0111; H = 1,00797; N = 14,0067; O = 15,9994; S = 32,064;

$$A = 135; U = 112; C = 111; G = 151;$$

The Digital Genetic Code

At the first stage of our research we replaced nucleotides from the Genetic Code with atomic weight of those nucleotides.

#### Mathematical Position of the Nucleotides in Codon3

The development of prediction methods based on digital theory is focused on the exploration of new digital formulas and algorithms. The genetic code is stored in DNA molecules as sequences of bases: adenine (A) which pairs with thymine (T), and cytosine (C) which pairs with guanine (G), The analog of DNA in a digital genetic algorithm is a number of atoms, atomic numbers, analog codes, etc.

At mathematical evolution of genetic processes, nucleotides TCAG are being transformed to codons UCAG and later to amino acids and various organic composition.

			Second Po	osition of Codon	
		U C		A	G
	F=	112,111,112 335 Ser 112,111,111 334 Ser 1	135,151,112 <b>398</b> Ser 35,151,111 <b>397</b> Ser 1	111,135,112 <b>358</b> His 11,135,111 <b>357</b> His	112,151,112 375 Cys 112,151,111 374 Cys
	U			11,135,135 <b>381</b> Gln 11,135,151 <b>397</b> Gln	112,151,135 398 Ter 6108 112,151,151 414 Trp
F		1401	1653	1493	<u>1561</u>
i r s t	C	151,135,111 397 Asp 5151,135,131 Glu 5151,135,151 437 Glu 6151,135,151 437 Glu 6151,135,151 437 Glu 6151,135,151 437	111,112,111 334 Leu 1 111,112,111 334 Leu 1 111,112,135 358 Leu 1 111,112,151 374 Leu 1	135,111,112   359   Thr	151,112,112     375     Val       151,112,111     374     Val       151,112,135     398     Val       151,112,151     414     Val
		1653	1401	1493	<u>1561</u>
s i t i o	A	112,135,112 359 Tyr 1 112,135,111 358 Tyr 1 112,135,135 382 Ter 1 112,135,151 398 Ter 1 1497	135,112,112   359     Ile	151,151,111 413 GI 151,151,135 437 GI	111,111,112   334   Pro
n	G	111,151,112 374 Arg 111,151,111 373 Arg 111,151,113 373 Arg 111,151,135 397 Arg 111,151,151 413 Arg 11557	151,111,112 374 Ala 151,111,111 373 Ala 151,111,135 397 Ala 151,111,151 413 Ala 1557	112,112,112 336 Phe 112,112,111 335 Phe 112,112,135 359 Leu 112,112,151 375 Leu 1405	135,135,112   382   Asn
		<mark>6108</mark>	6108	6108	6108

Diagonal D1 = 6108; Diagonal D2 = 6108

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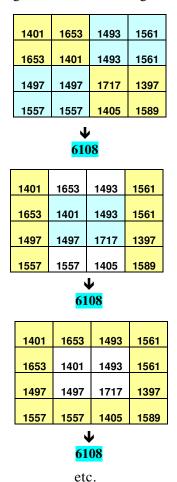
#### **Atomic Codon Square**

A atomic codon square of order n is an arrangement of  $n^2$  numbers, usually distinct integers, in a square, such that the n numbers in all rows, all columns, and both diagonals sum to the same constant. A digital square contains the integers from 1 to  $n^2$ . The term "digital square" is also sometimes used to refer to any of various types of word square.

Number of atoms 

D1 = (1401+1401+1717+1589) = 6108; D2 = (1561+1493+1497+1557) = 6108;

The constant sum in every row, column and diagonal is called the magic analogue constant or magic sum, M.



At this stage of our research we replaced nucleotides from the Amino Acid Code Matrix with analogue of the atomic weight in those nucleotides.

A = 135; U = 112; C = 111; G = 151;

A = 531; U = 211; C = 111; G = 151;

### **Analogue Codon Table**

		Second Position of Codon						
		U	С	A	G			
		211,111,211 <b>533</b> Ser	531,151,211 <b>0893</b> Ser	111,531,211 <b>0853</b> His	211,151,211 <b>573</b> Cys			
П			بلايا كالكال	11,531,111 <b>0753</b> His	211,151,111 473 Cys			
П	Ĭ.			11,531,531	211,151,531 <b>893</b> <i>Ter</i> <b>12048</b> 211,151,151 <b>513</b> Trp			
F		2292	3732	3572	2452			
i		151,531,211 <b>0893</b> Asp	111,211,211 <b>533</b> Leu	531,111,211 <b>0853</b> Thr	151,211,211 <b>573</b> Val			
S	C	151,531,111 <b>0793</b> Asp	111,211,111 433 Leu	531,111,111 <b>0753</b> Thr	151,211,111 473 Val			
t		151,531,531 1213 Glu 151,531,151 0833 Glu	111,211,531 <b>853</b> Leu 1111,211,151 <b>473</b> Leu	531,111,531 <b>1173</b> Thr 531,111,151 <b>0793</b> Thr	151,211,531   893   Val   1   151,211,151   513   Val			
P		3732	2292	3572	2452			
0		211,531,211 <b>0953</b> Tyr	531,211,211 <b>0953</b> IIe	151,151,211 <b>513</b> Gly	111,111,211 433 Pro			
s i		211,531,111 <b>0853</b> Tyr	531,211,111 <b>0853</b> IIe		111,111,111 333 Pro			
t	A	211,531,531 <b>1273</b> <i>Ter</i> 211,531,151 <b>0893</b> <i>Ter</i>	531,211,531 <b>1273</b> Ile   531,211,151 <b>0893</b> Met		111,111,531   <b>753</b>   Pro   <b>12048</b>			
0		3972	3972	2212	1892			
n		111,151,211 473 Arg	151,111,211 473 Ala	211,211,211 <b>633</b> Phe	531,531,211 <b>1273</b> Asn			
		111,151,111 373 Arg	151,111,111 373 Ala	211,211,111 <b>533</b> Phe	531,531,111 <b>1173</b> Asn			
	G	111,151,531 <b>793</b> Arg 111,151,151 <b>413</b> Arg	151,111,531 <b>793</b> Ala 151,111,151 <b>413</b> Ala	211,211,531 <b>953</b> Leu 211,211,151 <b>573</b> Leu	531,531,531 <b>1593</b> Lys <b>12048</b> 531,531,151 <b>1213</b> Lys			
		2052	2052	2692	5252			
		12048	12048	12048	12048			

Diagonal D1 = 3168; Diagonal D2 = 3168;

### **Analogue Codon Square**

A analogue codon square of order n is an arrangement of  $n^2$  numbers, usually distinct integers, in a square, such that the n numbers in all rows, all columns, and both diagonals sum to the same constant.

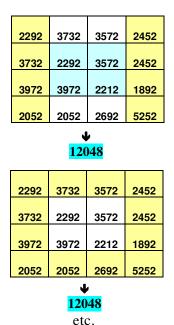
2292	3732	3572	2452	12048
3732	2292	3572	2452	12048
3972	3972	2212	1892	12048
2052	2052	2692	5252	12048
12048	12048	12048	12048	

D1 = 12048; D2 = 12048

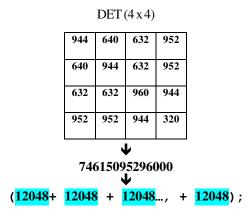
The constant sum in every row, column and diagonal is called the magic analogue constant or magic sum, M = 12048;

#### **Correlation:** 2292 3732 3572 2452 3732 2292 2452 3572 3972 1892 2052 2052 2692 5252 12048

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#### Determinsants in Digital Analogue Genetic Code



There is a mathematical balance within all of the phenomena in the analogue genetic code matrix.

Mathematical correlation of groups of nucleotides are a proof that genetic processes have evolved from one mathematical shape to another one. They are a proof that we can uncover some of hidden secrets in that science, with the help of mathematics.

It is obvious that digital matrix of amino acid code evolved from digital matrix of nucleotide code.

Mathematical correlation of groups of nucleotides are a proof that genetic processes have evolved from one mathematical shape to another one. They are a proof that we can uncover some of hidden secrets in that science, with the help of mathematics.

### **Perspectives**

#### About Importance of the Proposal

Development of science in following period will be based on contemporary digital technology. To conquer new technology it would be far more efficient to use method of reverse engineering for comprehension of phenomen in genetics. We'll give a brief description of that method.

The genetic code tables used by the modern science are characterized and determined by principles of biochemistry. However, if in those tables, instead of the UCAG nucleotides we put the number of atoms of those nucleotides, we will get the new tables of the genetic code characterized and determined by programmatic and information principles.

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Therefore, biochemistry can be explained through a phenomenon out of biochemistry.

Particularly interesting results we will get when determining numeric values for the information content of atoms and molecules. We will then find out that those values express physical and chemical characteristics of molecules. For example: in a DNA molecule, the polynucleotide chains are connected through an exact cyber-information connections. In those molecules there are also mathematical matrixes of DNA, represented by the number of atoms of four ATCG bases. These matrixes determine the positioning of nucleotides in that molecule. With this, the biological particularities of DNA are determined. Similar mathematical matrixes determine the positioning of nucleotides in the RNA molecule. In the amino acid proteins, they are interconnected into the respective mathematical chains. In those chains are also matrixes where particular mathematical principles apply, the principles that determine the positioning of each amino acid in the chain. Therefore, the herewith discussed research results show that the process of sequencing in bio-macromolecules is conditioned and determined not only through biochemical, but also through cybernetic information principles. The hypothesis here is that the processes in an organism occur only when certain mathematical conditions are met, i.e. when there is a certain mathematical correlation between parameters in those processes. That correlation is expressed by the respective methodology.

We would particularly like to stress here that the genetic, as well as biochemical information in a broader sense of the word, is determined and characterized by very complex cybernetic and information principles. The constantans in those principles are: the number of atoms and molecules, atomic numbers, atomic weight, physical and chemical parameters, even and odd values, codes and analogue codes, standard deviations, frequencies, primary and secondary values, and many other things.

### Where it Might be Useful

In view of this, our findings might have a series of impacts to the aforementioned work. We are devoted to provide a digital code for each of 20 native amino acids. These digital codes should more complete and better reflect the essence of each of the 20 amino acids. Therefore, it might stimulate a series of future work by using the author's digital codes to formulate the pseudo amino acid composition

for predicting protein structure class, subcellular location, membrane protein type, enzyme family class, GPCR type, protease type, protein-protein interaction, metabolic pathways, protein quaternary structure, and other protein attributes.

We can expect that this discovery will significantly speed up the research of mutational genesis of humans, molecular etymology, in applied biology and genetic engineering, and also it will provide discoveries in new medicines and methods of medicinal treatments.

### **Future Steps Required**

- 1.Establish scientific-research project team for development of advanced technologies in genetics, medicine and biochemistry.
- 2.Project team should make concrete program of scientific-research work, where they should define goals of research, indispensable facilities for implementation of project, project duration, budget, and other conditions.
- 3. Define rights and duties of all participants in implementation of project.
- 4. To implement project defined by project documentation.

### Research in the Field of Fundamental Sciences

- 1. Decode matrix of amino acid code and on the experimental way prove that the matrix really exists. And after that, use that matrix to conquer top technologies in the field of genetics.
- 2. Decode matrix of nucleotide code and digital codes which connect that matrix with matrix of amino acid code. And use that matrix to conquer top technologies in the field of biochemistry.
- 3. Decode matrix code in Tables of periodic system of chemical elements, and use that matrix to conquer top technologies in the field of chemistry.
- 4. Decode matrix code in the nature, and use that matrix to conquer top technologies in the field of all natural sciences.
  - 5. Decode matrix code of chromosomes in human body.
- 6. With the help of above mentioned matrixes, decode map of human DNA.
- 7. Decode matrix code of processes in the field of nuclear physics.
- 8. Decode insulin matrix code, as well as all other codes from the field of biochemistry.

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9. Other research (Matrix code in Pascal's triangle, Matrix code in astronomy, Matrix code in theoretical physics, determinism, etc.).

### Paragraph of Limitations

- 1. Confirm that the manuscript has been submitted solely to this journal and is not published, in press, or submitted elsewhere.
- 2. Confirm that all the research meets the ethical guidelines, including adherence to the legal requirements of the study country.
- 3. Confirm that you have completed and sent a Copyright Transfer Agreement (CTA) to the Editorial Office.

#### The Obtained Results

The obtained results are valid. In this manuscript, we proposed the universal genetic code. Mathematics could confirm this fact with 100% scientific accuracy. For example, Table mathematical position of the nucleotides in codon, Digital codon square, Analogue atomic genetic code, Correlation of the code and analogue code Analogue codon table, Analogue codon square, Determinsants in Digital analogue Genetic Code, Determinsants in Digital analogue Genetic Code, Atomic weight Atomic codon square, etc. This mathematic system represents that very universal formula of the genetic code which 100% scientific accuracy. was looking for.

#### Conclusion

It is a rewarding work to translate the biochemical language of amino acids into a digital language because it may be very useful for developing new methods for predicting protein sub cellular localization, membrane protein type, protein structure secondary prediction or any other protein attributes.

This is because ever since the concept of Chou's pseudo amino acid composition was proposed many efforts have been made trying to use various digital numbers to represent the 20 native amino acids in order to better reflect the sequence-order effects through the vehicle of pseudo amino acid composition. Some investigators used complexity measure factor some used the values derived from the cellular automata, some used hydrophobic and/or hydrophilic values, some were through Fourier transform, and some used the physicochemical distance.

Now, it is going to be possible to use the completely new strategy of research in genetics. However, observation of all these relations which are the outcome of the periodic law (actually, of the law of binary coding) is necessary, because it can be of great importance for decoding conformational forms and stereo-chemical and digital structure of proteins.

#### References

- Chou KC (1995) A novel approach to predicting protein structural classes in a (20-1)-D amino acid composition space, Proteins: Struct. Funct Gen 21: 319-344. » Pubmed » Google Scholar
- Chou KC (2000) Review: Prediction of protein structural classes and subcellular locations, Curr Prot Peptide Sci 1: 171-208. » CrossRef » Pubmed » Google Scholar
- Chou KC (2000) Prediction of protein subcellular locations by incorporating quasi-sequence-order effect, Biocheml Biophys. Res Commun 278: 477-483." Pubmed "Google Scholar"
- Chou KC (2001) Prediction of protein cellular attributes using pseudo amino acid composition, Proteins: Struct. Funct Genet 43: 246-255. "CrossRef" Pubmed "Google Scholar
- Chou KC (2002) In Weinrer Pw, Lu Q (eds) Gene Cloningand Expression technologies, Eaton Publishing. Westborough, MA.
- Chou KC (2005) Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes. Bioinformatics 21: 10-19.» CrossRef » Pubmed » Google Scholar
- 7. Chou KC (2005) Prediction of G-protein-coupled receptor classes, Journal of Proteome Research 4: 1413-1418.

  » Pubmed
- Chou KC, Cai YD (2003) Predicting protein quaternary structure by pseudo amino acid composition. Proteins: Struct Funct Genet 53: 282-289. "Pubmed" Google Scholar
- 9. Chou KC, Cai YD (2004) Predicting enzyme family class in a hybridization space Protein Sci 13: 2857-2863. » CrossRef » Pubmed » Google Scholar
- Chou KC, Cai YD (2005) Prediction of membrane protein types by incorporating amphipathic effects. J Chem Inform and Model 45: 407-413. " Pubmed " Google Scholar
- 11. Chou KC, Cai YD (2006) Prediction of protease types in a hybridization space. Biochem Biophys Res Comm 339: 1015-1020. "CrossRef" Pubmed "Google Scholar"

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Research Article JCSB/Vol.2 January-February 2009

- 12. Chou KC, Cai YD (2006) Predicting protein-protein interactions from sequences in a hybridization space. J Proteome Res 5: 316-322.» Pubmed » Google Scholar
- Chou KC, Cai YD (2006) Zhong WZ, Predicting networking couples for metabolic pathways of Arabidopsis. EXCLI J 5: 55-65.
- Chou KC, Elord DW (1999) Protein subcellular location prediction. Protein Eng 12: 107-118. "CrossRef" Pubmed "Google Scholar
- 15. Chou KC, Elord DW Prediction of membrane protein types and subcellular locations. Proteins Struct Funct Genet 34: 137-153. "Pubmed" Google Scholar
- Chou KC, Elrod DW (2002) Bioinformatical analysis of G-protein- coupled receptors. J Proteome Res 1: 429-433. "Pubmed" Google Scholar
- 17. Chou KC, Elrod DW Prediction of enzyme family classes. J Proteome Res 2: 183-190.» Pubmed » Google Scholar
- 18. Chou KC, Zhang CT (1994) Predicting protein folding types by distance functions that make allowances for amino acid interactions. J Biol Chem 269: 22014-22020. » CrossRef » Pubmed » Google Scholar
- 19. Chou KC, Zhang CT (1995) Review: Prediction of protein structural classes. Critical Reviews Biochem Mol Biol 30: 275-349. » CrossRef » Pubmed » Google Scholar
- 20. Kuriæ L (2007) The digital language of amino acids. Amino Acids January 25. » Pubmed » Google Scholar
- 21. Kuriæ L (1986) Mesure complexe des caracteristiques dynamiques de series temporelles "Journal de la Societe de statistique de Paris"- tome 127, No 2.1986.
- 22. Wang M, Yang J, Liu GP, Xu ZJ, Chou KC (2004) Weighted-support vector machines for predicting membrane protein types based on pseudo amino acid compo-

- sition. Protein Eng Des Select 17: 509-516. » CrossRef » Pubmed » Google Scholar
- 23. Wang M, Yang J, Liu GP, Xu ZJ, Chou KC (2005) SLLE for predicting membrane protein types. J Theor Biol 232: 7-15. » CrossRef » Pubmed » Google Scholar
- 24. Wang SQ, Yang J, Chou KC (2006) Using stacked generalization to predict membrane protein types based on pseudo amino acid composition. J Theor Biology doi:10.1016/j.jtbi.1005.1006. » CrossRef » Pubmed » Google Scholar
- 25. Xiao X, Shao S, Ding Y, Huang Z, Chen X, et al. (2005) An Application of Gene Comparative Image for Predicting the Effect on Replication Ratio by HBV Virus gene missense mutation. J Theor Biol 235: 555-565. » CrossRef » Pubmed » Google Scholar
- 26. Xiao X, Shao S, Ding Y, Huang Z, Huang Y, et al. (2005) Using complexity measure factor to predict protein subcellular location. Amino Acids 28: 57-61. "CrossRef" Pubmed "Google Scholar"
- 27. Xiao X, Shao S, Ding Y, Huang Z, Chen X, et al. (2005) Using cellular automata to generate Image representation for biological sequences. Amino Acids 28: 29-35.
  » Pubmed » Google Scholar
- 28. Xiao X, Shao SH, Huang ZD, Chou KC (2006) Using pseudo amino acid composition to predict protein structural classes: approached with complexity measure factor. J Comput Chem 27: 478-482. " CrossRef " Pubmed " Google Scholar
- 29. Xiao X, Shao SH, Ding YS, Huang ZD, Chou KC (2006) Using cellular automata images and pseudo amino acid composition to predict protein sub-cellular location. Amino Acids 30: 49-54.» Pubmed » Google Scholar
- 30. Zhang SW, Pan Q, Zhang HC, Shao ZC, Shi JY (2006) Prediction protein homo oligomer types by pseudo amino acid composition: Approached with an improved feature extraction and naive Bayes feature fusion. Amino Acids 30: 461-468.» Pubmed » Google Scholar